

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 13, 2004, 12:22:35 : Search time 5.72664 Seconds

(without alignments)  
1326.664 Million cell updates/sec

Title: US-09-990-586-79

Perfect score: 416

Sequence: 1 DIQMTQSPASLSASVGRVT.....QPEDFATYYCGGQTKLEIK 79

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	335	80.5	108	1 K1HUV	Ig kappa chain V-I
2	335	80.5	120	2 S46370	Ig kappa chain V-J
3	334	80.3	123	2 S40331	Ig kappa chain - h
4	330	79.3	107	2 S38269	Ig kappa chain V-I
5	330	79.3	127	2 S40367	Ig kappa chain V-J
6	330	79.3	129	2 S40369	Ig kappa chain - h
7	330	79.3	129	2 S52789	Ig kappa chain V-I
8	327	78.6	108	2 B49047	Ig kappa chain V-I
9	326	78.4	117	2 S46371	Ig kappa chain V-I
10	324	77.9	123	2 S40313	Ig kappa chain V-J
11	324	77.9	125	2 S40333	Ig kappa chain V-I
12	323.5	77.8	124	2 S40336	Ig kappa chain V-J
13	323.5	77.5	105	2 A27588	Ig kappa chain V-I
14	322.5	77.5	125	2 S40315	Ig kappa chain - h
15	322	77.4	108	1 K1HUV	Ig kappa chain V-I
16	322	77.4	108	1 K1HUV	Ig kappa chain V-I
17	322	77.4	108	1 K1HUV	Ig kappa chain V-I
18	322	77.4	108	1 K1HUV	Ig kappa chain V-I
19	322	77.4	122	2 S40314	Ig kappa chain - h
20	320	76.9	108	1 K1HUV	Ig kappa chain V-I
21	320	76.9	108	1 K1HUV	Ig kappa chain V-I
22	320	76.8	107	2 S40317	Ig kappa chain V-I
23	319.5	76.8	107	2 S38275	Ig kappa chain V-I
24	318.5	76.6	107	2 S47183	Ig kappa chain V-I
25	318	76.4	108	1 K1HUV	Ig kappa chain V-I
26	318	76.4	110	2 S44118	Ig kappa chain V-I
27	318	76.4	125	2 S40349	Ig kappa chain V-I
28	318	76.4	126	2 S40335	Ig kappa chain V-I
29	318	76.4	129	1 K1HUV	Ig kappa chain V-I

## ALIGNMENTS

30	318	76.4	129	2 S52793	Ig kappa chain V-I
31	317	76.2	107	2 U10139	Ig kappa chain V-I
32	317	76.2	108	1 K1HUV	Ig kappa chain V-I
33	317	76.2	108	1 K1HUV	Ig kappa chain V-I
34	317	76.2	108	1 K1HUV	Ig kappa chain V-I
35	317	76.2	109	2 S31981	Ig kappa chain - h
36	316.5	76.1	106	2 PC2397	anti-tetanus toxin
37	316	76.0	108	2 I39154	Ig kappa chain (BR
38	315	75.0	125	2 S40353	Ig kappa chain V-I
39	315	75.7	107	2 S38262	Ig kappa chain V-I
40	315	75.7	107	2 I69017	anti-HIV1 envelope
41	315	75.7	117	2 S46376	Ig kappa chain V-I
42	314	75.5	108	1 K1HUV	Ig kappa chain V-I
43	314	75.5	125	2 S40316	Ig kappa chain - h
44	313.5	75.4	108	2 S30521	Ig kappa chain V-I
45	313	75.2	108	1 K1HUV	Ig kappa chain V-I

## RESULT 1

K1HUV  
Ig kappa chain V-I region (Hau) - human

C:Species: Homo sapiens (man)  
C:Date: 24-Apr-1984 #sequence\_revision 02-Jul-1998 #text\_change 21-Jan-2000

C:Accession: A01668, S02574

R:Watanabe, S.; Hilschmann, N.  
Hoppe-Seyler's Z. Physiol. Chem. 351, 1291-1295, 1970

A:Title: The primary structure of a monoclonal kappa-type immunoglobulin L-chain of subg

A:Reference number: A01668; WUID:71032830; PMID:4097974

A:Accession: A01668

A:Molecule type: protein

A:Residues: 1-108 <WAT>

A:Note: the C region of this chain has the Inv (3) marker

R:Steiner, V.; Chang, J.Y.

FEBS Lett. 222, 6-10, 1987

A:Title: Chemical modification of the carboxyl groups of protein substrates enhances the

A:Reference number: S02572; WUID:88005152; PMID:315831

A:Contents: annotation

C:Comment: This is a Bence Jones protein.

C:Genetics:

A:Gene: GDB:IGKV1

A:Cross-references: GDB:136264

A:Map position: 2p12-2p12

C:Complex: an immunoglobulin heterotetramer subunit consists of two identical light (kap

tain disulfide bonds; in some cases, such as IgA and IgM, the subunits associate into 1a

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F,16-90/Domain: immunoglobulin homology <IMM>

F,123-88/Disulfide bonds: #status predicted

Query Match 80.5%; Score 335; DB 1; Length 108;

Best Local Similarity 67.3%; Pred. No. 4e-26; 2; Indels 28; Gaps 4;

Matches 72; Conservative 5; Mismatches 28; Gaps 4;

QY	1	DIQMTQSPASLSASVGRVTITTC-----NYLQPKGKSPQ-LTY-----GYPS 41
DB	1	DIQMTQSPASLSASVGRVTITTCRASQSSISYLYQKPKKQVLIYAASSLPSSVPS 60
QY	42	RFSGSGSGTDFTLTISLTPEDEPATYYC-----FGQGTKEIK 79
DB	61	RFSGSGSGTDFTLTISLTPEDEPATYYCQNVITRTSGQGRVETIK 107

## RESULT 2

S46370  
Ig kappa chain V-J region (T3-9) - human (fragment)

C:Species: Homo sapiens (man)  
C:Date: 27-Jan-1995 #sequence\_revision 01-Sep-1995 #text\_change 21-Jan-2000

C:Accession: S46370, S38644

R:Bensimon, C.; Chastagner, P.; Zouali, M.  
EMBO J. 13, 2951-2962, 1994

A>Title: Human lupus anti-DNA autoantibodies undergo essentially primary V(chI) gene re  
A:Reference number: S46369; MUID:94313975; PMID:8039491  
A:Accession: S46370  
A:Molecule type: mRNA  
A:Residues: 1-120 <BBN>  
A:Cross-references: EMBL:Z27171; NID:G415957; PIDN:CAA81695.1; PID:G415958  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotrimer; immunoglobulin  
F:26-100/Domain: immunoglobulin homology <IMM>

Query Match 80.5%; Score 335; DB 2; Length 120;  
Best Local Similarity 67.6%; Pred. No. 4.4e-26;  
Matches 73; Conservative 3; Mismatches 2; Indels 30; Gaps 4;

QY 1 DIQMTGSPASLSASVGDRTVITC-----WYLOKPKSPQ-LIY-----GVPS 41  
DB 11 DIQMTGSPSSLSASVGDRTVITCRASRISFLNWTQKPKAPQLIYAVGRLSQGVPS 70  
QY 42 RFGSGSGTDFPSFTISLSLOPEDFATYTC-----FGQGTKEIK 78  
DB 71 RFGSGSGTDFLTITISLSLOPEDFATYTCQGSFNPPEYFGQGTKEIK 118

RESULT 3  
S40331  
Ig kappa chain - human  
C:Species: Homo sapiens (man)  
C>Date: 06-Mar-1994 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000  
C:Accession: S40331  
R:Klein, R.; Jaenichen, R.; Zachau, H.G.  
Eur. J. Immunol. 23, 3248-3271, 1993  
A>Title: Expressed human immunoglobulin chi genes and their hypermutation.  
A:Reference number: S40312; MUID:94080891; PMID:8258341  
A:Accession: S40331  
A:Status: preliminary; translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-123 <KLB>  
A:Cross-references: EMBL:X72441; NID:G441350; PIDN:CAA51109.1; PID:G441351  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotrimer; immunoglobulin  
F:32-106/Domain: immunoglobulin homology <IMM>

Query Match 80.3%; Score 334; DB 2; Length 123;  
Best Local Similarity 67.3%; Pred. No. 5.7e-26;  
Matches 72; Conservative 5; Mismatches 2; Indels 28; Gaps 4;

QY 1 DIQMTGSPASLSASVGDRTVITC-----WYLOKPKSPQ-LIY-----GVPS 41  
DB 17 DIQMTGSPSSLSASVGDRTVITCRASQISISYLNWTQKPKAPQLIYAAASLSQGVPS 76  
QY 42 RFGSGSGTDFPSFTISLSLOPEDFATYTC-----FGQGTKEIK 79  
DB 77 RFGSGSGTDFLTITISLSLOPEDFATYTCQGSYSTPTFGQGTKEIK 123

RESULT 4  
S36269  
Ig lambda chain V region (clone alpha-TNF-A1) - human (fragment)  
C:Species: Homo sapiens (man)  
C>Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 21-Jan-2000  
C:Accession: S36269  
R:Giffiths, A.D.; Malmqvist, M.; Marks, U.D.; Bye, J.M.; Emberton, M.J.; McCafferty, J.  
EMBO J. 12, 725-734, 1993  
A>Title: Human anti-self antibodies with high specificity from phage display libraries.  
A:Reference number: S36256; MUID:93178448; PMID:7679950  
A:Accession: S36269  
A:Status: preliminary; nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-107 <GRI>  
A:Cross-references: EMBL:Z18838; NID:G33422; PIDN:CAA79290.1; PID:G939915  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotrimer; immunoglobulin  
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 79.3%; Score 330; DB 2; Length 107;  
Best Local Similarity 67.3%; Pred. No. 1.2e-25;  
Matches 72; Conservative 4; Mismatches 3; Indels 28; Gaps 4;

QY 1 DIQMTGSPASLSASVGDRTVITC-----WYLOKPKSPQ-LIY-----GVPS 41  
DB 1 DIQMTGSPSSLSASVGDRTVITCRASQIRNDLWYQKPKAPQLIYGTSLQGVPS 60  
QY 42 RFGSGSGTDFPSFTISLSLOPEDFATYTC-----FGQGTKEIK 79  
DB 61 RFGSGSGTDFLTITISLSLOPEDFATYTCQGSYNTPTFGQGTKEIK 107

RESULT 5  
S40367  
Ig kappa chain V-J-C region - human  
C:Species: Homo sapiens (man)  
C>Date: 19-May-1994 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000  
C:Accession: S40367  
R:Klein, R.; Jaenichen, R.; Zachau, H.G.  
Eur. J. Immunol. 23, 3248-3271, 1993  
A>Title: Expressed human immunoglobulin chi genes and their hypermutation.  
A:Reference number: S40312; MUID:94080891; PMID:8258341  
A:Accession: S40367  
A:Status: preliminary; translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-127 <KLB>  
A:Cross-references: EMBL:X72477  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotrimer; immunoglobulin  
F:33-107/Domain: immunoglobulin homology <IMM>

Query Match 79.3%; Score 330; DB 2; Length 127;  
Best Local Similarity 66.4%; Pred. No. 1.4e-25;  
Matches 71; Conservative 6; Mismatches 2; Indels 28; Gaps 4;

QY 1 DIQMTGSPASLSASVGDRTVITC-----WYLOKPKSPQ-LIY-----GVPS 41  
DB 18 DIQMTGSPSSLSASVGDRTVITCRASQISISYLNWTQKPKAPQLIYAAASLSQGVPS 77  
QY 42 RFGSGSGTDFPSFTISLSLOPEDFATYTC-----FGQGTKEIK 79  
DB 78 RFGSGSGTDFLTITISLSLOPEDFATYTCQGSYNTPTFGQGTKEIK 124

RESULT 6  
S40369  
Ig kappa chain - human  
C:Species: Homo sapiens (man)  
C>Date: 06-Mar-1994 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000  
C:Accession: S40369  
R:Klein, R.; Jaenichen, R.; Zachau, H.G.  
Eur. J. Immunol. 23, 3248-3271, 1993  
A>Title: Expressed human immunoglobulin chi genes and their hypermutation.  
A:Reference number: S40312; MUID:94080891; PMID:8258341  
A:Accession: S40369  
A:Status: preliminary; translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-129 <KLB>  
A:Cross-references: EMBL:X72479; NID:G441426; PIDN:CAA51147.1; PID:G441427  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotrimer; immunoglobulin  
F:37-111/Domain: immunoglobulin homology <IMM>

Query Match 79.3%; Score 330; DB 2; Length 129;  
Best Local Similarity 66.4%; Pred. No. 1.5e-25;  
Matches 71; Conservative 6; Mismatches 2; Indels 28; Gaps 4;

QY 1 DIQMTGSPASLSASVGDRTVITC-----WYLOKPKSPQ-LIY-----GVPS 41  
DB 22 DIQMTGSPSSLSASVGDRTVITCRASQISISYLNWTQKPKAPQLIYAAASLSQGVPS 81

```
QY 42 RFSGSGGTDFTFTISLQPEDFATYYC-----FGQGTKLEIK 79
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 82 KFSGSGGTDFTLTISLQPEDFATYYCQVNSYPTTFGQGTKLEIK 128

RESULT 7
Ig kappa chain V region - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 19-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C:Accession: S52789
R:Rocca, A.; Khamlichi, A.A.; Touchard, G.; Mougnot, B.; Ronco, P.; Denoroy, L.; Deret,
submitted to the EMBL Data Library, March 1995
A:Description: Light chain V region gene usage restriction and peculiarities in myeloma-
A:Reference number: S52789
A:Accession: S52789
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-129 <ROC>
A:Cross-references: EMBL:X85995; NID:G758588; PIDN:CAA59987.1; PID:G758589
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:38-112/Domain: immunoglobulin homology <IMM>

Query Match 79.3%; Score 330; DB 2; Length 129;
Best Local Similarity 65.4%; Pred. No. 1.5e-25;
Matches 70; Conservative 5; Mismatches 4; Indels 28; Gaps 3;

QY 1 DIQMTQSPASLSASVGRVITTC-----WYLPKPKGSPQ-LIY-----GVPS 41
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 23 DIQMTQSPSLASVGRVITTCASQDISNVLNWTQKPKGAPKLLIHAASLSTGVPS 82

QY 42 RFSGSGGTDFTFTISLQPEDFATYYC-----FGQGTKLEIK 79
      :|||:|||||:|||||:|||||:|||||:|||||:
Db 83 RFSGSGGTDFTLTISLQPEDFATYYCQVNLPTTFGGTKVLEIK 129

RESULT 8
B49047
Ig kappa chain V region (monoclonal striational autoantibody StrAB SA-1A) - human (fragm
C:Species: Homo sapiens (man)
C>Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C:Accession: B49047
R:Victor, K.D.; Pascual, V.; Williams, C.L.; Lennon, V.A.; Capra, J.D.
Eur. J. Immunol. 22, 2231-2236, 1992
A:Title: Human monoclonal striational autoantibodies isolated from thymic B lymphocytes
A:Reference number: A49047; MUID:92387224; PMID:1516616
A:Accession: B49047
A>Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-108 <VIC>
A:Experimental source: thymic B lymphocytes
A>Note: sequence extracted from NCBI backbone (NCBIN:113208, NCBIP:113209)
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 78.6%; Score 327; DB 2; Length 108;
Best Local Similarity 66.4%; Pred. No. 2.4e-25;
Matches 71; Conservative 5; Mismatches 3; Indels 28; Gaps 4;

QY 1 DIQMTQSPASLSASVGRVITTC-----WYLPKPKGSPQ-LIY-----GVPS 41
      :|||:|||||:|||||:|||||:|||||:|||||:
Db 1 DIQMTQSPSLASVGRVITTCASQSSISNVLNWTQKPKGAPKLLIYAASLQSGVPS 60

QY 42 RFSGSGGTDFTFTISLQPEDFATYYC-----FGQGTKLEIK 79
      :|||:|||||:|||||:|||||:|||||:|||||:
Db 61 RFSGSGGTDFTLTISLQPEDFATYYCQVNSYPTTFGQGTKVLEIK 107

RESULT 9
S46371
Ig kappa chain V-J region (T24-3) - human (fragment)
C:Species: Homo sapiens (man)
```

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C>Date: 27-Jan-1995 #sequence_revision 01-Sep-1995 #text_change 21-Jan-2000
C:Accession: S46371; S38645
R:Bansimon, C.; Chaetagner, P.; Zouali, M.
EMBO J. 13, 2951-2962, 1994
A:Title: Human lupus anti-DNA autoantibodies undergo essentially primary V(chi) gene rea
A:Reference number: S46369; MUID:94313975; PMID:8039491
A:Accession: S46371
A:Molecule type: mRNA
A:Residues: 1-117 <SEN>
A:Cross-references: EMBL:Z27172; NID:G415959; PIDN:CAA81596.1; PID:G415960
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:23-97/Domain: immunoglobulin homology <IMM>

Query Match 78.4%; Score 326; DB 2; Length 117;
Best Local Similarity 64.2%; Pred. No. 3.3e-25;
Matches 70; Conservative 7; Mismatches 2; Indels 30; Gaps 4;

QY 1 DIQMTQSPASLSASVGRVITTC-----WYLPKPKGSPQ-LIY-----GVPS 41
      :|||:|||||:|||||:|||||:|||||:|||||:
Db 8 DIQMTQSPSLASVGRVITTCRASRSISTWLAWYQKPKGAPKLLIYKASTLESQVPS 67

QY 42 RFSGSGGTDFTFTISLQPEDFATYYC-----FGQGTKLEIK 79
      :|||:|||||:|||||:|||||:|||||:|||||:
Db 68 RFSGSGGTEFTLTISLQPEDFATYYCQVNSYFPPTFGQGTKLEIK 116

RESULT 10
S40313
Ig kappa chain V-J region - human
C:Species: Homo sapiens (man)
C>Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40313
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40313
A>Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-123 <KLE>
A:Cross-references: EMBL:X72423; NID:G441314; PIDN:CAA51091.1; PID:G441315
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:32-106/Domain: immunoglobulin homology <IMM>

Query Match 78.4%; Score 326; DB 2; Length 123;
Best Local Similarity 65.4%; Pred. No. 3.5e-25;
Matches 70; Conservative 7; Mismatches 2; Indels 28; Gaps 4;

QY 1 DIQMTQSPASLSASVGRVITTC-----WYLPKPKGSPQ-LIY-----GVPS 41
      :|||:|||||:|||||:|||||:|||||:|||||:
Db 17 DIQMTQSPSLASVGRVITTCASQGINRDNLAWFOQKPKGAPKRLIYDAASLLSGVPS 76

QY 42 RFSGSGGTDFTFTISLQPEDFATYYC-----FGQGTKLEIK 79
      :|||:|||||:|||||:|||||:|||||:|||||:
Db 77 RFSGSGGTEFTLTISLQPEDFATYYCQVNSYFPPTFGQGTKVLEIK 123

RESULT 11
S40333
Ig kappa chain V-J region - human
C:Species: Homo sapiens (man)
C>Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40333
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40333
A>Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-125 <KLE>
```

[illegible]

Query Match 77.4%; Score 322; DB 1; Length 108;



Best Local Similarity 64.5%; Pred. No. 7.5e-25;  
Matches 69; Conservative 6; Mismatches 4; Indels 28; Gaps 4;  
QY 1 DIQMTQSPASISASVGRVTITC-----WYLQKPKSPQ-LIY-----GVPS 41  
Db 1 DIQMTQSPSSLSVSVGRVTITCQASQNVNAYLNWYQKPKLPALPKLIYCASTREAGVPS 60  
QY 42 RFGSGSGTDFSTISSLPEDFATYYC-----FGQTKLEIK 79  
Db 61 RFGSGSGTDFSTISSLPEDIATYYCQYNNWPPTFGQTKVEVK 107

Search completed: January 13, 2004, 12:44:39  
Job time : 5.72664 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 13, 2004, 12:19:34 ; Search time 3.44978 Seconds  
(without alignments)  
1076.912 Million cell updates/sec

Title: US-09-990-586-79

Perfect score: 416

Sequence: 1 DIQMTQSPASLSASVGRVT.....QPEDFATYCFGGQTKLEIK 79

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	335	80.5	108	1	KVIIH_HUMAN
2	322	77.4	108	1	KVIIH_HUMAN
3	322	77.4	108	1	KVIIH_HUMAN
4	322	77.4	108	1	KVIIH_HUMAN
5	320	76.9	108	1	KVIIH_HUMAN
6	320	76.9	108	1	KVIIH_HUMAN
7	318	76.4	108	1	KVIIH_HUMAN
8	318	76.4	108	1	KVIIH_HUMAN
9	317	76.2	108	1	KVIIH_HUMAN
10	317	76.2	108	1	KVIIH_HUMAN
11	317	76.2	108	1	KVIIH_HUMAN
12	314	75.5	108	1	KVIIH_HUMAN
13	313	75.2	108	1	KVIIH_HUMAN
14	313	75.2	108	1	KVIIH_HUMAN
15	312	75.0	108	1	KVIIH_HUMAN
16	309.5	74.4	107	1	KVIIH_HUMAN
17	306	73.6	129	1	KVIIH_HUMAN
18	304	73.1	108	1	KVIIH_HUMAN
19	302	72.6	108	1	KVIIH_HUMAN
20	302	72.6	108	1	KVIIH_HUMAN
21	299	71.9	108	1	KVIIH_HUMAN
22	295.5	71.0	109	1	KVIIH_HUMAN
23	292.5	70.3	117	1	KVIIH_HUMAN
24	292	70.2	108	1	KVIIH_HUMAN
25	290.5	69.8	117	1	KVIIH_HUMAN
26	277	66.6	108	1	KVIIH_HUMAN
27	274	65.9	112	1	KVIIH_HUMAN
28	273	65.6	108	1	KVIIH_HUMAN
29	272	65.4	108	1	KVIIH_HUMAN
30	272	65.4	149	1	KVIIH_HUMAN
31	271	65.1	108	1	KVIIH_HUMAN
32	271	65.1	114	1	KVIIH_HUMAN
33	270	64.9	108	1	KVIIH_HUMAN

34 270 64.9 108 1 KV5S MOUSE  
35 270 64.9 108 1 KV5T MOUSE  
36 269.5 64.8 115 1 KV5C MOUSE  
37 269 64.7 108 1 KV5P MOUSE  
38 268.5 64.5 109 1 KV3E\_HUMAN  
39 268.5 64.5 109 1 KV3G\_HUMAN  
40 268.5 64.5 129 1 KV3L\_HUMAN  
41 268 64.4 108 1 KV5K MOUSE  
42 268 64.4 108 1 KV5L MOUSE  
43 268 64.4 108 1 KV5N MOUSE  
44 268 64.4 134 1 KV4C\_HUMAN  
45 266.5 64.1 109 1 KV3D\_HUMAN

#### ALIGNMENTS

RESULT 1  
KV1H\_HUMAN STANDARD; PRT; 108 AA.  
AC P01600;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig kappa chain V-I region Hau.  
OS Homo sapiens (Human)  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID:9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=71032830; PubMed=4097974;  
RA Watanabe S., Hilschmann N.;  
RT The primary structure of a monoclonal kappa-type immunoglobulin L-chain of subgroup I (Bence-Jones Protein Hau): subdivision within RT subgroups.  
RL Hoppe-Seyler's Z. Physiol. Chem. 351:1291-1295(1970).  
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.  
CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.  
DR PIR; A01868; KIHUHU.  
DR HSSP; P80382; 1WT.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding activity; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_V.  
DR Pfam; PF00047; Ig\_1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG\_LIKE; 1.  
KW Immunoglobulin V region; Bence-Jones protein.  
FT DOMAIN 1 23  
FT COMPLEMENTARITY-DETERMINING-1.  
FT DOMAIN 24 34  
FT COMPLEMENTARITY-DETERMINING-2.  
FT DOMAIN 35 49  
FT COMPLEMENTARITY-DETERMINING-3.  
FT DOMAIN 50 56  
FT COMPLEMENTARITY-DETERMINING-4.  
FT DOMAIN 57 88  
FT DISULFID 89 97  
FT NON\_TER 98 107  
FT NON\_TER 108 108  
SQ SEQUENCE 108 AA; 11671 MW; 08D3A6160D8D0618 CRC64;

Query Match 80.5%; Score 335; DB 1; Length 108;  
Best Local Similarity 67.3%; Pred. No. 4.6e-31;  
Matches 72; Conservative 5; Mismatches 2; Indels 28; Gaps 4;  
QY 1 DIQMTQSPASLSASVGRVTITCRASQSISSYLSWYQKPKGAPQVLIYAASLPSGVPS 60  
DB 1 DIQMTQSPASLSASVGRVTITCRASQSISSYLSWYQKPKGAPQVLIYAASLPSGVPS 60  
QY 42 RFGSGSGDFTFTISSLOPEDFATYFC-----PQGTGLEIK 79  
DB 61 RFGSGSGDFTFTISSLOPEDFATYFCQNYITFTSFQGTTRVEIK 107

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RN RP SEQUENCE.
RX MEDLINE=77038198; PubMed=824717;
RA Capra J.D., Klapper D.G.;
RT "Complete amino acid sequence of the variable domains of two human
RT IgM anti-gamma globulins (Lay/Pom) with shared idiotypic
RT specificities.";
RL Scand. J. Immunol. 5:677-684 (1976).
CC -1- MISCELLANEOUS: THE SECOND AND THIRD HYPERVARIABLE REGIONS OF THIS
CC CHAIN ARE IDENTICAL WITH THOSE OF THE HUMAN POM V-III KAPPA CHAIN,
CC WITH WHICH IT SHARES CERTAIN IDIOTYPIC DETERMINANTS.
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
CC GLOBULIN ACTIVITY.
DR PIR; A01871; KIHULY.
DR HSSP; P01607; IREI.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 24 34
FT COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 35 49
FT COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 50 56
FT COMPLEMENTARITY-DETERMINING-4.
FT DOMAIN 57 88
FT DISULFID 98 107
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11934 MW; 739953A95431434A CRC64;

Query Match 77.4%; Score 322; DB 1; Length 108;
Best Local Similarity 64.5%; Pred. No. 1.4e-29;
Matches 69; Conservative 6; Mismatches 4; Indels 28; Gaps 4;

QY 1 DIQMTQSPASISASVGRVTITC-----WYLOKPKGKSPQ-LIY-----GVPS 41
DB 1 DIQMTQSPFSLSVSVGRVTITCQASQNVAYLNWYQKPKGLAPKLLIYGASTREAGVPS 60
QY 42 RFGSGSGTDFSTTISLQPEDFATYYC-----FGQGTKLEIK 79
DB 61 RFGSGSGTDFSTTISLQPEDFATYYCQQVNNWPPTEFGQGTKVEIK 107

RESULT 4
KVIM HUMAN
ID KVIM HUMAN STANDARD; PRT; 108 AA.
AC P01606;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region OU.
DE Ig kappa chain V-I region OU.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=70201507; PubMed=5447531;
RA Kohler H., Shimizu A., Paul C., Putnam F.W.;
RT "Macroglobulin structure: variable sequence of light and heavy
RT chains.";
RL Science 169:56-59 (1970).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S
CC MACROGLOBULIN.
DR PIR; A01872; KIHOUU.
DR HSSP; P01607; IREI.
```

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RESULT 2
KVIG HUMAN
ID KVIG HUMAN STANDARD; PRT; 108 AA.
AC P01599;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Gal.
DE Ig kappa chain V-I region Gal.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=75059122; PubMed=4215718;
RA Laure C.J., Watanabe S., Hilschmann N.;
RT "The primary structure of a monoclonal IgM-immunoglobulin
RT (macroglobulin Gal.), I. The amino acid sequence of the L-chain of
RT kappa-type, subgroup I.";
RL Hoppe-Sevler's Z. Physiol. Chem. 354:1503-1504 (1973).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S
CC MACROGLOBULIN.
DR PIR; A01867; KIHUGL.
DR HSSP; P01607; IREI.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 24 34
FT COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 35 49
FT COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 50 56
FT COMPLEMENTARITY-DETERMINING-4.
FT DOMAIN 57 88
FT DISULFID 98 107
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11814 MW; C1AD3CB0F600FF73 CRC64;

Query Match 77.4%; Score 322; DB 1; Length 108;
Best Local Similarity 64.5%; Pred. No. 1.4e-29;
Matches 69; Conservative 7; Mismatches 3; Indels 28; Gaps 4;

QY 1 DIQMTQSPASISASVGRVTITC-----WYLOKPKGKSP-OLIV-----GVPS 41
DB 1 DIQMTQSPFSLSVSVGRVTITCRASQIRNDLTWYQKPKGKPKKELIYAASNLQSGVPS 60
QY 42 RFGSGSGTDFSTTISLQPEDFATYYC-----FGQGTKLEIK 79
DB 61 RFGSGSGTDFSTTISLQPEDFATYYCQVNNWPPTEFGQGTKVEIK 107

RESULT 3
KVIM HUMAN
ID KVIM HUMAN STANDARD; PRT; 108 AA.
AC P01605;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Lay.
DE Ig kappa chain V-I region Lay.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
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DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 107
FT DISULFID 23 88
FT STRAND 4 7
FT STRAND 10 13
FT TURN 15 16
FT TURN 19 25
FT TURN 30 31
FT TURN 33 38
FT TURN 40 41
FT TURN 44 49
FT TURN 50 52
FT STRAND 53 54
FT TURN 56 57
FT TURN 60 61
FT STRAND 62 67
FT TURN 68 69
FT STRAND 70 75
FT HELIX 80 82
FT STRAND 85 90
FT STRAND 97 98
FT STRAND 102 106
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11777 MW; 8283D4A24105827E CRC64;

Query Match 77.4%; Score 322; DB 1; Length 108;
Best Local Similarity 59.8%; Pred. No. 1.4e-29;
Matches 64; Conservative 13; Mismatches 2; Indels 28; Gaps 4;

QY 1 DIQMTQSPASLSASVGRVTITC-----WYLQKPKSPQ-LIY-----GVPS 41
DB 1 DIQMTSPSSLSASVGRVTITCRASZTISYLBWYZZKPKAPBLIYASBLHSGVPS 60

QY 42 RFGSGSGTDFSTISSLPQDFATYYC-----FCQGTKLRI 78
DB 61 RFGSGSGTDFSTISSLPQDFATYYCQYQSLPYTFGGTKLQI 106

RESULT 5
KV10_HUMAN
ID KV10_HUMAN STANDARD; PRT; 108 AA.
AC P01607;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig kappa chain V-I region Rei.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=76023758; PubMed=8093229;
RA Palm W.; Hilschmann N.;
RT "The primary structure of a crystalline monoclonal immunoglobulin
kappa-type L-chain, subgroup I (Bence-Jones protein Rei); isolation
and characterization of the tryptic peptides; the complete amino acid
sequence of the protein; a contribution to the elucidation of the
three-dimensional structure of antibodies, in particular their
combining site."
RL Hoppe-Seyler's Z. Physiol. Chem. 356:167-191(1975).
RN [2]
RX X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RA MEDLINE=76039968; PubMed=1182131;
RA Epp O.; Lattman B.E.; Schiffer M.; Huber R.; Palm W.;
RT "The molecular structure of a dimer composed of the variable portions
of the Bence-Jones protein REI refined at 2.0-A resolution."
RL Biochemistry 14:4943-4952(1975).
CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
MARKER.
CC -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR PIR; A91663; K1HURE.
DR PDB; 1REI; 17-FEB-84.
DR PDB; 1AR2; 12-NOV-97.
DR PDB; 1BWV; 29-DEC-99.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
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CC WALDENSTROM'S MACROGLOBULINEMIA.
DR PIR; A01876; KIHUW.
DR HSP; P80362; IWL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG_LIKE; 1.
KW Immunoglobulin V region; Monoclonal antibody.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 FRAMEWORK-2.
FT DOMAIN 35 49 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11840 MW; 9249561F0945618C CRC64;

Query Match 76.9%; Score 320; DB 1; Length 108;
Best Local Similarity 63.6%; Pred. No. 2.3e-29;
Matches 68; Conservative 8; Mismatches 23; Indels 28; Gaps 4;

QY 1 DIQWTQSPASLSASVGRVITTC-----WYLPKPKSP-QLIY-----GVPS 41
DB 1 DIQWTQSPSSLSASVGRVITTCASQGIKNDLTWYQKQEGTAPKELIYGATSLQSGVPS 60

QY 42 RFGSGSGTDFSTISSLOPEDFATYTC-----FQGTKLEIK 79
DB 61 RFGSGSGTFTLTNSLOPEDFATYTCLOYSFPPTFGQGTKEVK 107

RESULT 7
KV1B_HUMAN
ID KV1B_HUMAN STANDARD; PRT; 108 AA.
AC P01594;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig kappa chain V-1 region AU.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=72189444; PubMed=5028201;
RA Schiechl H., Hilschmann N.;
RT "Rule of antibody structure. The primary structure of a monoclonal
RT immunoglobulin L-chain of the kappa-type, subgroup I (Bence-Jones
RT protein Au).";
RL Hoppe-Seyler's Z. Physiol. Chem. 353:345-370(1972).
RN [2]
RP X-RAY CRYSTALLOGRAPHY.
RX MEDLINE=77022433; PubMed=1234024;
RA Feilhammer H., Schiffer M., Epp O., Colman P.M., Lattman E.E.,
RA Schwager P., Steigemann W., Schramm H.J.;
RT "The structure determination of the variable portion of the
RT Bence-Jones protein Au.";
RL Biophys. Struct. Mech. 1:139-146(1975).
CC -1- MISCELLANEOUS: THE STRUCTURE OF THE V REGION WAS DETERMINED BY
CC MOLECULAR REPLACEMENT METHODS USING THE KNOWN STRUCTURE OF THE V
CC REGION OF THE KAPPA CHAIN REI.
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC PIR; A91653; KIHUW.
DR PDB; 1JVS; 30-JAN-02.
DR GO; GO:0005576; C:extracellular; NAS.

GO; GO:0003823; F:antigen binding activity; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IGV; 1.
PROSITE; PS0835; IG_LIKE; 1.
Immunoglobulin V region; Bence-Jones protein; 3D-structure.
DOMAIN 1 23 FRAMEWORK-1.
DOMAIN 24 34 FRAMEWORK-2.
DOMAIN 35 49 COMPLEMENTARITY-DETERMINING-1.
DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
DOMAIN 57 88 FRAMEWORK-3.
DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
DOMAIN 98 107 FRAMEWORK-4.
DISULFID 23 88 BY SIMILARITY.
NON TER 108 108
SEQUENCE 108 AA; 11939 MW; E8011187EE6F6B9 CRC64;

Query Match 76.4%; Score 318; DB 1; Length 108;
Best Local Similarity 64.5%; Pred. No. 3.9e-29;
Matches 69; Conservative 5; Mismatches 5; Indels 28; Gaps 4;

QY 1 DIQWTQSPASLSASVGRVITTC-----WYLPKPKSP-QLIY-----GVPS 41
DB 1 DIQWTQSPSSLSASVGRVITTCASQDISDYLNWYQKQKAPKELIYDASNLSEGVPS 60

QY 42 RFGSGSGTDFSTISSLOPEDFATYTC-----FQGTKLEIK 79
DB 61 RFGSGSGAHFTFTISSLOPEDFATYTCQVYDLPWTFGQGTKEIK 107

RESULT 8
KV1W_HUMAN
ID KV1W_HUMAN STANDARD; PRT; 129 AA.
AC P04431;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-1 region Walker precursor.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85014148; PubMed=6091049;
RA Kiobeck H.G.; Combrato G.; Zachau H.G.;
RT "Immunoglobulin genes of the kappa light chain type from two human
RT lymphoid cell lines are closely related.";
RL Nucleic Acids Res. 12:6995-7006(1984).
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; X00965; CAA25477.1; ALT_TERM.
CC FIR; A01893; KIHUW.
CC HSP; P01607; IRE1.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IGV; 1.
PROSITE; PS0835; IG_LIKE; 1.

```

Immunoglobulin V region; Signal.

KW SIGNAL 1 22 IG KAPPA CHAIN V-I REGION WALKER.  
 FT CHAIN 23 129  
 FT DOMAIN 23 45  
 FT DOMAIN 23 45  
 FT DOMAIN 46 56  
 FT DOMAIN 57 71  
 FT DOMAIN 72 78  
 FT DOMAIN 79 110  
 FT DOMAIN 111 119  
 FT DOMAIN 120 129  
 FT DOMAIN 129 129  
 FT DISULFID 45 110  
 FT NON TER 129 129  
 SQ SEQUENCE 129 AA; F941FA07D4AFC2F9 CRC64;

Query Match 76.4%; Score 318; DB 1; Length 129;  
 Best Local Similarity 65.4%; Pred. No. 4.7e-29;  
 Matches 70; Conservative 5; Mismatches 4; Indels 28; Gaps 4;

QY 1 DIQMTQSPASLSASVGDRTVITC-----WYLOKPGKSPQ-LIY-----GVPS 41  
 DB 23 DIQMTQSPSSUSASVGDRTVITCRASQSIGNYLWYQKPGKAPKFLIYAASSLQSGVTS 82

QY 42 RFGSGSGTDFSTISSIQLQPEDFATYYC-----FQGTGKLEIK 79  
 DB 83 RFGSGSGTDFTLTSSIQLQPEDSATYYCQSYSTLITFGQTRLEIK 129

RESULT 9  
 KV1C HUMAN  
 ID KV1C HUMAN STANDARD; PRT; 108 AA.  
 AC P01595;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Ig kappa chain V-I region B1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=73029807; PubMed=4563064;  
 RA Braun M., Leibold W., Barnikol H.U., Hilschmann N.;  
 RT "Principle of antibody structure. The primary structure of a  
 RT monoclonal kappa I-type immunoglobulin L-chain (Bence Jones protein  
 RT Bi). 3. The complete amino acid sequence and the genetic  
 RT significance of the variability principles for the mechanism of  
 RT antibody formation.";  
 RL Hoppe-Seyler's Z. Physiol. Chem. 353:1284-1306(1972).  
 CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.  
 CC -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.  
 DR PIR; A01863; KIHUBI.  
 DR HSSP; P01607; IREI.  
 DR GO; GO:0005576; C:extracellular; NAS.  
 DR GO; GO:0003823; F:antigen binding activity; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR Pfam; PF00047; IG\_1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS0835; IG LIKE; 1.  
 KW Immunoglobulin V region; Bence-Jones protein.  
 FT DOMAIN 1 23 FRAMEWORK-1.  
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.  
 FT DOMAIN 25 49 FRAMEWORK-2.  
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.  
 FT DOMAIN 57 88 FRAMEWORK-3.  
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.  
 FT DOMAIN 98 107 FRAMEWORK-4.  
 FT DISULFID 23 88  
 FT NON TER 108 108  
 SQ SEQUENCE 108 AA; 12026 MW; 7A83983986A431E7 CRC64;

Query Match 76.2%; Score 317; DB 1; Length 108;  
 Best Local Similarity 64.5%; Pred. No. 5e-29;  
 Matches 69; Conservative 5; Mismatches 5; Indels 28; Gaps 4;

QY 1 DIQMTQSPASLSASVGDRTVITC-----WYLOKPGKSPQ-LIY-----GVPS 41  
 DB 1 DIQMTQSPSSUSASVGDRTVITCRASQSIGNSRLIYQKPGKAPKFLIYDAENLIGVPS 60

QY 42 RFGSGSGTDFSTISSIQLQPEDFATYYC-----FQGTGKLEIK 79  
 DB 61 RFGSGSGTDFLTSIQLQPEDFATYYCQYYNLPYTFGQGTGKLEIK 107

RESULT 10  
 KV1F HUMAN  
 ID KV1F HUMAN STANDARD; PRT; 108 AA.  
 AC P01598;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig kappa chain V-I region EU.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=71064023; PubMed=5489770;  
 RA Gottlieb P.D., Cunningham B.A., Rutishauser U., Edelman G.M.;  
 RT "The covalent structure of a human gamma G-immunoglobulin. V. Amino  
 RT acid sequence of the light chain.";  
 RL Biochemistry 9:3155-3161(1970).  
 RN [2]  
 RP DISULFIDE BOND.  
 RX MEDLINE=71064027; PubMed=4923144;  
 RA Gall W.E., Edelman G.M.;  
 RT "The covalent structure of a human gamma G-immunoglobulin. X.  
 RT Intrachain disulfide bonds.";  
 RL Biochemistry 9:3188-3196(1970).  
 CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.  
 CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.  
 DR PIR; A90562; KIHUEU.  
 DR HSSP; P01607; IREI.  
 DR GO; GO:0005576; C:extracellular; NAS.  
 DR GO; GO:0003823; F:antigen binding activity; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_V.  
 DR Pfam; PF00047; IG; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS0835; IG LIKE; 1.  
 KW Immunoglobulin V region.  
 FT DOMAIN 1 23 FRAMEWORK-1.  
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.  
 FT DOMAIN 35 49 FRAMEWORK-2.  
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.  
 FT DOMAIN 57 88 FRAMEWORK-3.  
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.  
 FT DOMAIN 98 107 FRAMEWORK-4.  
 FT DISULFID 23 88  
 FT NON TER 108 108  
 SQ SEQUENCE 108 AA; 11788 MW; 9CD294F2F4D88823 CRC64;

Query Match 76.2%; Score 317; DB 1; Length 108;  
 Best Local Similarity 60.7%; Pred. No. 5e-29;  
 Matches 65; Conservative 10; Mismatches 28; Gaps 3;

QY 1 DIQMTQSPASLSASVGDRTVITC-----WYLOKPGKSPQ-LIY-----GVPS 41  
 DB 1 DIQMTQSPSSUSASVGDRTVITCRASQSIGNTWLWYQKPGKAPKFLIYKASLESIGVPS 60

QY 42 RFGSGSGTDFSTFISSLPEDFATYYC-----FGQTKLEIK 79  
Db 61 RFTGSGGTFTFISSLPEDFATYYCQYNSDKMFGGQTKVEVK 107

RESULT 11  
KV1P\_HUMAN  
ID KV1P\_HUMAN STANDARD; PRT; 108 AA.  
AC P01608;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig kappa chain V-I region Roy.  
OS Homo sapiens (Human)  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=68362076; PubMed=5595110;  
RA Hilschmann N.;  
RT "Chemical structure of 2 kappa-type Bence Jones proteins (Roy and Cum.)";  
RL Hoppe-Seyler's Z. Physiol. Chem. 348:1077-1080(1967).  
RN [2]  
RP REVISIONS TO 39 AND 41.  
RA Hilschmann N., Barnikol H.U., Hess M., Langer E., Ponstingl H., Steinmetz-Kayne M., Suter L., Watanabe S.;  
RL (In) Frazer F., Shugar D. (eds.);  
RL Gamma globulins: structure and function, pp.57-74, Academic Press, New York (1969).  
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2) MARKER.  
CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.  
DR PIR; A91638; KIHURY.  
DR HSSP; P80362; 1WTL.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding activity; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003006; IG\_MHC.  
DR Pfam; PF00047; IG; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS0835; IG\_LIKE; 1.  
KW Immunoglobulin V region; Bence-Jones protein.  
FT DOMAIN 1 23  
FT DOMAIN 24 34  
FT DOMAIN 35 49  
FT DOMAIN 50 56  
FT DOMAIN 57 88  
FT DOMAIN 89 97  
FT DOMAIN 98 107  
FT DISULFID 23 88  
FT NON\_TER 108 108  
SQ SEQUENCE 108 AA; 11782 MW; F5ACEDE5A313DF3A CRC64;

Query Match 76.2%; Score 317; DB 1; Length 108;  
Best Local Similarity 63.6%; Pred. No. 5e-29; Mismatches 7; Indels 28; Gaps 4;  
Matches 68; Conservative 7;

QY 1 DIQMTQSPASLSASVGRVTITC-----WYLOKPKGSPQ-LIY-----GVPS 41  
Db 1 DIQMTQSPFSLASVGRVTITCQASQDISIFLNWYQKPKAPKLLIYDASKLEAGVPS 60

QY 42 RFGSGSGTDFSTFISSLPEDFATYYC-----FGQTKLEIK 79  
Db 61 RFTGSGGTFTFISSLPEDFATYYCQYNSDKMFGGQTKVEVK 107

RESULT 12  
KV1K\_HUMAN  
ID KV1K\_HUMAN STANDARD; PRT; 108 AA.

AC P01603;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig kappa chain V-I region Ka.  
OS Homo sapiens (Human)  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=76189985; PubMed=818073;  
RA Shinoda T.;  
RT "Comparative structural studies on the light chains of human immunoglobulins. I. Protein Ka with the Inv(3) allotypic marker";  
RL J. Biochem. 77:1277-1296(1975).  
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.  
CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.  
DR PIR; A01869; KIHURA.  
DR HSSP; P80362; 1WTL.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding activity; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_V.  
DR Pfam; PF00047; IG; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS0835; IG\_LIKE; 1.  
KW Immunoglobulin V region; Bence-Jones protein.  
FT DOMAIN 1 23  
FT DOMAIN 24 34  
FT DOMAIN 35 49  
FT DOMAIN 50 56  
FT DOMAIN 57 88  
FT DOMAIN 89 97  
FT DOMAIN 98 107  
FT DISULFID 23 88  
FT NON\_TER 108 108  
SQ SEQUENCE 108 AA; 11900 MW; 768839FBED5A2F4B CRC64;

Query Match 75.5%; Score 314; DB 1; Length 108;  
Best Local Similarity 58.9%; Pred. No. 1.1e-28; Mismatches 13; Conservative 13; Indels 28; Gaps 4;  
Matches 63;

QY 1 DIQMTQSPASLSASVGRVTITC-----WYLOKPKGSPQ-LIY-----GVPS 41  
Db 1 DIQMTQSPFSLASVGRVTITCQASQDISIFLNWYQKPKAPKLLIYDASKLEAGVPS 60

QY 42 RFGSGSGTDFSTFISSLPEDFATYYC-----FGQTKLEIK 79  
Db 61 RFTGSGGTFTFISSLPEDFATYYCQYNSDKMFGGQTKVEVK 107

RESULT 13  
KV1V\_HUMAN  
ID KV1V\_HUMAN STANDARD; PRT; 108 AA.  
AC P04430;  
DT 13-AUG-1987 (Rel. 05, Created)  
DT 13-AUG-1987 (Rel. 05, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig kappa chain V-I region BAN.  
OS Homo sapiens (Human)  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=86174817; PubMed=3083240;  
RA Dwulet F.E., O'Connor T.P., Benson M.D.;  
RT "Polymorphism in a kappa I primary (AL) amyloid protein (BAN)";  
RL Mol. Immunol. 23:73-78(1986).  
DR PIR; A01878; KIHUBN.

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DR HSSP; P80362; 1WTL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; P:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 1.
KW Immunoglobulin V region; Amyloid.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11840 MW; CD3FD944FE96FD37 CRC64;

Query Match 75.2%; Score 313; DB 1; Length 108;
Best Local Similarity 62.6%; Pred. No. 1.4e-28;
Matches 67; Conservative 8; Mismatches 4; Indels 28; Gaps 4;

QY 1 DIQMTQSPASLSASVGRVITTC-----WYLOKPKSPQ-LIY-----GVPS 41
DB 1 DIQMTQSPSSLSASVGRVITTCRASQVYVAVFQKPKAPKSLIYDASTLQSGVPS 60
QY 42 RFGSGSGTDFSTFISSLPQEDPATYYC-----FGQGTKLEIK 79
DB 61 NFGSGSGTDFSTFISSLPQEDPATYYCQVNSFYFTFGQGTKVQIK 107

RESULT 14
KVIA_HUMAN STANDARD; PRT; 108 AA.
ID KVIA_HUMAN STANDARD; PRT; 108 AA.
AC P80362;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ig kappa chain V-I region WAT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE, AND X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX MEDLINE=95086080; PubMed=7939311;
Huang D.-B., Chang C.-H., Ainsworth C., Bruenger A.T., Eulitz M.,
Solomon A., Stevens F.J., Schiffer M.;
"Comparison of crystal structures of two homologous proteins:
structural origin of altered domain interactions in immunoglobulin
light-chain dimers";
RL Biochemistry 33:14848-14857(1994).
RN [2]
RP SEQUENCE OF 1-35.
RX MEDLINE=81267384; PubMed=6167731;
Stevens F.J., Westholm F.A., Panagiotopoulos N., Schiffer M.,
Popp R.A., Solomon A.;
"Characterization and preliminary crystallographic data on the VL-
related fragment of the human kappa Bence Jones protein Wat.";
RL J. Mol. Biol. 147:185-193(1981).
CC -1- MISCELLANEOUS: THIS IS A BENICE-JONES PROTEIN.
DR PDB; 1WTL; 01-NOV-94.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; P:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.

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DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein; 3D-structure.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11737 MW; D9D941B3F0FAE697 CRC64;

Query Match 75.2%; Score 313; DB 1; Length 108;
Best Local Similarity 62.6%; Pred. No. 1.4e-28;
Matches 67; Conservative 9; Mismatches 3; Indels 28; Gaps 4;

QY 1 DIQMTQSPASLSASVGRVITTC-----WYLOKPKSPQ-LIY-----GVPS 41
DB 1 DIQMTQSPSSLSASVGRVITTCRASQDITVNVAVFQKPKVLIYGASILETGVP 60
QY 42 RFGSGSGTDFSTFISSLPQEDPATYYC-----FGQGTKLEIK 79
DB 61 RFGSGSGTDFSTFISSLPQEDPATYYCQYDTLPLTFGGGTRVDIK 107

RESULT 15
KVIA_HUMAN STANDARD; PRT; 108 AA.
ID KVIA_HUMAN STANDARD; PRT; 108 AA.
AC P01593;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region AG.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=69234734; PubMed=4893682;
Titani K., Shinoda T., Putnam F.W.;
"The amino acid sequence of a kappa type Bence-Jones protein. 3. The
complete sequence and the location of the disulfide bridges.";
RL J. Biol. Chem. 244:3550-3560(1969).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
DR PIR; A01861; KIHUAG.
DR HSSP; P01607; IREI.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; P:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.

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DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11992 MW; E3B3B246C18F0C4F CRC64;

Query Match 75.0%; Score 312; DB 1; Length 108;
Best Local Similarity 64.5%; Pred. No. 1.8e-28;
Matches 69; Conservative 4; Mismatches 6; Indels 28; Gaps 4;

Qy 1 DIQWTQSPASLSASVGDRTVITC-----WYLOKPKSPQ-LIY-----GVPS 41
Db 1 DIQWTQSPSLSASVGDRTVITCQASQDINHLYNWYQGGPKAPKILIIDASNLETGVPS 60

Qy 42 RFSGSGGTDFTFTISLSQPEDPATYYC-----FGQGTKLEIK 79
Db 61 RFSGSGGTDFTFTISGLQPEDATYYCQOYDTLPRTFGQGTKLEIK 107
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Job time : 4.44978 secs



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RESULT 2  
ID Q96SA9 PRELIMINARY; PRT; 107 AA.  
AC Q96SA9  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Anti-streptococcal/anti-myoisin immunoglobulin kappa light chain  
DE variable region (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98375893; PubMed=9712075;  
RA Adderson E.E., Shikman A.R., Ward K.E., Cunningham M.W.;  
RT "Molecular analysis of polyclonal antibodies from  
RT rheumatic carditis: human anti-N-acetylglucosamine/anti-myoisin  
RT antibody V region genes";  
RL J. Immunol. 161:2020-2031(1998).  
DR EMBL; U96396; AAB68785.1; -  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_V.  
DR Pfam; PF00047; IG; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS0835; IG\_LIKE; 1.  
DR NON\_TER 1  
FT NON\_TER 107  
SQ SEQUENCE 107 AA; 11520 MW; 4BB43E9C5B577F16 CRC64;  
Query Match 78.7%; Score 327.5; DB 4; Length 107;  
Best Local Similarity 67.0%; Pred. No. 2.4e-31;  
Matches 71; Conservative 5; Mismatches 3; Indels 27; Gaps 4;  
QY 1 DIQWTSPPSLASVSGDRVTTCRASQSISSYLNWYQKPKAPNLLIYAASSLSQGVPS 41  
Db 1 DIQWTSPPSLASVSGDRVTTCRASQSISSYLNWYQKPKAPNLLIYAASSLSQGVPS 60  
QY 42 RFSGSGSGTDFSTISSLOPEDFATYYC-----FGQGTKEIK 79  
Db 61 RFSGSGSGTDFTLTSSLOPEDFATYYCQSYSTSTWTFEGGTKEIK 106  
RESULT 3  
ID Q9UL70 PRELIMINARY; PRT; 108 AA.  
AC Q9UL70  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Myosin-reactive immunoglobulin light chain variable region  
DE (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98277139; PubMed=9614934;  
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,  
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
RT fetus";  
RL Clin. Immunol. Immunopathol. 87:184-192 (1998).  
Query Match 74.4%; Score 309.5; DB 4; Length 107;  
Best Local Similarity 63.2%; Pred. No. 3.4e-29;  
Matches 67; Conservative 6; Mismatches 6; Indels 27; Gaps 4;  
QY 1 DIQWTSPPSLASVSGDRVTTCRASQSISSYLNWYQKPKAPNLLIYAASSLSQGVPS 41  
Db 1 DIQWTSPPSLASVSGDRVTTCRASQSISSYLNWYQKPKAPNLLIYAASSLSQGVPS 60  
QY 42 RFSGSGSGTDFSTISSLOPEDFATYYC-----FGQGTKEIK 79  
Db 61 RFSGSGSGTDFTLTSSLOPEDFATYYCQSYSTSTWTFEGGTKEIK 106  
RESULT 5  
Q9UL79

DR EMBL; AF035044; AAD56280.1; -  
DR HSSP; P01607; 1REI.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_V.  
DR Pfam; PF00047; IG; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS0835; IG\_LIKE; 1.  
DR NON\_TER 1  
FT NON\_TER 108  
SQ SEQUENCE 108 AA; 11633 MW; B7BEDC3E41FCCA37 CRC64;  
Query Match 77.2%; Score 321; DB 4; Length 108;  
Best Local Similarity 66.4%; Pred. No. 1.5e-30;  
Matches 71; Conservative 3; Mismatches 5; Indels 28; Gaps 4;  
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Db 1 DIQWTSPPSLASVSGDRVTTCRASQSISSYLNWYQKPKAPNLLIYAASSLSQGVPS 60  
QY 42 RFSGSGSGTDFSTISSLOPEDFATYYC-----FGQGTKEIK 79  
Db 61 RFSGSGSGTDFTLTSSLOPEDFATYYCQSYSTSTWTFEGGTKEIK 107  
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Q9UL81 PRELIMINARY; PRT; 107 AA.  
AC Q9UL81  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Myosin-reactive immunoglobulin light chain variable region  
DE (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98277139; PubMed=9614934;  
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,  
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
RT fetus";  
RL Clin. Immunol. Immunopathol. 87:184-192 (1998).  
DR EMBL; AF035033; AAD56269.1; -  
DR HSSP; P01607; 1REI.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_V.  
DR Pfam; PF00047; IG; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS0835; IG\_LIKE; 1.  
DR NON\_TER 1  
FT NON\_TER 107  
SQ SEQUENCE 107 AA; 11501 MW; 070549FDE0754748 CRC64;  
Query Match 74.4%; Score 309.5; DB 4; Length 107;  
Best Local Similarity 63.2%; Pred. No. 3.4e-29;  
Matches 67; Conservative 6; Mismatches 6; Indels 27; Gaps 4;  
QY 1 DIQWTSPPSLASVSGDRVTTCRASQSISSYLNWYQKPKAPNLLIYAASSLSQGVPS 41  
Db 1 DIQWTSPPSLASVSGDRVTTCRASQSISSYLNWYQKPKAPNLLIYAASSLSQGVPS 60  
QY 42 RFSGSGSGTDFSTISSLOPEDFATYYC-----FGQGTKEIK 79  
Db 61 RFSGSGSGTDFTLTSSLOPEDFATYYCQSYSTSTWTFEGGTKEIK 106  
RESULT 5  
Q9UL79

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Query Match          71.9%; Score 299; DB 11; Length 109;
Best Local Similarity 60.7%; Pred.No.6.2e-28;
Matches 65; Conservative

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DB      1 DIQTQPASLSASVGTEVTITCRAGNIHNYLAWYQQKGSKPQLLYNNAKTLDGVPS 60

QY      42 RFGSGSGTDFSTTISSLOPEFATYYC-----FCGQTKLEIK 79
DB      61 RFGSGSGTGYSLKINSLOPEDFGSYICQHFWSTPTWTGGGTKEIK 107

RESULT 7
QBVCFO  QBVCFO PRELIMINARY; PRT; 234 AA.
ID       Q8VCP0
AC       Q8VCP0;
DT       01-MAR-2002 (TrEMBLrel. 20, Created)
DI       01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DE       01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DS       Hypothetical 25.7 kDa protein.
OS       Mus musculus (Mouse).
OC       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC       Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN       [1]
RP       SEQUENCE FROM N.A.
RC       TISSUE=Colon;
RL       Strausberg R.;
RR       Submitted (DEC-2001) to the EMBL/GenBank/DDAJ databases.
DR       EMBL; BC019474; AAL19474.1; -.
DR       InterPro; IPR003006; IG_MHC.
DR       InterPro; IPR003596; IG_V.
DR       Pfam; PF00047; Ig; 2.
DR       SMART; SM00406; IGV; 1.
DR       PROSITE; PS00290; IG_MHC; 1.
KW       Hypothetical protein_
SQ       SEQUENCE 234 AA; 25702 MW; 102551C58AC2FA9F CRC64;

Query Match          70.4%; Score 293; DB 11; Length 234;
Best Local Similarity 59.8%; Pred.No.8.3e-27;
Matches 64; Conservative

QY      1 DIQTQPASLSASVSGDRVTITC-----WYLQKPGKSPQLIY-----GVPS 41
DB      21 DIQTQPASLSASVGTEVTITCRAGENISYLAWYQQKGSKPQLLYNNAKTLDGVPS 80

QY      42 RFGSGSGTDFSTTISSLOPEFATYYC-----FCGQTKLEIK 79
DB      81 RFGSRSGTGSLKINSLOPEDFGSYICQHSHGIPFTFGSGTKLEIK 127

RESULT 8
QBVCFO  QBVCFO PRELIMINARY; PRT; 298 AA.
ID       Q9QYF0
AC       Q9QYF0;
DT       01-WAY-2000 (TrEMBLrel. 13, Created)
DI       01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
DE       01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
DS       CN 8 scfV.
OS       Mus musculus (Mouse).
OC       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC       Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN       [1]
RP       SEQUENCE FROM N.A.
RC       STRAIN=Balb/c; TISSUE=Spleen;
RR       MEDLINE=20183931; PubMed=10706631;
RX       Shinozawa N., Demura T., Fukuda H.;
RT       "Isolation of a vascular cell wall-specific monoclonal antibody
RT       recognizing a cell polarity by using a phase display subtraction

```

```
RT method.":
RL Proc. Natl. Acad. Sci. U.S.A. 97:2585-2590 (2000).
DR ENBL; AB036411; BAA8633.1; -.
DR HSPF; P01607; IREI.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_2.
DR SMART; SM00406; IGV; 2.
DR PROSITE; PS50835; IG_LIKE; 2.
SQ SEQUENCE 298 AA; 31867 MW; E0F96B8A17004317 CRC64;

Query Match 70.4%; Score 293; DB 11; Length 298;
Best Local Similarity 58.9%; Pred. No. 1.1e-26;
Matches 63; Conservative 7; Mismatches 9; Indels 28; Gaps 3;

QY 1 DIQWTQSPASLSASVGRVTITC-----WYLOKPGKSPQLIY-----GVPS 41
DB 173 DIETQSPASLSASVGRVTITCRASGNHYNLYAWYQKQKSPQLVYNKTLADGVPS 232
QY 42 RFGSGSGTDFSTFISSLPQEDFATYYC-----FGQGTKLEIK 79
DB 233 RFGSGSGTQSLKINSLOPEDRGSYYCQHFWTPTPTFGGKTKLEIK 279

RESULT 9
Q96PF6 PRELIMINARY; PRT; 116 AA.
AC Q96PF6; 2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Kappa 1 light chain variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN 1
SQ SEQUENCE 116 AA; 12735 MW; E796FC2217BFCF57 CRC64;

Query Match 69.0%; Score 287; DB 4; Length 116;
Best Local Similarity 57.9%; Pred. No. 1.8e-26;
Matches 62; Conservative 9; Mismatches 8; Indels 28; Gaps 4;

QY 1 DIQWTQSPASLSASVGRVTITC-----WYLOKPGKSPQLIY-----GVPS 41
DB 1 DIQWTQSPSSLSASVGRVTITCQASQDIANHLNWKYQKPGKFLIYDGSFLKTVPS 60
QY 42 RFGSGSGTDFSTFISSLPQEDFATYYC-----FGQGTKLEIK 79
DB 61 RFGSGGSATNFTVTISSLQPEDFATYYCQVHHLPTFTFGPKTVDFK 107

RESULT 10
Q921A6 PRELIMINARY; PRT; 241 AA.
AC Q921A6; 2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Anti-CEA 79 single chain Fv fragment (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN 1
SQ SEQUENCE 241 AA; 26086 MW; 0276887248B9C771 CRC64;

Query Match 67.4%; Score 280.5; DB 11; Length 241;
Best Local Similarity 55.7%; Pred. No. 2.6e-25;
Matches 59; Conservative 12; Mismatches 8; Indels 27; Gaps 4;

QY 1 DIQWTQSPASLSASVGRVTITC-----WYLOKPGKSPQLIY-----GVPS 41
DB 134 DIETQSPSSLSASLGKVVITTCASQDINKYAWYQKPGKSPSAHTLHYIQGPS 193
QY 42 RFGSGSGTDFSTFISSLPQEDFATYYC-----FGQGTKLEIK 79
DB 194 RFGSGSGRDYFSISNLEPEDIATYCYLHYDNLHTFGGKTKLEIK 239

RESULT 11
Q91WS9 PRELIMINARY; PRT; 233 AA.
AC Q91WS9; 2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical 25.8 kDa protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN 1
SQ SEQUENCE 233 AA; 25781 MW; B1C184DA149A16EB CRC64;

Query Match 67.3%; Score 280; DB 11; Length 233;
Best Local Similarity 58.9%; Pred. No. 2.9e-25;
```



Tue Jan 13 13:22:02 2004

DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
DE Hypothetical 25.9 kDa protein.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Colon;  
RA Strausberg R.;  
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL: BC015292; AH15292.1; -.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_v.  
DR InterPro; IPR001865; Ribosomal\_S2.  
DR Pfam; PF00047; IG; 2.  
DR SMART; SMO0406; IGV; 1.  
DR PROSITE; PS00290; IG\_MHC; 1.  
DR PROSITE; PS00962; RIBOSOMAL\_S2\_1; 1.  
KW Hypothetical protein.  
SQ SEQUENCE 234 AA; 25929 MW; B0D0B0E6EB7812D2 CRC64;  
  
Query Match 64.7%; Score 269; DB 11; Length 234;  
Best Local Similarity 56.1%; Pred. No. 6e-24;  
Matches 60; Conservative 9; Mismatches 10; Indels 28; Gaps 4;  
  
Qy 1 DIQWTQSPASLSASVGRVITC-----WYLOKP-GKSPOLIY-----GVPS 41  
Db 21 DIQWTQTSLSASLSGRVITC-----WYLOKP-GKSPOLIY-----GVPS 41  
  
Qy 42 RFGSGSGTDYSLTISNLEQSDIATYFCQQQNTPTPTFGSGTKLVK 79  
Db 81 RFGSGSGTDYSLTISNLEQSDIATYFCQQQNTPTPTFGSGTKLVK 127

Search completed: January 13, 2004, 12:43:05  
Job time : 17.1441 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 13, 2004, 12:18:44 ; Search time 18.4218 Seconds  
(without alignments)  
680.681 Million cell updates/sec

Title: US-09-990-586-79

Perfect score: 416

Sequence: 1 DIQMTSPASLSASVGRVT.....QPEDPATYTCFGQGYLEIK 79

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- A\_Geneseq\_19Jun03:\*
- 1: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:\*
  - 2: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:\*
  - 3: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:\*
  - 4: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:\*
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  - 7: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:\*
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  - 9: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:\*
  - 10: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1989.DAT:\*
  - 11: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1990.DAT:\*
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  - 13: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:\*
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  - 19: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:\*
  - 20: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:\*
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  - 23: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:\*
  - 24: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	376.5	90.5	80	ABG74720	Murine humanised M
2	337.5	81.1	110	AAW76130	Human ICR-1.1 V-K
3	337.5	81.1	110	AAW71260	Humanised murine a
4	337.5	81.1	110	AAW00786	Antibody against I
5	337.5	81.1	110	AAW81454	Humanised antibody
6	337.5	81.1	110	AAW13050	Humanised ICR-1.1
7	337.5	81.1	110	AAW32449	Humanised ICR-1.1
8	337.5	81.1	110	AAW50757	Humanised murine a
9	337.5	81.1	110	AAW70942	Humanised monoclon

10	335.5	80.6	126	21	AAW77599	Anti-human VEGF re
11	335.5	80.6	126	22	AAW78868	Anti-human Flt-1 a
12	335	80.5	110	13	AAW30147	431/26 VK hum. Sy
13	335	80.5	111	15	AAW47935	Humanised light ch
14	335	80.5	111	20	AAW89351	Humanised 23F2G 11
15	335	80.5	213	17	AAW04301	Antibody fusion pr
16	335	80.5	909	15	AAW50092	Humanised anti-CEA
17	334.5	80.4	107	15	AAW47222	Antibody light cha
18	334.5	80.4	107	18	AAW41397	Anti-CEA antibody
19	334.5	80.4	107	18	AAW41390	Anti-CEA antibody
20	334.5	80.4	107	24	ABP96012	HSA antibody relat
21	334.5	80.4	108	22	AAE12062	Human anti-tissue
22	334.5	80.4	125	16	AAW67656	Anti-human IL-6 ch
23	334.5	80.4	126	16	AAW89479	Anti-human IL-4 hu
24	334.5	80.4	128	21	AAW77597	Anti-human VEGF re
25	334.5	80.4	128	21	AAW78866	Anti-human Flt-1 a
26	334.5	80.4	212	23	AAU72815	DNA encoding TRA-8
27	334.5	80.4	232	16	AAW80616	Anti-human IL-4 hu
28	334.5	80.4	235	18	AAW41398	Humanised antibody
29	334.5	80.4	235	18	AAW41411	Humanised light ch
30	334.5	80.4	241	20	AAW21882	Amino acid sequenc
31	334	80.3	107	12	AAW11987	Human anti-placenta
32	334	80.3	107	15	AAW55125	Mouse-human chimera
33	334	80.3	107	15	AAW60304	Chimeric anti HIV
34	334	80.3	107	19	AAW86804	Variable Light dom
35	334	80.3	107	19	AAW70623	Humanised murine a
36	334	80.3	107	20	AAW87455	Humanised anti-ALP
37	334	80.3	107	22	AAW62085	Humanised Fab vers
38	334	80.3	107	22	AAW62087	Human VI consensus
39	334	80.3	107	22	AAW60398	Humanised anti-Erb
40	334	80.3	107	22	AAW60400	Consensus human 11
41	334	80.3	107	22	AAW61583	Humanised Fab vers
42	334	80.3	107	22	AAW61585	Human variable lig
43	334	80.3	107	23	ABP61192	Humanised anti-VEG
44	334	80.3	107	24	ABW18721	Antibody library r
45	334	80.3	108	13	AAW70618	Anti-VEGF humanise

ALIGNMENTS

RESULT 1  
ABG74720  
ID ABG74720 standard; Protein; 80 AA.  
XX  
XX ABG74720;  
XX  
XX  
DT 10-MAY-2003 (first entry)  
DE Murine humanised Mu007-associated protein L1.

XX Murine; light chain; variable region; antibody; Crohn's disease;  
XX human interleukin (IL)-1beta; anti-rheumatic; antiarthritic; humanised;  
XX antinflammatory; osteopathic; antiallergic; cerebroprotective;  
XX antiaschmatic; immunosuppressive; antibacterial; vaccine; Mu007;  
XX rheumatoid arthritis; osteoarthritis; cartilage destruction;  
XX allergy; septic shock; endotoxic shock; septicemia; stroke; asthma;  
XX graft versus host disease; inflammatory bowel disease; LI.

OS Unidentified.  
XX  
XX WO2003010282-A2.  
PN  
XX  
XX 06-FEB-2003.

XX 18-JUL-2002; 2002WO-US21281.  
XX  
XX 26-JUL-2001; 2001US-307973P.  
PR  
XX 14-AUG-2001; 2001US-312278P.  
XX  
XX (ELIL) LILLY & CO ELI.  
PA  
XX Bright SW, Jia AY, Kuhstoss SA, Manetta JV, Teurushita N;  
PI



PI Vasquez MJ;  
 XX WPI; 2003-248068/24.  
 XX  
 XX New IL-beta antibodies, useful for treating allergy, septic or  
 PT endotoxic shock, septicemia, stroke, asthma, graft versus host disease,  
 PT Crohn's disease, or inflammatory bowel disease -  
 XX  
 PS Disclosure; Fig 1; 98pp; English.  
 XX  
 XX This invention describes a novel antibody that specifically binds mature  
 CC human interleukin (IL)-beta, and binds the same epitope on mature human  
 CC IL-beta as mouse monoclonal antibody Mu007 or humanized antibody Hu007.  
 CC The antibody of the invention have antirheumatic, antiarthritic,  
 CC antiinflammatory, osteopathic, anti-allergic, cerebroprotective,  
 CC antitubercular, immunosuppressive and antibacterial activity and can be  
 CC used in a vaccine. The antibody is useful for manufacturing a medicament  
 CC for treating rheumatoid arthritis or osteoarthritis, or for inhibiting  
 CC cartilage destruction in a subject. The antibody is also useful for  
 CC treating allergy, septic or endotoxic shock, septicemia, stroke, asthma,  
 CC graft versus host disease, Crohn's disease, or inflammatory bowel  
 CC disease. This sequence represents a protein associated with the  
 CC humanised murine Mu007 antibody described in the disclosure of the  
 CC invention.  
 XX  
 SQ Sequence 80 AA;  
 Query Match 90.5%; Score 376.5; DB 24; Length 80;  
 Best Local Similarity 90.0%; Pred. No. 6.8e-27;  
 Matches 72; Conservative 5; Mismatches 2; Indels 1; Gaps 1;  
 QY 1 DIQMTQSPASLSASVGRVTITCWYLQPKSPQ-LIYGVPRFSGSGGDTFSTISL 59  
 DB 1 DIQMTQSPASLSASVGRVTITCWYQPKSPQKAPKSLIYGVPRFSGSGGDTFSTISL 60  
 QY 60 QPEDFATYYCFGGTKLEIK 79  
 DB 61 QPEDFATYYCFGGTKLEIK 80  
 RESULT 2  
 AAW76130  
 ID AAW76130 standard; Protein; 110 AA.  
 AC AAW76130;  
 DT 20-NOV-1998 (first entry)  
 XX Human ICR-1.1 V-K region PCR product protein.  
 XX  
 XX Interleukin adhesion molecule; human; ICAM-R; modulator; 14.3.3 family;  
 KW HSI-beta; tubulin; inhibitor; stimulator; effector; immune response;  
 KW inflammation; disorder; T cell activation; macrophage; Crohn's disease;  
 KW adult respiratory distress syndrome; stroke; multiple sclerosis; asthma;  
 KW rheumatoid arthritis; tumour growth; human immune deficiency virus;  
 KW infection; diabetes; graft vs. host disease; passive immunisation.  
 XX  
 OS Homo sapiens.  
 XX  
 XX US5773218-A.  
 XX  
 XX 30-JUN-1998.  
 XX  
 XX 07-JUN-1995; 95US-0482882.  
 XX  
 XX 05-AUG-1994; 94US-0286754.  
 XX  
 XX 27-JAN-1992; 92US-0827689.  
 XX  
 XX 26-MAY-1992; 92US-0889724.  
 XX  
 XX 05-JUN-1992; 92US-0894061.  
 XX  
 XX 22-JAN-1993; 93US-0009266.  
 XX  
 XX 26-JAN-1993; 93WO-US000787.  
 XX  
 XX 05-AUG-1993; 93US-0102852.  
 XX  
 XX 07-JUN-1995; 95US-0482882.

XX  
 PA (ICOS-) ICOS CORP.  
 XX Gallatin WM, Vazeux R;  
 PI  
 XX  
 DR WPI; 1998-386989/33.  
 DR N-PSDB; AAV56428.  
 XX  
 PT Identifying compounds that modulate interaction of intercellular  
 PT adhesion molecule R - with ligands HSI-beta and tubulin using  
 PT two-hybrid assay, useful for treating inflammation, T cell  
 PT activation etc.  
 XX  
 PS Example 13; Column 135-136; 108pp; English.  
 XX  
 XX This sequence represents a human ICR-1.1 V-K region amplified PCR  
 CC product. This sequence is used in the isolation of a novel human  
 CC intercellular adhesion molecule, ICAM-R. This sequence is used in a  
 CC method which investigates modulators of the interaction between ICAM-R  
 CC and the 14.3.3 family member HSI-beta and tubulin. An anti-ICAM-R  
 CC antibody optionally coupled to toxin or radionuclide, or an ICAM-R  
 CC peptide, can block, inhibit or stimulate ligand/receptor interactions  
 CC involving ICAM-R, particularly its effector functions involved in  
 CC (non)specific immune responses. ICAM-R related agents may be used to  
 CC treat or monitor inflammation, disorders involving T cell activation or  
 CC macrophages, e.g. adult respiratory distress syndrome, stroke, Crohn's  
 CC disease, multiple sclerosis, rheumatoid arthritis, asthma, tumour growth,  
 CC human immune deficiency virus infection, diabetes, graft vs. host disease  
 CC and many others. Antibodies may also be used for passive immunisation,  
 CC for purifying, detecting or quantifying ICAM-R and for identifying  
 CC ICAM-R expressing cells.  
 XX  
 SQ Sequence 110 AA;  
 Query Match 81.1%; Score 337.5; DB 19; Length 110;  
 Best Local Similarity 88.9%; Pred. No. 3e-23;  
 Matches 73; Conservative 4; Mismatches 2; Indels 27; Gaps 4;  
 QY 1 DIQMTQSPASLSASVGRVTITC-----WYLQPKSPQ-LIY-----GVPSR 42  
 DB 5 DIQMTQSPSSLSASVGRVTITCSASSSVSYIYVQKPKAPKLLIYLTSLASGVPSR 64  
 QY 43 FSGSGSGTDFSTISLQPEDFATYYC-----FGGQTKLEIK 79  
 DB 65 FSGSGSGTDFLTITSLQPEDFATYYCQOWKSIPLTFGGQTKLEIK 110  
 RESULT 3  
 AAW71260  
 ID AAW71260 standard; Protein; 110 AA.  
 XX  
 XX AAW71260;  
 XX  
 XX 25-MAR-2003 (updated)  
 DT 18-NOV-1998 (first entry)  
 XX  
 XX Humanised murine antibody ICR-1.1 light chain amino acid sequence.  
 XX  
 XX Human; ICAM-R; intercellular adhesion molecule; adhesion; treatment;  
 KW inflammatory condition; asthma; tumour growth; metastasis;  
 KW vital infection; antibody ICR-1.1.  
 XX  
 OS Synthetic.  
 OS Mus sp.  
 OS Homo sapiens.  
 XX  
 XX US5811517-A.  
 XX  
 XX 22-SEP-1998.  
 XX  
 XX 07-JUN-1995; 95US-0483389.  
 XX  
 XX 05-AUG-1994; 94US-0286754.

PR 26-JAN-1993; 93WO-US00787.  
 PR 27-JAN-1992; 92US-0827689.  
 PR 28-MAY-1992; 92US-0899724.  
 PR 05-JUN-1992; 92US-0894061.  
 PR 22-JAN-1993; 93US-0009266.  
 PR 05-AUG-1993; 93US-0102852.  
 XX XX  
 PA (ICOS-) ICOS CORP.  
 XX XX  
 FI Gallatin WM, Vazeux R;  
 XX XX  
 DR WPI; 1998-530940/45.  
 DR N-PSDB; AAV54866.

XX XX  
 PT DNA encoding mutant ICAM-R polypeptide(s) - useful for diagnosis  
 PT and treatment of cell adhesion based disease conditions e.g.  
 PT inflammation or asthma

XX XX  
 PS Example 13; Columns 135-136; 111pp; English.

XX XX  
 CC The present sequence represents the humanised light chain of murine  
 CC antibody ICR-1.1. This antibody is specific for ICAM-R (intercellular  
 CC adhesion molecule-R). ICAMs are polypeptides that are expressed on blood  
 CC vessel endothelial cell surfaces and are involved in the adhesion events  
 CC in various conditions. ICAM-R variants (see AAW71264-65) can be used to  
 CC treat or monitor inflammatory conditions involving specific or  
 CC nonspecific immune responses, asthma, tumour growth and/or metastasis  
 CC and viral infections. The ICAM variants are produced recombinantly, from  
 CC expression libraries of mutated sequences, and the ones that are  
 CC claimed are the ones that have been found to be especially involved in  
 CC adhesion events. They can also be used to raise antibodies, also for  
 CC use as therapeutic or diagnostic agents.  
 CC (Updated on 25-MAR-2003 to correct PR field.)

XX XX  
 SQ Sequence 110 AA;

Query Match 81.1%; Score 337.5; DB 19; Length 110;  
 Best Local Similarity 68.9%; Pred. No. 3e-23; Indels 27; Gaps 4;  
 Matches 73; Conservative 4; Mismatches 2

QY 1 DIQMTQSPASLSASVGRVITTC-----WYLOKPKSPQ-LIY-----GVPSR 42  
 DB 5 DIQMTQSPSSLSASVGRVITTCASSSVSYIYWKQKPGKAPKLLIYLTSLASGVPSR 64  
 QY 43 FSGSGSGTDFSTSSLOPEDFATYYC-----FCQGTKLEIK 79  
 DB 65 FSGSGSGTDFLTITSSLOPEDFATYYCQWKSIPLTFQGTKLEIK 110

RESULT 4

AAAY00786  
 ID AAY00786 standard; Protein; 110 AA.

XX XX  
 AC AAY00786;

XX XX  
 DT 14-MAY-1999 (first entry)

XX XX  
 DE Antibody against ICAM-R.

XX XX  
 KW ICAM; immunoglobulin-like loop; intercellular adhesion molecule receptor;  
 KW alpha d/CD18; antibody; immunisation; inflammatory response; asthma;  
 KW tumour growth; viral infection; therapy.

XX OS Mus sp.

XX XX US5980268-A.

XX XX 09-MAR-1999.

XX XX 07-JUN-1995; 95US-0483932.

XX XX 05-AUG-1994; 94US-0286754.

PR 27-JAN-1992; 92US-0827689.

PR 26-MAY-1992; 92US-0889724.  
 PR 05-JUN-1992; 92US-0894061.  
 PR 22-JAN-1993; 93US-0009266.  
 PR 26-JAN-1993; 93WO-US00787.  
 PR 05-AUG-1993; 93US-0102852.  
 PR 07-JUN-1995; 95US-0483932.  
 XX XX

XX PA (ICOS-) ICOS CORP.

XX XX Gallatin WM, Vazeux R;

XX XX WPI; 1999-204041/17.

DR N-PSDB; AAX21883.

XX XX  
 PT New intercellular adhesion molecule receptor (ICAM-R) specific  
 PT antibodies - useful for modulating ligand/receptor binding and  
 PT biological activities involving ICAM-R, especially those of the  
 PT specific and non-specific immune systems

XX PS Example 13; Column 135-136; 108pp; English.

XX XX  
 CC This sequence represents an antibody specific for ICAM-R.  
 CC The invention relates to antibodies (Ab) which bind specifically  
 CC to the intercellular adhesion molecule receptor (ICAM-R), inhibiting the  
 CC interaction between ICAM-R and alpha d/CD18. Abs with specific ICAM-R  
 CC binding are useful in compositions for immunisation, and for purifying  
 CC ICAM-R polypeptides and identifying cells expressing ICAM-R on their cell  
 CC surface, modulating ligand/receptor binding and biological activities  
 CC involving ICAM-R, especially inflammatory responses of the specific  
 CC immune system, the non-specific immune system, monitoring and treating  
 CC asthma, tumour growth, and/or metastasis, and viral infection (e.g. HIV  
 CC infection). In particular diseases involving an essential T cell  
 CC activation (e.g. asthma, psoriasis, diabetes, graft vs. host disease,  
 CC tissue transplant rejection, and multiple sclerosis) may be treated with  
 CC anti-ICAM-R antibodies. The Abs specifically bind to and identify ICAM-R  
 CC and disrupt ICAM-R to cell adhesion molecule, especially alpha d/CD18  
 CC binding.

XX XX  
 SQ Sequence 110 AA;

Query Match 81.1%; Score 337.5; DB 20; Length 110;  
 Best Local Similarity 68.9%; Pred. No. 3e-23; Indels 27; Gaps 4;  
 Matches 73; Conservative 4; Mismatches 2

QY 1 DIQMTQSPASLSASVGRVITTC-----WYLOKPKSPQ-LIY-----GVPSR 42  
 DB 5 DIQMTQSPSSLSASVGRVITTCASSSVSYIYWKQKPGKAPKLLIYLTSLASGVPSR 64  
 QY 43 FSGSGSGTDFSTSSLOPEDFATYYC-----FCQGTKLEIK 79  
 DB 65 FSGSGSGTDFLTITSSLOPEDFATYYCQWKSIPLTFQGTKLEIK 110

RESULT 5

AAW81454

ID AAW81454 standard; Protein; 110 AA.

XX XX  
 AC AAW81454;

XX XX  
 DT 17-FEB-1999 (first entry)

XX XX Humanised antibody ICR-1.1 V $\kappa$  region (HuVK).

XX XX  
 KW Intercellular adhesion molecule polypeptide; ICAM-R; humanised; ICR-1.1;  
 KW ICR-8.1; monoclonal antibody; therapeutic; inflammatory; asthma; tumour;  
 KW graft-versus-host disease; viral infection; toxin; radionuclide;  
 KW neovascularisation site.

XX OS Mus sp.

XX OS Homo sapiens.

XX XX US5837822-A.

PD 17-NOV-1998. 95US-0487113.  
XX 07-JUN-1995; 95US-0487113.  
XX 07-JUN-1995; 95US-0487113.  
PR 27-JAN-1992; 92US-0827689.  
PR 26-MAY-1992; 92US-0889724.  
PR 05-JUN-1992; 92US-0894061.  
PR 22-JAN-1993; 93US-0009266.  
PR 26-JAN-1993; 93US-0009266.  
PR 03-AUG-1993; 93US-0102852.  
XX (ICOS-) ICOS CORP.  
XX Gallatin WM, Vazeux R;  
PI WPI; 1999-023535/02.  
XX N-PSDB; AAV69196.  
XX Humanised antibodies specific for intercellular adhesion molecule  
PT polypeptide - useful for therapeutic or diagnostic purposes  
XX  
XX Example 13; Columns 145-148; 116pp; English.  
XX The invention relates to humanised ICR-1.1 and ICR-8.1 antibodies  
CC targeted to the human intercellular adhesion molecule polypeptide  
CC (ICAM-R) polypeptide. Antibodies specific for ICAM-R's are potentially  
CC useful as therapeutic compounds, for treating e.g. immune-mediated  
CC inflammatory conditions (e.g. graft-versus-host disease), asthma,  
CC tumours or viral infections. Monoclonal antibodies specific for ICAM-R,  
CC or their conjugates formed with e.g. toxins or radionuclides are useful  
CC for therapeutically targeting or detecting neovascularisation sites.  
CC The present sequence represents the amino acid sequence of the V $\kappa$  region  
CC of the humanised antibody ICR-1.1.  
XX  
XX Sequence 110 AA;  
SQ  
Query Match 81.1%; Score 337.5; DB 20; Length 110;  
Best Local Similarity 68.9%; Pred. No. 3e-23;  
Matches 73; Conservative 4; Mismatches 2; Indels 27; Gaps 4;  
Qy 1 DIQMTQSPASLSASVGRVITTC-----WYLOKPGKSPQ-LIY-----GVPSR 42  
Db 5 DIQMTQSPSSLSASVGRVITTCSSASSSVSYIYQKPKGKAPKLLIYLTSLNLSGVPSR 64  
Qy 43 FSGSGSGTDFPSFTISSLPQDFATYYC-----FGQGTKLEIK 79  
Db 65 FSGSGSGTDFTLTISSLPQDFATYYCQQWKSIPLTFGQGTKLEIK 110  
RESULT 6  
AAB13050  
ID AAB13050 standard; Protein; 110 AA.  
XX AC AAB13050;  
XX 19-DEC-2000 (first entry)  
XX Humanised ICR-1.1 V $\kappa$  protein sequence.  
XX Anti-human immunodeficiency virus; HIV; cytostatic; ICAM-R; ARDS; stroke;  
XX intercellular adhesion molecule; immunoglobulin heavy chain; septicemia;  
XX inflammatory conditions; glomerulonephritis; arthritis; dermatosis;  
XX haemodialysis; leukapheresis; ulcerative colitis; Crohn's disease;  
XX necrotising enterocolitis; atherosclerosis; psoriasis; asthma;  
XX transplant rejection; diabetes; tumour.  
XX Synthetic.  
XX OS US6100383-A.  
XX FN 08-AUG-2000.  
XX PD 08-AUG-2000.  
XX

PF 07-JUN-1995; 95US-0475680.  
XX 05-AUG-1994; 94US-0286754.  
PR 26-JAN-1993; 93WO-US00787.  
PR 27-JAN-1992; 92US-0827689.  
PR 26-MAY-1992; 92US-0889724.  
PR 05-JUN-1992; 92US-0894061.  
PR 22-JAN-1993; 93US-0009266.  
PR 05-AUG-1993; 93US-0102852.  
XX (ICOS-) ICOS CORP.  
XX Gallatin WM, Vazeux R;  
PI WPI; 2000-542449/49.  
XX N-PSDB; AAA97170.  
XX Hybrid fusion proteins comprising intercellular adhesion molecule or  
PT its variants useful, for treating inflammatory conditions, Crohn's  
PT disease, atherosclerosis and diabetes -  
XX  
XX Example 13; Column 135-138; 109pp; English.  
XX This invention relates to a hybrid fusion protein comprising an  
CC intercellular adhesion molecule (ICAM-R) amino acid fragment at its  
CC amino terminus and a constant domain of an immunoglobulin heavy chain at  
CC its carboxy terminus. ICAM-R polypeptides are useful for treating and  
CC monitoring inflammatory conditions such as adult respiratory distress  
CC syndrome, multiple organ injury syndrome secondary to septicemia or  
CC trauma, reperfusion injury of tissue, acute glomerulonephritis, reactive  
CC arthritis, dermatosis, stroke, thermal injury, haemodialysis,  
CC leukapheresis, ulcerative colitis, Crohn's disease, necrotising  
CC enterocolitis, granulocyte transfusion associated syndrome,  
CC atherosclerosis and cytokine induced toxicity. ICAM-R polypeptides are  
CC also useful for treating conditions resulting from a response of the  
CC specific immune system in a mammal e.g. psoriasis, organ/tissue  
CC transplant rejection and autoimmune diseases including Raynaud's  
CC syndrome, autoimmune thyroiditis, multiple sclerosis, rheumatoid  
CC arthritis, diabetes and lupus erythematosus. ICAM-R products and ICAM-R  
CC related products are also useful in monitoring and treating asthma,  
CC tumour growth and/or metastasis, and viral infection (e.g. HIV  
CC infection). Sequences AAA97090 and AAB13036 represent the human ICAM-R  
CC DNA and protein sequences. Sequences AAA97091-A97112 represent ICAM-R  
CC DNA fragments, PCR primers and probes, all used in the identification of  
CC the ICAM-R DNA sequence. AAA97113-A97123 and AAA97129-A97152 represent  
CC primers used in the production of humanised anti-ICAM-R antibody ICR-8.1,  
CC and fragments of the humanised antibody. Sequences AAA97124-A97128,  
CC AAA97132, AAA97144 represent ICR-8.1 sequences. Sequences AAA97153-A97176  
CC excluding AAA97155-A97156 represent primers used in the production of  
CC humanised anti-ICAM-R antibody ICR-1.1, and fragments of the humanised  
CC antibody. Sequences AAA97155-A97156 and AAB13047-B13048 represent murine  
CC ICR-1.1 sequences. DNA and peptide sequences used in the production of  
CC the chimeric protein of the invention include AAA97177-A97188 and  
CC AAB13050-B13051.  
XX  
XX Sequence 110 AA;  
SQ  
Query Match 81.1%; Score 337.5; DB 21; Length 110;  
Best Local Similarity 68.9%; Pred. No. 3e-23;  
Matches 73; Conservative 4; Mismatches 2; Indels 27; Gaps 4;  
Qy 1 DIQMTQSPASLSASVGRVITTC-----WYLOKPGKSPQ-LIY-----GVPSR 42  
Db 5 DIQMTQSPSSLSASVGRVITTCSSASSSVSYIYQKPKGKAPKLLIYLTSLNLSGVPSR 64  
Qy 43 FSGSGSGTDFPSFTISSLPQDFATYYC-----FGQGTKLEIK 79  
Db 65 FSGSGSGTDFTLTISSLPQDFATYYCQQWKSIPLTFGQGTKLEIK 110  
RESULT 7  
AAY82449  
ID AAY82449 standard; Protein; 110 AA.

XX AC AAY82449;  
 XX DT 28-JUN-2000 (first entry)  
 XX DE Humanised ICR-1.1 antibody HuVK protein sequence SEQ ID NO:96.  
 XX DE Human; ICAM-R; chromosome 19; intracellular adhesion molecule receptor;  
 XX KW CAM; ICAM-1; ICAM-2; humanised; antibody; mutagenic; chimeric; vulnary;  
 XX KW nephropathic; antiarthritis; cerebroprotective; antitumor; cytosaric;  
 XX KW antiarteriosclerotic; immunosuppressive; antidiabetic; neuroprotective;  
 XX KW antihypertensive; dermatological; antiasmatic; antiviral; antinflammatory;  
 XX KW anti-HIV; vasotropic; antipsoriatic; immunomodulator; antirheumatic;  
 XX KW cell adhesion mediator; inflammatory condition; immunisation;  
 XX KW immune response.  
 XX OS Mus sp.  
 XX OS Homo sapiens.  
 XX PN US6040176-A.  
 XX PD 21-MAR-2000.  
 XX PF 12-SEP-1996; 96US-0714017.  
 XX PR 05-AUG-1994; 94US-0286754.  
 XX PR 27-JAN-1992; 92US-0827689.  
 XX PR 26-MAY-1992; 92US-0889724.  
 XX PR 05-JUN-1992; 92US-0894061.  
 XX PR 22-JAN-1993; 93US-0009266.  
 XX PR 26-JAN-1993; 93WO-US00787.  
 XX PR 05-AUG-1993; 93US-0102852.  
 XX PF (ICOS-) ICOS CORP.  
 XX PI Gallatin WM, Vazeux R;  
 XX DR WPI; 2000-270138/23.  
 XX PT Novel monoclonal antibody directed against ICAM-R proteins useful for  
 XX PT treating acute glomerulonephritis, ulcerative colitis, psoriasis,  
 XX PT rheumatoid arthritis, diabetes, multiple sclerosis, asthma and viral  
 XX PT infection -  
 XX PS Example 13; Column 151-153; 117pp; English.  
 XX CC The present invention describes a monoclonal antibody (MAB) (I),  
 XX CC produced by the hybridoma cell line 81K2F (ATCC HB 11692). Also described  
 XX CC are: (1) a hybridoma cell line 81K2F; and (2) a MAB (III), that competes  
 XX CC with (1) for binding to ICAM-R (intracellular adhesion molecule  
 XX CC receptor) (III). (II) mimics the activity of natural binding proteins  
 XX CC through which intercellular and intracellular activities of (III) are  
 XX CC modulated. (II) is also used for modulating the immune responses. (I) is  
 XX CC used for immunisation as well as for purifying (III). They are also  
 XX CC useful in modulating the ligand/receptor binding biological activity  
 XX CC involving (III) especially those effector functions of (III) involved in  
 XX CC specific and non-specific immune system responses. Inflammatory  
 XX CC conditions which may be treated or monitored with related products of  
 XX CC (III) include conditions resulting from a response of the non-specific  
 XX CC immune system in a mammal e.g. adult respiratory distress syndrome,  
 XX CC multiple organ injury syndrome secondary to septicemia or trauma,  
 XX CC reperfusion injury of tissue, acute glomerulonephritis, reactive  
 XX CC arthritis, stroke, ulcerative colitis and atherosclerosis, and conditions  
 XX CC resulting from a response of the specific immune system in a mammal, e.g.  
 XX CC psoriasis, organ/tissue transplantation rejection, autoimmune diseases  
 XX CC such as autoimmune thyroiditis, multiple sclerosis, rheumatoid arthritis,  
 XX CC diabetes and lupus erythematosus. AA08236 to AA08334, and AA82435 to  
 XX CC AA82451 represent sequences used in the exemplification of the present  
 XX CC invention.  
 XX SQ Sequence 110 AA;  
 XX Query Match 81.1%; Score 337.5; DB 21; Length 110;  
 XX Best Local Similarity 68.9%; Pred. No. 3e-23;  
 XX Matches 73; Conservative 4; Mismatches 2; Indels 27; Gaps 4;  
 XX QY 1 DIQMTQSPASLSASVGRVTITC-----WYLOKPGKSPQ-LIY-----GVPSR 42  
 XX DB 5 DIQMTQSPSSLSASVGRVTITCASSSVSVIYQYQKPGKAPKLLIYLTSLNLSGVPSR 64  
 XX QY 43 FSGSGSGTDFSTISSLPEDFATYYC-----FGQGTKLEIK 79  
 XX DB 65 FSGSGSGTDFLTITSSLPEDFATYYCQWKSIPLTFGQGTKLEIK 110  
 XX RESULT 8  
 XX AAY50757  
 XX ID AAY50757 standard; Protein; 110 AA.  
 XX AC AAY50757;  
 XX DT 16-FEB-2000 (first entry)  
 XX DE Humanised murine antibody ICR-1.1 VK protein.  
 XX KW ICAM-R; murine; intercellular adhesion molecule; phosphorylation;  
 XX KW protein kinase C; modulator; ICR-1.1; antibody.  
 XX OS Synthetic.  
 XX OS Mus sp.  
 XX OS Homo sapiens.  
 XX PN US5989843-A.  
 XX PD 23-NOV-1999.  
 XX PF 27-SEP-1996; 96US-0720420.  
 XX PR 27-JAN-1992; 92US-0827689.  
 XX PR 26-MAY-1992; 92US-0889724.  
 XX PR 05-JUN-1992; 92US-0894061.  
 XX PR 22-JAN-1993; 93US-0009266.  
 XX PR 26-JAN-1993; 93WO-US00787.  
 XX PR 05-AUG-1993; 93US-0102852.  
 XX PR 07-JUN-1995; 95US-0487113.  
 XX PF (ICOS-) ICOS CORP.  
 XX PI Gallatin WM, Vazeux R;  
 XX DR WPI; 2000-022778/02.  
 XX DR N-PSDB; AA224342.  
 XX PT Identifying modulators of protein kinase C phosphorylation of human  
 XX PT intercellular adhesion molecule polypeptide -  
 XX PS Example 14; Column 153-154; 122pp; English.  
 XX CC This invention describes a novel method for identifying a compound that  
 XX CC modulates phosphorylation of human intercellular adhesion molecule  
 XX CC polypeptide (ICAM-R) by protein kinase C isoform. The method comprises:  
 XX CC (a) exposing a purified peptide consisting of the cytoplasmic domain of  
 XX CC ICAM-R to protein kinase C isoform and labeled adenosine triphosphate in  
 XX CC the presence and absence of a test compound; (b) measuring labeled  
 XX CC phosphate transferred to the peptide; and (c) identifying a test compound  
 XX CC that affects transfer of the labeled phosphate as a modulator of the  
 XX CC method is useful for identifying compounds that modulate the  
 XX CC phosphorylation of human intercellular adhesion molecule polypeptide  
 XX CC which might form the basis for the development of therapeutic and  
 XX CC diagnostic agents. This sequence represents the humanised murine ICR-1.1  
 XX CC antibody VK region which is used in the method of the invention.  
 XX SQ Sequence 110 AA;  
 XX Query Match 81.1%; Score 337.5; DB 21; Length 110;  
 XX Best Local Similarity 68.9%; Pred. No. 3e-23;

Matches 73; Conservative 4; Mismatches 2; Indels 27; Gaps 4;

QY 1 DIQMTQSPASLSASVGRVTITC-----WYLOKPKSPQ-LIY-----GVPSR 42  
 DB 5 DIQMTQSPSLSASVGRVTITCSASSSVSYIYWYQCKPKAPKLLIYLTSLASGVPSR 64  
 QY 43 FSGSGSGTDFSTFISSLOPEDFATYYC-----FGQGTKLEIK 79  
 DB 65 FSGSGSGTDFTLTISSLQPEDFATYYCQWKSIPLTFGGGTKLEIK 110

RESULT 9  
 AAU70942  
 ID AAU70942 standard; Protein; 110 AA.  
 XX  
 AC AAU70942;  
 XX  
 DT 26-FEB-2002 (first entry)  
 XX  
 DE Humanised monoclonal antibody ICR-1.1 VK region.  
 XX  
 KW Human; intercellular adhesion molecule; ICAM; antiinflammatory; stroke;  
 KW antibacterial; vulnerrary; vasotrophic; nephrotropic; antiarthritic;  
 KW cerebroprotective; dermatological; antiulcer; immunosuppressive; tumour;  
 KW antipruritic; antiarteriosclerotic; neuroprotective; antithyroid;  
 KW virucide; antirheumatic; antidiabetic; antiaschmatic; cytostatic; asthma;  
 KW hybridoma cell line; ATCC HB 12190; inflammation; septicaemia; trauma;  
 KW adult respiratory distress syndrome; multiple organ injury syndrome;  
 KW tissue reperfusion injury; acute glomerulonephritis; arthritis; vaccine;  
 KW dermatosis; thermal injury; haemodialysis; leukopheresis; psoriasis;  
 KW Crohn's disease; ulcerative colitis; multiple sclerosis; infection.  
 XX  
 OS Synthetic.  
 XX  
 XX US2001029293-A1.  
 XX  
 XX 11-OCT-2001.  
 XX  
 XX 03-JAN-2001; 2001US-0753436.  
 XX  
 XX 24-AUG-1999; 99US-0382289.  
 XX 27-JAN-1992; 92US-0827689.  
 XX 26-MAY-1992; 92US-0889724.  
 XX 05-JUN-1992; 92US-0894061.  
 XX 22-JAN-1993; 93US-0009266.  
 XX 26-JAN-1993; 93WO-US00787.  
 XX 05-AUG-1993; 93US-0102852.  
 XX 07-JUN-1995; 95US-0487113.  
 XX  
 XX (ICOS-) ICOS CORP.  
 XX  
 XX Gallatin WM, Vazeux R;  
 XX  
 XX WPI; 2002-009992/01.  
 XX N-PSDB; ABK09359.  
 XX  
 XX Novel hybridoma cell line useful for producing monoclonal antibody for  
 XX treating inflammatory conditions, immune system disorders and  
 XX infectious diseases, is deposited under specified ATCC accession number  
 XX  
 XX  
 XX Page 83; Example 14; 126pp; English.  
 XX  
 XX The invention relates to a novel hybridoma cell line (I) ATCC HB 12190.  
 XX (I) is useful for producing an intercellular adhesion molecule (ICAM)  
 XX monoclonal antibody (II). (II) is useful for treating inflammatory  
 XX conditions including adult respiratory distress syndrome, multiple organ  
 XX injury syndrome secondary to septicemia or trauma, tissue reperfusion  
 XX injury, acute glomerulonephritis, reactive arthritis, dermatosis with  
 XX acute inflammatory components, stroke, thermal injury, haemodialysis,  
 XX leukopheresis, ulcerative colitis, Crohn's disease, necrotising  
 XX enterocolitis, granulocyte transfusion associated syndrome, diabetes,  
 XX atherosclerosis, cytokine-induced toxicity, psoriasis, organ/tissue

transplant rejection, autoimmune diseases including Raynaud's syndrome,  
 autoimmune thyroiditis, multiple sclerosis, rheumatoid arthritis,  
 lupus erythematosus, asthma, tumour growth and/or metastasis, viral  
 infection, tissue transplant rejection, graft versus host disease and  
 multiple sclerosis. (II) is also useful for immunisation, for purifying  
 ICAM-R polypeptides and for identifying cells that display the  
 polypeptides on their surfaces. AAU70928-AAU70946 represent ICAM  
 amino acid sequences of the invention.

XX Sequence 110 AA;

Query Match 81.1%; Score 337.5; DB 23; Length 110;  
 Best Local Similarity 68.9%; Pred. No. 3e-23;  
 Matches 73; Conservative 4; Mismatches 2; Indels 27; Gaps 4;  
 QY 1 DIQMTQSPASLSASVGRVTITC-----WYLOKPKSPQ-LIY-----GVPSR 42  
 DB 5 DIQMTQSPSLSASVGRVTITCSASSSVSYIYWYQCKPKAPKLLIYLTSLASGVPSR 64  
 QY 43 FSGSGSGTDFSTFISSLOPEDFATYYC-----FGQGTKLEIK 79  
 DB 65 FSGSGSGTDFTLTISSLQPEDFATYYCQWKSIPLTFGGGTKLEIK 110

# RESULT 10

AAU77599  
 ID AAU77599 standard; peptide; 126 AA.

XX  
 AC AAU77599;  
 XX

XX 08-MAY-2000 (first entry)  
 XX

XX Anti-human VEGF receptor Flt-1 antibody related peptide sequence #94.  
 XX

XX Antibody; human; vascular endothelial growth factor; VEGF receptor;  
 KW Flt-1; neovascularisation; cell proliferation; metastasis; tumour;  
 KW rheumatoid arthritis; retinopathy; psoriasis.  
 XX  
 OS Mus musculus.

XX  
 XX WO9960025-A1.  
 XX

XX 25-NOV-1999.  
 XX

XX 20-MAY-1999; 99WO-JP02661.  
 XX

XX 20-MAY-1998; 98JP-0139000.  
 XX

XX (KYOW ) KYOWA HAKKO KOGYO KK.  
 XX

XX Shitara K, Ito M, Kawada Y, Nakamura K;  
 XX

XX WPI; 2000-072431/06.  
 XX

XX N-PSDB; AAZ87771.  
 XX

XX Gene recombinant antibodies, useful for diagnosis and as remedies for  
 XX diseases due to abnormal neovascularization e.g. proliferation or  
 XX metastasis of solid tumor, rheumatoid arthritis, diabetic retinopathy  
 XX and psoriasis  
 XX  
 XX Claim 28; Page 202; 210pp; Japanese.  
 XX  
 XX The invention relates to a gene recombinant antibody that has specific  
 XX reaction with human vascular endothelial growth factor (VEGF) receptor  
 XX Flt-1. The antibodies are useful for diagnosis and as remedies for  
 XX diseases due to abnormal neovascularisation such as proliferation or  
 XX metastasis of solid tumor, arthritis in rheumatoid arthritis, diabetic  
 XX retinopathy, premature retinopathy and psoriasis.  
 XX  
 XX Sequence 126 AA;

XX Query Match 80.6%; Score 335.5; DB 21; Length 126;  
 XX Best Local Similarity 69.2%; Pred. No. 5.2e-23;

Matches 72; Conservative 5; Mismatches 2; Indels 25; Gaps 4;

QY 1 DIQMTQSPASLSASVGDRTVITC-----WYLPKPKSPQ-LIY-----GVPSR 42  
Db 23 DIQMTQSPSSLSASVGDRTVITCSASSSVSYMHYQKPGKAPKLLIYRTSNLASGVPSR 82  
QY 43 FSGSGSGTDFSTLTISSLOPEDFATYYC-----FGQGTKLEIK 79  
Db 83 FSGSGSGTDFLTITSSLOPEDFATYYCHQWSMYTFGQGTKVEIK 126

RESULT 11  
AAB78868  
ID AAB78868 standard; Protein; 126 AA.  
XX  
AC AAB78868;  
XX  
DT 20-APR-2001 (first entry)  
XX  
DE Anti-human Flt-1 antibody VL CDR protein sequence SEQ ID 90.  
XX  
KW Differentiation; monocyte; macrophage; haematopoietic stem cell; cancer;  
KW vascular endothelial growth factor; VEGF; Flt-1; inflammation; antibody;  
KW delayed hypersensitivity; malignant tumour; arteriosclerosis.  
XX  
OS Synthetic.  
XX  
FN WO200079275-A1.  
XX  
PD 28-DEC-2000.  
XX  
PF 16-JUN-2000; 2000WO-JP03957.  
XX  
PR 17-JUN-1999; 95JP-0171709.  
XX  
XX (KYOW ) KYOWA HAKKO KOGYO KK.  
XX  
PA Shitara K, Shibuya M;  
PI  
XX  
XX WPI; 2001-080847/09.  
DR N-PSDB; AAF70244.  
XX  
Substances binding to human vascular endothelial growth factor receptor  
Flt-1, used for diagnosis and treatment of inflammatory diseases,  
arteriosclerosis, cancer and delayed hypersensitivity -  
Example 3; Page 157; 164pp; Japanese.  
XX  
This invention relates to a reagent for detecting differentiation of  
monocytes and macrophages from haematopoietic stem cells, containing a  
substance which binds to human vascular endothelial growth factor (VEGF)  
receptor Flt-1. The invention also includes a method for diagnosing a  
disease in which the differentiation of monocytes and macrophages is  
implicated, using the reagent, and an agent for the treatment of diseases  
diagnosed using the method containing a substance which binds to Flt-1  
or a substance which inhibits the signal transduction of Flt-1. Diseases  
CC hypersensitivity, malignant tumours and arteriosclerosis.  
CC AAF70190 - AAF70244, AAF70251 and AAF70258 represent DNA sequences  
CC encoding anti-human Flt-1 monoclonal antibody fragments, and  
CC oligonucleotides used in the construction of the antibody. The monoclonal  
antibody is used in the reagent of the invention. PCR primers AAF70245 -  
CC AAF78870 (excluding AAF70251) are used in the isolation of the antibody  
CC DNA sequences. Protein sequences AAB78848 - AAB78870 represent fragments  
CC of the anti-human Flt-1 antibody.  
XX  
Sequence 126 AA;  
Query Match 80.6%; Score 335.5; DB 22; Length 126;  
Best Local Similarity 69.2%; Pred. No. 5.2e-23;  
Matches 72; Conservative 5; Mismatches 2; Indels 25; Gaps 4;

QY 1 DIQMTQSPASLSASVGDRTVITC-----WYLPKPKSPQ-LIY-----GVPSR 42

Db 23 DIQMTQSPSSLSASVGDRTVITCSASSSVSYMHYQKPGKAPKLLIYRTSNLASGVPSR 82  
QY 43 FSGSGSGTDFSTLTISSLOPEDFATYYC-----FGQGTKLEIK 79  
Db 83 FSGSGSGTDFLTITSSLOPEDFATYYCHQWSMYTFGQGTKVEIK 126

RESULT 12  
AAR30147  
ID AAR30147 standard; Protein; 110 AA.  
XX  
AC AAR30147;  
XX  
DT 25-MAR-2003 (updated)  
DT 11-FEB-1993 (first entry)  
XX  
DE 431/26 VK hum.  
XX  
KW VH; VK; huTUMAK-L-beta-Gluc; monoclonal antibody; tumour; linker;  
KW beta-glucuronidase; hinge; prodrug.  
XX  
OS Synthetic.  
XX  
FN EP501215-A2.  
XX  
PD 02-SEP-1992.  
XX  
PF 10-FEB-1992; 92EP-0102197.  
XX  
PR 28-FEB-1991; 91DE-4106389.  
XX  
XX (BEHW ) BEHRINGWERKE AG.  
XX (FARH ) HOECHST AG.  
XX  
PI Bosslet K, Czech J, Hoffman D, Kolar C, Sedlacek H;  
PI Seemann G, Hoffmann D;  
XX  
XX WPI; 1992-293718/36.  
DR N-PSDB; AAQ26758.  
XX  
Fusion protein for diagnosis and treatment - comprises humanised,  
tumour-specific monoclonal antibody (fragment), linker and  
beta-glucuronidase  
XX  
Disclosure; Page 19; 34pp; German.  
XX  
The 431/26 VH and VK antibody fragments represented in AAQ26757-58 are  
CC pref. for the prodn. of the fusion proteins of formula huTUMAK-L-beta-  
CC Gluc (I) (huTUMAK= humanised, tumour-specific monoclonal antibody, or  
CC its tumour-binding fragments); L= linker; beta-Gluc= human beta-  
CC glucuronidase). BetaGlc Linker 1 and betaGlc Linker 2  
CC oligonucleotides are given in AAQ26759-60. Hinge 1 and hinge 2b  
CC oligonucleotides are given in AAQ26761-62.  
CC (I) are used to activate prodrugs. The antibody component provides  
CC for specific targeting to tumours while the beta-Gluc component  
CC activates a suitable prodrug by cleavage of glucuronic acid. The  
CC combination of the prodrug and (I) is useful in tumour treatment or  
CC diagnosis.  
CC (Updated on 25-MAR-2003 to correct PN field.)  
CC (Updated on 25-MAR-2003 to correct PA field.)  
XX  
Sequence 110 AA;  
Query Match 80.5%; Score 335; DB 13; Length 110;  
Best Local Similarity 68.6%; Pred. No. 5.1e-23;  
Matches 72; Conservative 5; Mismatches 2; Indels 26; Gaps 4;

QY 1 DIQMTQSPASLSASVGDRTVITC-----WYLPKPKSPQ-LIY-----GVPSR 42  
Db 5 DIQMTQSPSSLSASVGDRTVITCSASSSVSYMHYQKPGKAPKLLIYRTSNLASGVPSR 64  
QY 43 FSGSGSGTDFSTLTISSLOPEDFATYYC-----FGQGTKLEIK 79

Db 65 FGSGSGTDTFTTISLQPEDATYYCHQWSSYPFGQGTKEIK 109

RESULT 13  
ID AAR47935 standard; Protein; 111 AA.  
AC AAR47935;  
XX  
DT 25-MAR-2003 (updated)  
DT 10-MAR-2003 (updated)  
DT 24-JUL-1994 (first entry)  
XX  
DE Humanised light chain region of 23F2G.  
XX  
KW Amplification; 23F2G; humanised antibody; heavy chain; light chain;  
KW hybridoma; inflammation; CD18; human leukocyte integrins; mab 60.3;  
KW monoclonal antibody; LFA-1; adhesion; migration; multiple  
KW sclerosis; MS.  
XX  
OS Mus sp.  
OS Synthetic.  
XX  
PN W09402175-A1.  
XX  
PD 03-FEB-1994.  
XX  
PF 16-JUL-1993; 93WO-US06734.  
XX  
PR 16-JUL-1992; 92US-0915068.  
PR 10-MAY-1993; 93US-0060899.  
XX  
PA (ICOS-) ICOS CORP.  
PA (UNIW ) UNIV WASHINGTON.  
XX  
PI Rose LM;  
XX  
DR WPI; 1994-048551/06.  
DR N-PSDB; AAQ55917.  
XX  
XX Antibodies immunologically reactive with the CD18 of human  
PT leukocyte integrins and/or competing with mab 60.3 for binding to  
PT human LFA-1 - for alleviating symptoms associated with  
PT inflammatory disease states  
XX  
PS Example 6; Page 45; 58pp; English.

XX Total RNA was isolated from the hybridoma cell line 23F2G and first  
CC strand cDNA was synthesised using the total RNA as a template. The  
CC first strand cDNA was used as a template for PCR to obtain double  
CC stranded DNA fragments encoding the variable regions of both the  
CC heavy and light chains of monoclonal antibody 23F2G. The sequence  
CC shown is a humanised form of the light chain variable region of MAb  
CC 23F2G. The humanised form of MAb 23F2G may be administered to  
CC alleviate symptoms associated with inflammatory disease states, esp.  
CC for the inhibition of inflammatory processes associated with  
CC multiple sclerosis. The MAb blocks leukocyte adhesion and  
CC migration to inflammatory sites. The MAb is an anti-CD18 integrin  
CC antibody which competes with MAb 60.3 for binding to LFA-1.  
CC See also AAR47931-6.  
CC (Updated on 10-MAR-2003 to add missing OS field.)  
CC (Updated on 25-MAR-2003 to correct PN field.)  
XX  
SQ Sequence 111 AA;  
Query Match 80.5%; Score 335; DB 15; Length 111;  
Best Local Similarity 65.8%; Pred. No. 5.1e-23;  
Matches 73; Conservative 4; Mismatches 2; Indels 32; Gaps 4;

QY 1 DIQMTQSPASLSASVGRVTITC-----WYLOKPKSPQ-LIY----- 37  
Db 1 DIQMTQSPSSLSASVGRVTITCRASERVESYGNFMWYQCKPKAPKLLIYPSNLQS 60

QY 38 GVPSPRFGSGSGTDFSTFTTISLQPEDFATYYC-----FGQGTKEIK 79  
Db 61 GVPSPRFGSGSGTDFSTFTTISLQPEDFATYYCHQDNEDPPTFGQGTKEIK 111

RESULT 14  
ID AAW89351 standard; Protein; 111 AA.  
XX  
AC AAW89351;  
XX  
DT 02-MAR-1999 (first entry)  
XX  
DE Humanised 23F2G light chain variable region.  
XX  
KW Mouse; humanised; antibody; heavy chain variable region; light chain;  
KW 23F2G; inflammatory disease; multiple sclerosis; common beta chain;  
KW CD18; human leukocyte integrin.  
XX  
OS Mus sp.  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN US854070-A.  
XX  
PD 29-DEC-1998.  
XX  
PF 21-JAN-1997; 97US-0785571.  
XX  
PR 16-JUL-1993; 93US-0094535.  
PR 16-JUL-1992; 92US-0915068.  
PR 10-MAY-1993; 93US-0060699.  
PR 28-FEB-1995; 95US-0396089.  
PR 21-JAN-1997; 97US-0785571.  
XX  
PA (ICOS-) ICOS CORP.  
PA (UNIW ) UNIV WASHINGTON.  
XX  
PI Rose LM;  
XX  
DR WPI; 1999-094920/08.  
DR N-PSDB; AAV81909.  
XX  
XX Hybridomas that secrete anti-CD18 antibody - useful for treating  
PT inflammation specifically multiple sclerosis  
XX  
PS Example 6; Column 27-30; 24pp; English.

XX The present invention describes the hybridoma cell line 23F2G  
CC (ATCC HB 11801) and the Chinese hamster ovary (CHO) cell lines 6S6  
CC (ATCC CRL 11398) and B13-24 (ATCC CRL 11397). Monoclonal antibody (Mab)  
CC 23F2G (and its humanised variants 6S6 and B13-24) is an anti-human CD18  
CC antibody for the treatment of inflammation, specifically multiple  
CC sclerosis. The present sequence represents humanised 23F2G light chain  
CC variable region from the present invention.  
XX  
SQ Sequence 111 AA;  
Query Match 80.5%; Score 335; DB 20; Length 111;  
Best Local Similarity 65.8%; Pred. No. 5.1e-23;  
Matches 73; Conservative 4; Mismatches 2; Indels 32; Gaps 4;

QY 1 DIQMTQSPASLSASVGRVTITC-----WYLOKPKSPQ-LIY----- 37  
Db 1 DIQMTQSPSSLSASVGRVTITCRASERVESYGNFMWYQCKPKAPKLLIYASNL 60  
QY 38 GVPSPRFGSGSGTDFSTFTTISLQPEDFATYYC-----FGQGTKEIK 79  
Db 61 GVPSPRFGSGSGTDFSTFTTISLQPEDFATYYCHQDNEDPPTFGQGTKEIK 111

RESULT 15

```

AAW04301
ID AAW04301 standard; Protein; 213 AA.
XX
AC AAW04301;
XX
DT 25-MAR-2003 (updated)
DT 14-FEB-1997 (first entry)
XX
DE Antibody fusion protein..
XX
KW Antibody; fusion protein; recombinant antibody; tumour therapy;
KW prodrug.
XX
OS Synthetic.
XX
PN EP737747-A2.
XX
PD 16-OCT-1996.
XX
PF 13-MAR-1996; 96EP-0103913.
XX
PR 11-APR-1995; 95DE-1013676.
XX.
PA (BEHW ) BEHRINGWERKE AG.
XX
PI Bosslet K, Czech J, Oppen M;
XX
DR WPI; 1996-457328/46.
DR N-PSDB; AAT38397.
XX
PT prodn. of recombinant antibody (Ab), Ab fragment or Ab/enzyme fusion
PT protein - by cytoplasmic expression in thio:redoxin:reductase
PT deficient E. coli
XX
PS Example 1; Figure 5a; 12pp; German.
CC
CC production of recombinant antibodies (Ab), Ab fragments or Ab
CC fragment/enzyme fusion proteins can be used for tumour therapy,
CC especially when the fusion protein comprises a tumour-specific
CC Ab fragment and an enzyme capable of converting a non-toxic prodrug
CC to a toxic drug. The fusion proteins are constructed in expression
CC vectors and expressed in thio:redoxin:reductase deficient E.coli,
CC allowing expression products to be isolated in soluble functional
CC form without renaturation. The Ab fragment is an FAb fragment or an
CC antigen binding region. In the fusion protein, the Ab component is
CC humanised and the enzyme component is a human cytoplasmic enzyme.
CC This fusion protein comprises the antibody constant and variable
CC light chain regions.
CC (Updated on 25-MAR-2003 to correct PR field.)
XX
SQ Sequence 213 AA;
Query Match 80.5%; Score 335; DB 17; Length 213;
Best Local Similarity 68.6%; Pred.No.9.4e-23;
Matches 72; Conservative 5; Mismatches 2; Indels 26; Gaps 4;
QY 1 DIQMTQSPASLSASVGDRTITC-----WYLPKPKSPQ-LIY-----GVPSR 42
DB 2 DIQMTQSPSSLSASVGDRTITCSTSSSVSYMHYQKPKGKAPKLLIYSTNLSAGVPSR 61
QY 43 FSGSGGTDFSTISSLOPEFATYYC-----FGQGTKLEIK 79
DB 62 FSGSGGTDFSTISSLOPEIATYYCHQWSISYPTFGQGTKVEIK 106
Search completed: January 13, 2004, 12:38:23
Job time : 19.4218 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 13, 2004, 12:33:50 ; Search time 6.83057 Seconds  
(without alignments)  
489.353 Million cell updates/sec

Title: US-09-990-586-79

Perfect score: 416

Sequence: 1 DIQMQSPASLSASVGRVT.....QPEDFATYVCGGKLEIK 79

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.\*  
1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep.\*  
2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	377.5	90.7	80	2 US-08-553-501A-85	Sequence 85, Appl
2	377.5	90.7	80	2 US-08-765-783A-104	Sequence 104, App
3	377.5	90.7	80	3 US-09-205-231-85	Sequence 85, Appl
4	377.5	90.7	80	3 US-09-416-557-104	Sequence 104, App
5	364	87.5	87	3 US-08-646-265A-112	Sequence 112, App
6	358.5	86.2	80	3 US-08-554-840-10	Sequence 10, Appl
7	358.5	86.2	80	4 US-08-925-339-10	Sequence 10, Appl
8	358.5	86.2	80	4 US-09-332-595-10	Sequence 10, Appl
9	349.5	84.0	80	3 US-08-554-840-12	Sequence 12, Appl
10	349.5	84.0	80	4 US-08-925-339-12	Sequence 12, Appl
11	349.5	84.0	80	4 US-09-332-595-12	Sequence 12, Appl
12	345.5	83.1	98	2 US-08-553-501A-87	Sequence 87, Appl
13	345.5	83.1	98	3 US-09-205-231-87	Sequence 87, Appl
14	337.5	81.1	110	1 US-08-483-889-96	Sequence 96, Appl
15	337.5	81.1	110	2 US-08-483-889-96	Sequence 96, Appl
16	337.5	81.1	110	2 US-08-487-113D-96	Sequence 96, Appl
17	337.5	81.1	110	2 US-08-473-503-96	Sequence 96, Appl
18	337.5	81.1	110	2 US-08-483-932-96	Sequence 96, Appl
19	337.5	81.1	110	2 US-08-720-420A-96	Sequence 96, Appl
20	337.5	81.1	110	3 US-08-714-017-96	Sequence 96, Appl
21	337.5	81.1	110	3 US-08-475-680-96	Sequence 96, Appl
22	335	80.5	110	4 US-09-343-698-8	Sequence 8, Appl
23	335	80.5	213	3 US-08-630-820-6	Sequence 6, Appl
24	334.5	80.4	106	2 US-08-553-501A-86	Sequence 86, Appl
25	334.5	80.4	106	3 US-09-205-231-86	Sequence 86, Appl
26	334.5	80.4	107	1 US-08-459-310-14	Sequence 14, Appl
27	334.5	80.4	107	1 US-08-459-310-17	Sequence 17, Appl

Query Match 90.7%; Score 377.5; DB 2; Length 80;

Sequence 50, Appl  
Sequence 71, Appl  
Sequence 55, Appl  
Sequence 55, Appl  
Sequence 80, Appl  
Sequence 52, Appl  
Sequence 99, Appl  
Sequence 12, Appl  
Sequence 18, Appl  
Sequence 18, Appl  
Sequence 130, App  
Sequence 18, Appl  
Sequence 18, Appl  
Sequence 2, Appl  
Sequence 3, Appl  
Sequence 10, Appl  
Sequence 32, Appl  
Sequence 3, Appl

334.5 80.4 107 3 US-09-171-945-50  
334.5 80.4 107 3 US-09-171-945-71  
334.5 80.4 125 2 US-08-553-501A-55  
334.5 80.4 125 3 US-09-205-231-55  
334.5 80.4 232 1 US-08-704-744-80  
334.5 80.4 235 3 US-09-171-945-52  
334.5 80.4 235 3 US-09-171-945-99  
334 80.3 107 1 US-08-491-845-12  
334 80.3 107 2 US-07-934-373C-18  
334 80.3 107 3 US-08-437-642B-18  
334 80.3 107 3 US-08-646-265A-130  
334 80.3 107 4 US-08-146-206C-18  
334 80.3 107 5 PCT-US93-07832-18  
334 80.3 108 3 US-08-974-899-2  
334 80.3 108 3 US-08-974-899-3  
334 80.3 108 4 US-08-407-620A-10  
334 80.3 108 4 US-08-407-620A-32  
334 80.3 109 2 US-07-934-373C-3

ALIGNMENTS

RESULT 1  
US-08-553-501A-85  
; Sequence 85, Application US/08553501A  
; Patent No. 5856135  
; GENERAL INFORMATION:  
; APPLICANT: TSUCHIYA, Masayuki  
; APPLICANT: SAITO, Koh  
; APPLICANT: HIRATA, Yuichi  
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN  
; TITLE OF INVENTION: INTERLEUKIN-6  
; NUMBER OF SEQUENCES: 91  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20007-5109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/553,501A  
; FILING DATE: 20-FEB-1996  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/JP94/00859  
; FILING DATE: 30-MAY-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 5-129787  
; FILING DATE: 31-MAY-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: WEGNER, Harold C.  
; REGISTRATION NUMBER: 25,258  
; REFERENCE/DOCKET NUMBER: 53466/177/AAOK  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)672-5300  
; TELEFAX: (202)672-5399  
; TELEX: 904136  
; INFORMATION FOR SEQ ID NO: 85:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 80 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-553-501A-85

Best Local Similarity 90.0%; Pred. No. 1.5e-29; Mismatches 2; Indels 1; Gaps 1;  
Matches 72; Conservative 5;

QY 1 DIQMTQSPASLSASVGDRTVITCWYLOKPGKSPQ-LIYGVPSRFSGSGGTDFSTFISL 59  
DB 1 DIQMTQSPSSLSASVGDRTVITCWYQKPGKAPKLLIYGVPSRFSGSGGTDFSTFISL 60

QY 60 QPEDFATYYCFGGQTKLEIK 79  
DB 61 QPEDATYYCFGGQTKVEIK 80

## RESULT 2

US-08-765-783A-104  
; Sequence 104, Application US/08765783A  
; Patent No. 5994524  
; GENERAL INFORMATION:  
; APPLICANT: Matsushima, Kouji  
; APPLICANT: Matsumoto, Yoshihiro  
; APPLICANT: Yamada, Yoshiaki  
; APPLICANT: Sato, Koh  
; APPLICANT: Tsuchiya, Masayuki  
; APPLICANT: Yamazaki, Tatsumi  
; TITLE OF INVENTION: Reshaped Human Antibody to  
; TITLE OF INVENTION: Interleukin-8  
; NUMBER OF SEQUENCES: 105  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 2000 Pennsylvania Avenue, NW, suite 5500  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20006-1888

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/765,783A  
FILING DATE: 07-MAR-1997  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:

FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Murashige, Kate H

REGISTRATION NUMBER: 29,959  
REFERENCE/DOCKET NUMBER: 35029-20001.20  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-887-1500  
TELEFAX: 202-822-0168  
TELEX:

INFORMATION FOR SEQ ID NO: 104:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 80 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear

US-08-765-783A-104

Query Match 90.7%; Score 377.5; DB 2; Length 80;  
Best Local Similarity 90.0%; Pred. No. 1.5e-29;  
Matches 72; Conservative 5; Mismatches 2; Indels 1; Gaps 1;

QY 1 DIQMTQSPASLSASVGDRTVITCWYLOKPGKSPQ-LIYGVPSRFSGSGGTDFSTFISL 59  
DB 1 DIQMTQSPSSLSASVGDRTVITCWYQKPGKAPKLLIYGVPSRFSGSGGTDFSTFISL 60

QY 60 QPEDFATYYCFGGQTKLEIK 79  
DB 61 QPEDATYYCFGGQTKVEIK 80

## RESULT 3

US-09-205-231-85  
; Sequence 85, Application US/09205231  
; Patent No. 6121423  
; GENERAL INFORMATION:  
; APPLICANT: TSUCHIYA, Masayuki  
; APPLICANT: SAITO, Koh  
; APPLICANT: HIRATA, Yuichi  
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN  
; TITLE OF INVENTION: INTERLEUKIN-6  
; NUMBER OF SEQUENCES: 91  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/205,231

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 5-129787

FILING DATE: 31-MAY-1993

ATTORNEY/AGENT INFORMATION:

NAME: WEGNER, Harold C.

REGISTRATION NUMBER: 25,258

REFERENCE/DOCKET NUMBER: 53466/177/AAOK

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)672-5300

TELEFAX: (202)672-5399

TELEX: 904136

INFORMATION FOR SEQ ID NO: 85:

SEQUENCE CHARACTERISTICS:

LENGTH: 80 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

US-09-205-231-85

Query Match 90.7%; Score 377.5; DB 3; Length 80;  
Best Local Similarity 90.0%; Pred. No. 1.5e-29;  
Matches 72; Conservative 5; Mismatches 2; Indels 1; Gaps 1;

QY 1 DIQMTQSPASLSASVGDRTVITCWYLOKPGKSPQ-LIYGVPSRFSGSGGTDFSTFISL 59  
DB 1 DIQMTQSPSSLSASVGDRTVITCWYQKPGKAPKLLIYGVPSRFSGSGGTDFSTFISL 60

QY 60 QPEDFATYYCFGGQTKLEIK 79

DB 61 QPEDATYYCFGGQTKVEIK 80

## RESULT 4

US-09-416-557-104  
; Sequence 104, Application US/09416557  
; Patent No. 6245894  
; GENERAL INFORMATION:  
; APPLICANT: Matsushima, Kouji  
; APPLICANT: Matsumoto, Yoshihiro  
; APPLICANT: Yamada, Yoshiaki

APPLICANT: Sato, Koh  
APPLICANT: Tsuchiya, Masayuki  
APPLICANT: Yamazaki, Tatsumi  
TITLE OF INVENTION: Reshaped Human Antibody to Interleukin-8  
NUMBER OF SEQUENCES: 105  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FOERSTER  
STREET: 2000 Pennsylvania Avenue, NW, suite 5500  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20006-1898  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/416,557  
FILING DATE: 12-October-1999  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/765,783  
FILING DATE: 7-March-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Murashige, Kate H  
REGISTRATION NUMBER: 29,959  
REFERENCE/DOCKET NUMBER: 35029-20001.10  
TELEPHONE: 202-887-1500  
TELEFAX: 202-822-0168  
TELEX:  
INFORMATION FOR SEQ ID NO: 104:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 80 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-416-557-104  
Query Match 90.7%; Score 377.5; DB 3; Length 80;  
Best Local Similarity 90.0%; Pred. No. 1.5e-29;  
Matches 72; Conservative 5; Mismatches 2; Indels 1; Gaps 1;  
QY 1 DIQMTQSPASLSASVGDRTVITTCWYQKPKSPQ-LIYGVPSRFGSGSGTDFSTISL 59  
Db 1 DIQMTQSPSLSASVGDRTVITTCWYQKPKAPKLLIYGVPSRFGSGSGTDFSTISL 60  
QY 60 QPEDFATYYCFQGQTKLEIK 79  
Db 61 QPEDATYYCFQGQTKVEIK 80  
RESULT 5  
US-08-646-265A-112  
Sequence 112, Application US/08646265A  
Patent No. 6214973  
GENERAL INFORMATION:  
APPLICANT: OHTOMO, Toshihiko  
APPLICANT: SATO, Koh  
APPLICANT: TSUCHIYA, Masayuki  
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN MEDULLOBLASTOMA CELLS  
NUMBER OF SEQUENCES: 132  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/646,265A  
FILING DATE: 09-SEP-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/JP94/01763  
FILING DATE: 19-OCT-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 5-291078  
FILING DATE: 19-NOV-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: WEGNER, Harold C.  
REGISTRATION NUMBER: 25,258  
REFERENCE/DOCKET NUMBER: 53466/184  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 112:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 87 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-646-265A-112  
Query Match 87.5%; Score 364; DB 3; Length 87;  
Best Local Similarity 82.8%; Pred. No. 3.3e-28;  
Matches 72; Conservative 5; Mismatches 2; Indels 8; Gaps 2;  
QY 1 DIQMTQSPASLSASVGDRTVITTCWYQKPKSPQ-LIY-----GVPSRFGSGSGTDF 52  
Db 1 DIQMTQSPSLSASVGDRTVITTCWYQKPKAPKLLIYASVYSGVPSRFGSGSGTDF 60  
QY 53 SFTISSLQPEDFATYYCFQGQTKLEIK 79  
Db 61 TFTISSLQPEDATYYCFQGQTKVEIK 87  
RESULT 6  
US-08-554-840-10  
Sequence 10, Application US/08554840  
Patent No. 6001358  
GENERAL INFORMATION:  
APPLICANT: BLACK, Amelia  
APPLICANT: HANNA, Nabil  
APPLICANT: PADIAN, Eduardo A.  
APPLICANT: NEWMAN, Roland A.  
TITLE OF INVENTION: HUMANIZED ANTIBODIES TO HUMAN gp39,  
TITLE OF INVENTION: COMPOSITIONS CONTAINING AND THERAPEUTIC USE THEREOF  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Burns, Doane, Swecker & Mathis  
STREET: P.O. Box 1404  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: United States  
ZIP: 22313-1404  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/554,840  
FILING DATE: 07-NOV-1995  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Teskin, Robin L.

REGISTRATION NUMBER: 35,030  
REFERENCE/DOCKET NUMBER: 012712-127  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 836-6620  
TELEFAX: (703) 836-2021  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 80 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-554-840-10

Query Match 86.2%; Score 358.5; DB 3; Length 80;  
Best Local Similarity 85.0%; Pred. No. 1e-27;  
Matches 68; Conservative 8; Mismatches 3; Indels 1; Gaps 1;

QY 1 DIQMTQSPASLSASVGDRTVITTCWYLOKPGKSPQ-LIYGVPFRFSGSGGTDFSTISL 59  
DB 1 DIQMTQSPSTLSASVGDRTVITTCWYQKPGKAPKVLIIYGVPSRFGSGGTFTLTISL 60

QY 60 QPEDFATYYCFGQGTKEIK 79  
DB 61 QSDDFATYYCFGQGTKEIK 80

RESULT 8  
US-09-332-595-10  
Sequence 10, Application US/09332595  
Patent No. 6506383  
GENERAL INFORMATION:  
APPLICANT: BLACK, Amelia  
APPLICANT: HANNA, Nabil  
APPLICANT: PADLAN, Eduardo A.  
APPLICANT: NEWMAN, Roland A.  
TITLE OF INVENTION: HUMANIZED ANTIBODIES TO HUMAN GP39,  
TITLE OF INVENTION: COMPOSITIONS CONTAINING AND THERAPEUTIC USE THEREOF  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Burns, Doane, Swecker & Mathis  
STREET: P.O. Box 1404  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: United States  
ZIP: 22313-1404  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/332,595  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/554,840  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Teskin, Robin L.  
REGISTRATION NUMBER: 35,030  
REFERENCE/DOCKET NUMBER: 012712-127  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 836-6620  
TELEFAX: (703) 836-2021  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 80 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-332-595-10

Query Match 86.2%; Score 358.5; DB 4; Length 80;  
Best Local Similarity 85.0%; Pred. No. 1e-27;  
Matches 68; Conservative 8; Mismatches 3; Indels 1; Gaps 1;

QY 1 DIQMTQSPASLSASVGDRTVITTCWYLOKPGKSPQ-LIYGVPFRFSGSGGTDFSTISL 59  
DB 1 DIQMTQSPSTLSASVGDRTVITTCWYQKPGKAPKVLIIYGVPSRFGSGGTFTLTISL 60

QY 60 QPEDFATYYCFGQGTKEIK 79  
DB 61 QSDDFATYYCFGQGTKEIK 80

REGISTRATION NUMBER: 35,030  
REFERENCE/DOCKET NUMBER: 012712-127  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 836-6620  
TELEFAX: (703) 836-2021  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 80 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-554-840-10

Query Match 86.2%; Score 358.5; DB 3; Length 80;  
Best Local Similarity 85.0%; Pred. No. 1e-27;  
Matches 68; Conservative 8; Mismatches 3; Indels 1; Gaps 1;

QY 1 DIQMTQSPASLSASVGDRTVITTCWYLOKPGKSPQ-LIYGVPFRFSGSGGTDFSTISL 59  
DB 1 DIQMTQSPSTLSASVGDRTVITTCWYQKPGKAPKVLIIYGVPSRFGSGGTFTLTISL 60

QY 60 QPEDFATYYCFGQGTKEIK 79  
DB 61 QSDDFATYYCFGQGTKEIK 80

RESULT 7  
US-08-925-339-10  
Sequence 10, Application US/08925339  
Patent No. 6440418  
GENERAL INFORMATION:  
APPLICANT: BLACK, Amelia  
APPLICANT: HANNA, Nabil  
APPLICANT: PADLAN, Eduardo A.  
APPLICANT: NEWMAN, Roland A.  
TITLE OF INVENTION: HUMANIZED ANTIBODIES TO HUMAN GP39,  
TITLE OF INVENTION: COMPOSITIONS CONTAINING AND THERAPEUTIC USE THEREOF  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Burns, Doane, Swecker & Mathis  
STREET: P.O. Box 1404  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: United States  
ZIP: 22313-1404  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/925,339  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/554,840  
FILING DATE: 07-NOV-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Teskin, Robin L.  
REGISTRATION NUMBER: 35,030  
REFERENCE/DOCKET NUMBER: 012712-127  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 836-6620  
TELEFAX: (703) 836-2021  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 80 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-925-339-10

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RESULT 9
US-08-554-840-12
; Sequence 12, Application US/08554840
; Patent No. 6001358
; GENERAL INFORMATION:
; APPLICANT: BLACK, Amelia
; APPLICANT: HANNA, Nabil
; APPLICANT: PADLAN, Eduardo A.
; APPLICANT: NEWMAN, Roland A.
; TITLE OF INVENTION: HUMANIZED ANTIBODIES TO HUMAN gp39.
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/554,840
; FILING DATE: 07-NOV-1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-127
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 80 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-554-840-12

Query Match      84.0%; Score 349.5; DB 3; Length 80;
Best Local Similarity 85.0%; Pred. No. 7.3e-27;
Matches 68; Conservative 4; Mismatches 7; Indels 1; Gaps 1;

QY 1 DIQMTQSPASLSASVGRVTITCWYLOKPGKSPQ-LIYGVPSPRSGSGGTDFSTISL 59
Db 1 DIVMTQSPFLSASVGRVTITCWYQKPKSLIYGVDPFRSGSGGTDFLTITSL 60

QY 60 QPEDFATYVCFGGTKLEIK 79
Db 61 QPEDFADYFCFGGTKLEIK 80

RESULT 10
US-08-925-339-12
; Sequence 12, Application US/08925339
; Patent No. 6440418
; GENERAL INFORMATION:
; APPLICANT: BLACK, Amelia
; APPLICANT: HANNA, Nabil
; APPLICANT: PADLAN, Eduardo A.
; APPLICANT: NEWMAN, Roland A.
; TITLE OF INVENTION: HUMANIZED ANTIBODIES TO HUMAN gp39.
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/332,595
; FILING DATE:
; CLASSIFICATION:
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; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/925,339
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/554,840
; FILING DATE: 07-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-127
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 80 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-925-339-12

Query Match      84.0%; Score 349.5; DB 4; Length 80;
Best Local Similarity 85.0%; Pred. No. 7.3e-27;
Matches 68; Conservative 4; Mismatches 7; Indels 1; Gaps 1;

QY 1 DIQMTQSPASLSASVGRVTITCWYLOKPGKSPQ-LIYGVPSPRSGSGGTDFSTISL 59
Db 1 DIVMTQSPFLSASVGRVTITCWYQKPKSLIYGVDPFRSGSGGTDFLTITSL 60

QY 60 QPEDFATYVCFGGTKLEIK 79
Db 61 QPEDFADYFCFGGTKLEIK 80

RESULT 11
US-09-332-595-12
; Sequence 12, Application US/09332595
; Patent No. 6506383
; GENERAL INFORMATION:
; APPLICANT: BLACK, Amelia
; APPLICANT: HANNA, Nabil
; APPLICANT: PADLAN, Eduardo A.
; APPLICANT: NEWMAN, Roland A.
; TITLE OF INVENTION: HUMANIZED ANTIBODIES TO HUMAN gp39.
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/332,595
; FILING DATE:
; CLASSIFICATION:
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/554,840
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-127
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 80 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-332-595-12

Query Match      84.0%; Score 349.5; DB 4; Length 80;
Best Local Similarity 85.0%; Pred. No. 7.3e-27;
Matches 68; Conservative 4; Mismatches 7; Indels 1; Gaps 1;

QY 1 DIQWTQSPASLSASVGRVITTCWYLOKPKSPQ-LIYGVPSFSGSGTDFSFITSL 59
Db 1 DIVNTQSPFLSASVGRVITTCWYQOKPKSPALLIYGVDRFSGSGTDFITLITSL 60
QY 60 QPEDFATYFCGGGTGLEIK 79
Db 61 QPEDFADYFCGGGTGLEIK 80

RESULT 12
US-08-553-501A-87
; Sequence 87, Application US/08553501A
; Patent No. 5856135
; GENERAL INFORMATION:
; APPLICANT: TSUCHIYA, Masayuki
; APPLICANT: SATO, Koh
; APPLICANT: HIRATA, Yuichi
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
; TITLE OF INVENTION: INTERLEUKIN-6
; NUMBER OF SEQUENCES: 91
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/553,501A
; FILING DATE: 20-FEB-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/553,501
; FILING DATE: 20-FEB-1996
; APPLICATION NUMBER: WO PCT/JP94/00859
; FILING DATE: 30-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 5-129787
; FILING DATE: 31-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: WEGNER, Harold C.
; REGISTRATION NUMBER: 25,258
; REFERENCE/DOCKET NUMBER: 53466/177/AAOK
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 87:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 98 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-205-231-87

Query Match      83.1%; Score 345.5; DB 3; Length 98;
Best Local Similarity 72.4%; Pred. No. 2.2e-26;
Matches 71; Conservative 6; Mismatches 2; Indels 19; Gaps 3;

QY 1 DIQWTQSPASLSASVGRVITTC-----WYLOKPKSPQ-LIY-----GVPS 41
Db 1 DIQWTQSPFLSASVGRVITTCRASNIYSNLAWQOKPKAPKLLIYAATYVLADGVPS 60
QY 42 RFGSGSGTDFSFITSLQLPEDFATYFCGGGTGLEIK 79
Db 61 RFGSGSGTDFITSLQLPEDATYFCGGGTGLEIK 98

RESULT 13
US-09-205-231-87
; Sequence 87, Application US/09205231
; Patent No. 6121423
; GENERAL INFORMATION:
; APPLICANT: TSUCHIYA, Masayuki
; APPLICANT: SATO, Koh
; APPLICANT: HIRATA, Yuichi
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
; TITLE OF INVENTION: INTERLEUKIN-6
; NUMBER OF SEQUENCES: 91
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/205,231
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/553,501
; FILING DATE: 20-FEB-1996
; APPLICATION NUMBER: WO PCT/JP94/00859
; FILING DATE: 30-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 5-129787
; FILING DATE: 31-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: WEGNER, Harold C.
; REGISTRATION NUMBER: 25,258
; REFERENCE/DOCKET NUMBER: 53466/177/AAOK
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 87:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 98 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-205-231-87

Query Match      83.1%; Score 345.5; DB 3; Length 98;
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Best Local Similarity 72.4%; Pred. No. 2.2e-26;  
Matches 71; Conservative 6; Mismatches 2; Indels 19; Gaps 3;

QY 1 DIQMTQSPASLSASVGDRTVITC-----WYLOKPKSPQ-LIY-----GVPS 41

Db 1 DIQMTQSPSSLSASVGDRTVITC-----WYLOKPKSPQ-LIY-----GVPS 41

QY 42 RFGSGSGTDFSTFISSLOPEDFATYYCFGGTKLEIK 79

Db 61 RFGSGSGTDFSTFISSLOPEDFATYYCFGGTKLEIK 98

RESULT 14

US-08-482-882-96  
; Sequence 96, Application US/08482882  
; Patent No. 5773218  
; GENERAL INFORMATION:  
; APPLICANT: Gallatin, W. Michael  
; APPLICANT: Vazeux, Rosemay  
; TITLE OF INVENTION: ICM-Related Materials and Methods  
; NUMBER OF SEQUENCES: 116  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 S. Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/482,882  
FILING DATE: 07-JUN-1995

CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/286,754

FILING DATE: 05-AUG-1993  
APPLICATION NUMBER: US 08/102,852

FILING DATE: 05-AUG-1993  
APPLICATION NUMBER: US 08/009,266

FILING DATE: 22-JAN-1993  
APPLICATION NUMBER: US 07/894,061

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/889,724

FILING DATE: 26-MAY-1992  
APPLICATION NUMBER: US 07/827,689

FILING DATE: 27-JAN-1992  
ATTORNEY/AGENT INFORMATION:

NAME: No. 5773218 and, Greta E.  
REGISTRATION NUMBER: 35,302

REFERENCE/DOCKET NUMBER: 32178  
TELEPHONE: (312) 474-6300

TELEFAX: (312) 474-0448  
TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 96:  
SEQUENCE CHARACTERISTICS:

LENGTH: 110 amino acids  
TYPE: amino acid

TOPOLOGY: linear  
MOLECULE TYPE: protein

US-08-482-882-96

Query Match 81.1%; Score 337.5; DB 1; Length 110;

Best Local Similarity 68.9%; Pred. No. 1.4e-25;  
Matches 73; Conservative 4; Mismatches 2; Indels 27; Gaps 4;

QY 1 DIQMTQSPASLSASVGDRTVITC-----WYLOKPKSPQ-LIY-----GVPSR 42

Db 5 DIQMTQSPSSLSASVGDRTVITC-----WYLOKPKSPQ-LIY-----GVPSR 64

QY 43 RFGSGSGTDFSTFISSLOPEDFATYYC-----FGGTKLEIK 79

Db 65 RFGSGSGTDFSTFISSLOPEDFATYYCQWKSIPLTFGGTKLEIK 110

RESULT 15

US-08-483-389-96  
; Sequence 96, Application US/08483389  
; Patent No. 5811517  
; GENERAL INFORMATION:  
; APPLICANT: Gallatin, W. Michael  
; APPLICANT: Vazeux, Rosemay  
; TITLE OF INVENTION: ICM-RELATED PROTEIN  
; NUMBER OF SEQUENCES: 118  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 233 South Wacker Drive/6300 Sears Tower  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: United States of America  
; ZIP: 60606

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/483,389  
FILING DATE: 07-JUN-1995

CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/102,852

FILING DATE: 05-AUG-1993  
APPLICATION NUMBER: US 08/009,266

FILING DATE: 22-JAN-1993  
APPLICATION NUMBER: US 07/894,061

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/889,724

FILING DATE: 26-MAY-1992  
APPLICATION NUMBER: US 07/827,689

FILING DATE: 27-JAN-1992  
ATTORNEY/AGENT INFORMATION:

NAME: Sub, Young J.  
REGISTRATION NUMBER: P-41,337

REFERENCE/DOCKET NUMBER: 27866/32760  
TELEPHONE: (312) 474-6300

TELEFAX: (312) 474-0448  
TELEX: (312) 474-6600

INFORMATION FOR SEQ ID NO: 96:  
SEQUENCE CHARACTERISTICS:

LENGTH: 110 amino acids  
TYPE: amino acid

TOPOLOGY: linear  
MOLECULE TYPE: protein

US-08-483-389-96

Query Match 81.1%; Score 337.5; DB 2; Length 110;

Best Local Similarity 68.9%; Pred. No. 1.4e-25;  
Matches 73; Conservative 4; Mismatches 2; Indels 27; Gaps 4;

QY 1 DIQMTQSPASLSASVGDRTVITC-----WYLOKPKSPQ-LIY-----GVPSR 42

Db 5 DIQMTQSPSSLSASVGDRTVITC-----WYLOKPKSPQ-LIY-----GVPSR 64

Qy 43 FSGSGTDFSTISSLOPEDPATYYC-----FGGTKLEIK 79  
Db 65 FSGSGTDFSTISSLOPEDPATYYCQQWKSIPLTFFGGTKLEIK 110

Search completed: January 13, 2004, 12:46:32  
Job time : 7.83057 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 13, 2004, 12:22:35 ; Search time 6.30655 Seconds  
(without alignments)  
1326.664 Million cell updates/sec

Title: US-09-990-586-90

Perfect score: 448

Sequence: 1 QIQLVQSGGELVKPGASVRV.....DTAVFCARWGQTTTVSS 87

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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2: PIR2.\*  
3: PIR3.\*  
4: PIR4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	345.5	77.1	119	2 A24672	Ig heavy chain pre
2	343.5	76.7	469	2 S37483	Ig gamma-2a chain
3	341	76.1	138	2 S21810	Ig heavy chain v r
4	340	75.9	246	2 S38950	Ig gamma chain m
5	340	75.9	446	2 S40295	Ig gamma-2a chain
6	339.5	75.8	137	2 H32513	Ig heavy chain pre
7	337.5	75.3	120	2 B22769	Ig heavy chain v r
8	337.5	75.3	141	2 J10076	Ig heavy chain pre
9	337	75.2	116	2 S55542	Ig heavy chain v r
10	337	75.2	119	2 PH0961	Ig heavy chain v r
11	336.5	75.1	120	2 S41394	Ig heavy chain v r
12	335.5	74.9	116	2 S33751	Ig heavy chain v r
13	335.5	74.9	122	2 PH0958	Ig heavy chain pre
14	335.5	74.9	139	1 MMS18	Ig heavy chain pre
15	335.5	74.9	287	4 PC4402	peB leader/Ig hea
16	334.5	74.7	118	2 S36265	Ig heavy chain v r
17	334.5	74.7	119	2 F30502	Ig heavy chain v r
18	333.5	74.4	118	2 C30560	Ig heavy chain v r
19	333	74.3	119	2 S20640	Ig heavy chain v r
20	332.5	74.2	115	2 A54378	Ig heavy chain v r
21	332.5	74.2	116	2 PH0959	Ig heavy chain v r
22	332.5	74.2	136	2 J10077	Ig heavy chain pre
23	332.5	74.2	136	2 PH0960	Ig heavy chain v r
24	332	74.1	121	2 H37266	Ig heavy chain v r
25	331.5	74.0	115	2 P30238	Ig heavy chain v r
26	331.5	74.0	118	2 S38717	Ig heavy chain v r
27	331.5	74.0	139	2 PS0024	Ig heavy chain pre
28	331	73.9	142	2 A32483	Ig heavy chain v r
29	330.5	73.8	120	2 G38195	Ig heavy chain v r

30	330.5	73.8	120	2 PH0962	Ig heavy chain v r
31	330.5	73.8	128	2 PH0952	Ig heavy chain v r
32	330.5	73.8	132	2 PH0954	Ig heavy chain v r
33	330	73.7	138	2 E32513	Ig heavy chain pre
34	329.5	73.5	137	1 G2MS43	Ig heavy chain pre
35	329.5	73.5	139	2 A37609	Ig heavy chain v r
36	329	73.4	117	1 MEMS4E	Ig heavy chain v r
37	329	73.4	117	1 MEMS35	Ig heavy chain v r
38	329	73.4	121	2 F37266	Ig heavy chain v r
39	329	73.4	127	2 PH0955	Ig heavy chain v r
40	329	73.4	140	2 T01407	Ig heavy chain (my
41	328	73.2	119	2 S03077	Ig heavy chain v r
42	328	73.2	120	2 S25175	Ig heavy chain v r
43	328	73.2	123	2 S20645	Ig heavy chain v r
44	328	73.2	136	2 PL0208	Ig heavy chain pre
45	327.5	73.1	120	2 F28195	Ig heavy chain v r

#### ALIGNMENTS

##### RESULT 1

A24672 Ig heavy chain precursor V region (VMU-3.2) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 19-Nov-1988 #sequence\_revision 19-Nov-1988 #text\_change 23-Jul-1999

C/Accession: A24672

R/Winter, E., Radbruch, A., Krawinkel, U.

EMBO J. 4, 2861-2867, 1985

A/Reference number: A91022; MUID:86055722; PMID:2998759

A/Accession: A24672

A/Molecule type: DNA

A/Residues: 1-119 <WIN>

A/Cross-references: GB:X03088; NID:952378; PIDN:CAA26881.1; PID:G773578

A/Note: this sequence was determined from the germline gene

C/Superfamily: Immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotrimer; immunoglobulin

F/4-119/Product: Ig heavy chain V region VMU-3.2 #status predicted <MAT>

F/18-101/Domain: immunoglobulin homology <IMM>

Query Match 77.1%; Score 345.5; DB 2; Length 119;  
Best Local Similarity 62.1%; Pred. No. 5.4e-27;  
Matches 72; Conservative 10; Mismatches 5; Indels 29; Gaps 3;

QY	1	QIQLVQSGGELVKPGASVRVSKASGYFT-----WVRQSPGKGLW----	43
DB	4	QYQLQSGPELVKPGASVKISKASGYAFSSMMNWKQRPCKGLEWIGRIYFGDITNY	63
QY	44	-----GKALTVDKSTSTAYMELSLRSEDITAYFCAR-----WGQTTTVSS	87
DB	64	NGKFKGKATLTADKSSSTAYMQLSLTSDSAVYFCARDYDYGSDYWGQTTTVSS	119

##### RESULT 2

S37483

Ig gamma-2a chain - mouse

C/Species: Mus musculus (house mouse)

C/Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 23-Jul-1999

C/Accession: S37483

R/Ducancel, F.F.D.

submitted to the EMBL Data Library, February 1993

A/Reference number: S37483

A/Accession: S37483

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-469 <DUC>

A/Cross-references: EMBL:X70423; NID:G406252; PIDN:CAA49868.1; PID:G406253

C/Superfamily: immunoglobulin C region; immunoglobulin homology

C/Keywords: immunoglobulin

F/276-345/Domain: immunoglobulin homology <IMM>

Query Match 76.7%; Score 343.5; DB 2; Length 469;  
Best Local Similarity 60.8%; Pred. No. 3.3e-26;

Matches 73; Conservative 9; Mismatches 5; Indels 33; Gaps 3;

QY 1 QIQLVQSGGELVKPGASVRVSCASGYST-----WVRSPOGKLEWI----- 43  
DB 20 QIQLQSGGPELVKPGASVRVSCASGYSTFYIHWVKRPGGKLEWIGWIYPSGNTKY 79  
QY 44 -----GKATLTVDKSTSTAYMELSSLSRSEDVAVFCAR-----WGQGTITVTSS 87  
DB 80 NENFKGKATLTVDTSSTAYMQLSSLTSEDVAVFCARANGATATLLDYGQGTITVTSS 139

RESULT 3  
S21810  
Ig heavy chain V region - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 23-Jul-1999  
C:Accession: S21810  
R:Ostermeyer, M.; Brack, C.H.; Traunecker, A.; Koehler, G.  
submitted to the EMBL Data Library, January 1991  
A:Description: Nucleotide sequence of a rearranged VDJ-region of a mouse Ig mu heavy chain  
A:Reference number: S21810  
A:Accession: S21810  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-138 <OST>  
A:Cross-references: EMBL:X56936; NID:G54163; PIDN:CAA40257.1; PID:G54164  
C:Genetics:  
A:Introns: 15/3  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotrimer; immunoglobulin  
F:137-201/Domain: immunoglobulin homology <IMM>

Query Match 76.1%; Score 341; DB 2; Length 138;  
Best Local Similarity 60.5%; Pred. No. 1.7e-26;  
Matches 72; Conservative 9; Mismatches 6; Indels 32; Gaps 3;

QY 1 QIQLVQSGGELVKPGASVRVSCASGYST-----WVRSPOGKLEWI----- 43  
DB 20 QVQLQSGGPELVKPGASVRVSCASGYSTFYIHWVKRPGGKLEWIGWIYPSGNTKY 79  
QY 44 -----GKATLTVDKSTSTAYMELSSLSRSEDVAVFCAR-----WGQGTITVTSS 87  
DB 80 NENFKGKATLTADKSSSTAYMQLSSLTSEDVAVFCARNYSSYGLAYWGQGTITVTSA 138

RESULT 4  
S38950  
Ig gamma chain - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 19-May-1994 #sequence\_revision 10-Nov-1995 #text\_change 16-Jul-1999  
C:Accession: S38950  
R:Kleber, S.; Kratzin, H.D.; Zimmermann, B.; Vaesen, M.; Frosch, M.; Weisgerber, C.; B.  
Biochem. Hoppe-Seyler 374, 993-1000, 1993  
A:Title: Primary structure of the murine monoclonal IgG2a antibody mAb735 against alpha  
A:Reference number: S38950; MUID:94128242; PMID:8297501  
A:Accession: S38950  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-246 <KLE>  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: immunoglobulin  
F:137-201/Domain: immunoglobulin homology <IMM>

Query Match 75.9%; Score 340; DB 2; Length 246;  
Best Local Similarity 61.5%; Pred. No. 3.8e-26;  
Matches 72; Conservative 10; Mismatches 5; Indels 30; Gaps 3;

QY 1 QIQLVQSGGELVKPGASVRVSCASGYST-----WVRSPOGKLEWI----- 43  
DB 1 QIQLQSGGPELVKPGASVRVSCASGYSTFYIHWVKRPGGKLEWIGWIYPSGNTKY 60  
QY 44 -----GKATLTVDKSTSTAYMELSSLSRSEDVAVFCAR-----WGQGTITVTSS 87

DB 61 NENFKGKATLTVDTSSTAYMQLSSLTSEDVAVFCARGKFAMDYWGQGTITVTSS 117

RESULT 5  
S40295  
Ig gamma-2a chain (mAb735) - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 07-Apr-1994 #sequence\_revision 07-Apr-1994 #text\_change 16-Jul-1999  
C:Accession: S40295  
R:Kleber, S.; Kratzin, H.D.; Zimmermann, B.; Vaesen, M.; Frosch, M.; Weisgerber, C.; B.  
submitted to the EMBL Data Library, January 1993  
A:Description: Primary structure of the murine monoclonal IgG2a antibody mAb735 against  
A:Reference number: S40295  
A:Accession: S40295  
A:Molecule type: protein  
A:Residues: 1-446 <KLE>  
C:Genetics:  
A:Map position: 12  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: disulfide bond; glycoprotein; immunoglobulin; pyroglutamic acid  
F:1-446/Product: Ig gamma-2a chain #status experimental <MA>  
F:1-117/Domain: V-D-J region <VDJ>  
F:118-446/Domain: C region <CHR>  
F:118-214/Domain: C1 region <CH1>  
F:215-230/Region: hinge  
F:231-340/Domain: C2 region <CH2>  
F:341-446/Domain: C3 region <CH3>  
F:360-427/Domain: immunoglobulin homology <IMM>  
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F:22-96,144-199,261-321,367-425/Disulfide bonds: #status predicted  
F:132/Disulfide bonds: interchain (to light chain) #status predicted  
F:224, 227, 229/Disulfide bonds: interchain #status predicted  
F:297/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 75.9%; Score 340; DB 2; Length 446;  
Best Local Similarity 61.5%; Pred. No. 6.9e-26;  
Matches 72; Conservative 10; Mismatches 5; Indels 30; Gaps 3;

QY 1 QIQLVQSGGELVKPGASVRVSCASGYST-----WVRSPOGKLEWI----- 43  
DB 1 QIQLQSGGPELVKPGASVRVSCASGYSTFYIHWVKRPGGKLEWIGWIYPSGNTKY 60  
QY 44 -----GKATLTVDKSTSTAYMELSSLSRSEDVAVFCAR-----WGQGTITVTSS 87  
DB 61 NENFKGKATLTVDTSSTAYMQLSSLTSEDVAVFCARGKFAMDYWGQGTITVTSS 117

RESULT 6  
H32513  
Ig heavy chain precursor V region (BXW16) - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 21-May-1990 #sequence\_revision 31-Dec-1990 #text\_change 21-Jan-2000  
C:Accession: H32513  
R:Kofler, R.; Strohal, R.; Balderas, R.S.; Johnson, M.E.; Noonan, D.J.; Duchosal, M.A.;  
J. Clin. Invest. 92, 852-860, 1998  
A:Title: Immunoglobulin kappa light chain variable region gene complex organization and  
A:Reference number: A94689; MUID:88331394; PMID:9338286  
A:Accession: H32513  
A:Molecule type: DNA  
A:Residues: 1-137 <KOF>  
A:Cross-references: GB:M20831; NID:G196949; PIDN:AAA38848.1; PID:G196950  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotrimer; immunoglobulin  
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 75.8%; Score 339.5; DB 2; Length 137;  
Best Local Similarity 61.0%; Pred. No. 2.4e-26;  
Matches 72; Conservative 10; Mismatches 5; Indels 31; Gaps 3;

QY 1 QIQLVQSGGELVKPGASVRVSCASGYST-----WVRSPOGKLEWI----- 43  
DB 20 EIQLOQSGAELVKPGASVRVSCASGYSTFYIHWVKRPGGKLEWIGWIYPSGNTKY 79

```
QY 44 -----GKATLTVDKSTAYMELSLRSRSDTAVYFCAR-----WGQGTIVTVSS 87
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 80 NQKFKGKATLTVDKSSSTAYMQLNSLTSEDSAVYVCARKNYGSSFDYWGQGTIVTVSS 137

RESULT 7
B22769
IG heavy chain V region (BI-8.VI/V2) - mouse (tentative sequence)
C:Species: Mus musculus (house mouse)
C>Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 16-Aug-1996
C:Accession: B22769
R:Didrop, R.; Bruggemann, M.; Radbruch, A.; Rajewsky, K.; Beyreuther, K.
EMBO J. 1, 635-640, 1982
A:Title: Immunoglobulin V region variants in hybridoma cells. II. Recombination between
A:Reference number: A90971; MUID:84236026; PMID:7188353
A:Accession: B22769
A:Molecule type: protein
A:Residues: 1-120 <DI>
A>Note: the sequences of two spontaneously arising somatic variants, BI-8.VI and BI-8.V2
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 75.3%; Score 337.5; DB 2; Length 120;
Best Local Similarity 59.2%; Pred. No. 3.3e-26;
Matches 71; Conservative 10; Mismatches 6; Indels 33; Gaps 3;

QY 1 QIQLVSGGELVKPGASVRVSKASGYST-----WVRQSPGKLEWIG----- 43
Db 1 QVLOQPGAEVLKPGASVKVSKASGYFTSYWVHWVQRPGQGLEWIGRIHPDSDTNY 60

QY 44 -----GKATLTVDKSTAYMELSLRSRSDTAVYFCAR-----WGQGTIVTVSS 87
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 NQKFKGKATLTVDKPSSTAYMQLNSLTSEDSAVYVCARYDYGSYFDYWGQGTIVTVSS 120

RESULT 8
JL0076
IG heavy chain precursor V region (anti-phenylloxazolone, 18C10) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 23-Jul-1999
C:Accession: JL0076
Mol. Immunol. 25, 859-865, 1988
R:Kaartinen, M.; Rocca-Serra, J.; Maekela, O.
A:Title: Combinatorial association of V genes: one VH gene codes for three non-cross-react
A:Reference number: JL0076; MUID:89096973; PMID:3211160
A:Accession: JL0076
A:Molecule type: mRNA
A:Residues: 1-141 <KAA>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-141/Product: Ig heavy chain #status predicted <MAT>
F:34-117/Domain: immunoglobulin homology <IMM>
F:50-54/Region: complementarity-determining 1
F:69-85/Region: complementarity-determining 2
F:123-135/Region: J2 segment
F:136-141/Region: C

Query Match 75.3%; Score 337.5; DB 2; Length 141;
Best Local Similarity 60.3%; Pred. No. 3.9e-26;
Matches 70; Conservative 11; Mismatches 6; Indels 29; Gaps 3;

QY 1 QIQLVSGGELVKPGASVRVSKASGYST-----WVRQSPGKLEWIG----- 44
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 20 QVLOQPGAEVLKPGASVKLSKASGYFTSYWVHWVQRPGQGLEWIGRIDPNSGGTKY 79

QY 45 -----KATLTVDKSTAYMELSLRSRSDTAVYFCAR-----WGQGTIVTVSS 87
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 80 NEKFKSKATLTVDKPSSTAYMQLNSLTSEDSAVYVCAREGPAGDYWGQGTIVTVSS 135
```

```
RESULT 9
S55542
IG heavy chain V region pe2 - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 23-Jul-1999
C:Accession: S55542
R:Boettger, V.; Boettger, A.; Lane, E.B.; Spruce, B.A.
J. Mol. Biol. 247, 932-946, 1995
A:Title: Comprehensive epitope analysis of monoclonal anti-proenkephalin antibodies usin
utations in the variable region genes.
A:Reference number: S55528; MUID:95239763; PMID:7536850
A:Accession: S55542
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-116 <BOE>
A:Cross-references: EMBL:X82581; NID:G854302; PIDN:CAA57917.1; PID:G854303
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:14-97/Domain: immunoglobulin homology <IMM>

Query Match 75.2%; Score 337; DB 2; Length 116;
Best Local Similarity 60.3%; Pred. No. 3.6e-26;
Matches 70; Conservative 11; Mismatches 5; Indels 30; Gaps 3;

QY 2 QIQLVSGGELVKPGASVRVSKASGYST-----WVRQSPGKLEWIG----- 44
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 VQLQSGAEVLKPGASVKLSKASGYFTTRYVYVWVQRPGQGLEWIGEINPSNGTTFN 60

QY 45 -----KATLTVDKSTAYMELSLRSRSDTAVYFCAR-----WGQGTIVTVSS 87
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 EKFKSKATLTVDKSSSTAYMQLNSLTSEDSAVYVTRGVASMDYWGQGTIVTVSS 116

RESULT 10
PH0961
IG heavy chain V region (G6+ T-133) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
C:Accession: PH0961
R:Martin, T.; Duffv, S.F.; Carson, D.A.; Kipps, T.J.
J. Exp. Med. 175, 993-991, 1992
A:Title: Evidence for somatic selection of natural autoantibodies.
A:Reference number: PH0952; MUID:92202880; PMID:1552291
A:Accession: PH0961
A>Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-119 <NAR>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-30/Region: framework 1
F:15-98/Domain: immunoglobulin homology <IMM>
F:31-35/Region: complementarity-determining 1
F:36-50/Region: framework 2
F:51-67/Region: complementarity-determining 2
F:68-98/Region: framework 3
F:99-107/Region: complementarity-determining 3

Query Match 75.2%; Score 337; DB 2; Length 119;
Best Local Similarity 58.0%; Pred. No. 3.7e-26;
Matches 69; Conservative 13; Mismatches 5; Indels 32; Gaps 3;

QY 1 QIQLVSGGELVKPGASVRVSKASG-----YSFTVVRQSPGKLEWIG----- 43
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 QVLOVSGAEVFKPGSVKSVKASGDTTSSVAISWVRQAPGQGLEWGMGIPIPTANY 60

QY 44 -----GKATLTVDKSTAYMELSLRSRSDTAVYFCAR-----WGQGTIVTVSS 87
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 AQKQGRVITADESTAYMELSLRSRSDTAVYVCARGVYVYGVMDVWGQGTIVTVSS 119

RESULT 11
S41394
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Ig heavy chain V region - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 20-Jun-2000  
C:Accession: S41394  
R:Margartite, C.; Gilbert, D.; Brard, F.; Tron, F.  
submitted to the EMBL Data Library, January 1994  
A:Description: Structural characterization of an (NZB X NZW)F1 mouse-derived IgM anti-DN  
A:Reference number: S41393  
A:Accession: S41394  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-120 <MAR>  
A:Cross-references: EMBL:Z29586; NID:G452354; PIDN:CAA82703.1; PID:gi334080  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:15-98/Domain: immunoglobulin homology <IMW>  
Query Match 75.1%; Score 336.5; DB 2; Length 120;  
Best Local Similarity 58.3%; Pred. No. 4.1e-26;  
Matches 70; Conservative 12; Mismatches 5; Indels 33; Gaps 3;  
Qy 1 QIQLVQSGGELVKPGASVRVSCKASGYFT-----WVROSPGKGLWEI----- 43  
Db 1 EVQLQSGGELVKPGASVKLSKASGYFTSYWVHWKQRPQGLEWIGIEDPSDSYTY 60  
Qy 44 -----GKATLTVDKSTSTAYMELSSLRSEDTAVYFCAR-----WQGGTTVTYSS 87  
Db 61 NQKFKGKATLTVDKSSSTAYMQSSLTSDSAVYVCARRYGSRVSMQWGGQTSVTYSS 120  
RESULT 12  
S53751  
antibody Fab Jcl 103 heavy chain - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 23-Aug-1995 #sequence\_revision 19-Oct-1995 #text\_change 17-Mar-1999  
C:Accession: S53751  
R:Pokkuluri, P.R.; Bouthillier, F.; Li, Y.; Kuderova, A.; Lee, J.; Cygler, M.  
J. Mol. Biol. 243, 283-297, 1994  
A:Title: Preparation, characterization and crystallization of an antibody Fab fragment  
A:Reference number: S53750; MUID:95018269; PMID:7523684  
A:Accession: S53751  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-116 <POX>  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
F:15-98/Domain: immunoglobulin homology <IMW>  
Query Match 74.9%; Score 335.5; DB 2; Length 116;  
Best Local Similarity 60.3%; Pred. No. 5e-26;  
Matches 70; Conservative 11; Mismatches 6; Indels 29; Gaps 3;  
Qy 1 QIQLVQSGGELVKPGASVRVSCKASGYFT-----WVROSPGKGLWEI----- 43  
Db 1 QVQLQSGGELVKPGASVKLSKASGYFTSYWVHWKQRPQGLEWIGIEDPSDSYTY 60  
Qy 44 -----GKATLTVDKSTSTAYMELSSLRSEDTAVYFCAR-----WQGGTTVTYSS 87  
Db 61 NQKFKGKATLTVDSSSTAYMQSSLTSDSAVYVCANLRGYDYGQGGTTLTVSS 116  
RESULT 13  
PH0958  
Ig heavy chain V region (G6+ CUL-HUR) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 16-Aug-1996  
C:Accession: PH0958  
R:Martin, T.; Duffy, S.P.; Carson, D.A.; Kipps, T.J.  
J. Exp. Med. 175, 983-991, 1992  
A:Title: Evidence for somatic selection of natural autoantibodies.  
A:Reference number: PH0952; MUID:92202880; PMID:1552291  
A:Accession: PH0958  
A:Status: nucleic acid sequence not shown  
A:Molecule type: DNA

A:Residues: 1-122 <MAR>  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:1-30/Region: framework 1  
F:15-98/Domain: immunoglobulin homology <IMW>  
F:31-35/Region: complementarity-determining 1  
F:36-50/Region: framework 2  
F:51-67/Region: complementarity-determining 2  
F:68-98/Region: framework 3  
F:99-110/Region: complementarity-determining 3  
Query Match 74.9%; Score 335.5; DB 2; Length 122;  
Best Local Similarity 56.6%; Pred. No. 5.3e-26;  
Matches 69; Conservative 13; Mismatches 5; Indels 35; Gaps 3;  
Qy 1 QIQLVQSGGELVKPGASVRVSCKASG-----YGFVWROSPGKGLWEI----- 43  
Db 1 QVQLVQSGAEVKPGSSVKVCKASGTFSSYVAISWVRQAPGQGLEWMGGIIFPGTANY 60  
Qy 44 -----GKATLTVDKSTSTAYMELSSLRSEDTAVYFCAR-----WQGGTTVTY 85  
Db 61 AQKPGQRTITADESTSTAYMELSSLRSEDTAVYCARVNPFLFFAVGMDVWGGTITV 120  
Qy 86 SS 87  
Db 121 SS 122  
RESULT 14  
MHMS18  
Ig heavy chain precursor V region (B1-8) - mouse  
N:Contains: Ig heavy chain precursor V region 186-2  
C:Species: Mus musculus (house mouse)  
C:Date: 02-Apr-1982 #sequence\_revision 02-Apr-1982 #text\_change 22-Jun-1999  
C:Accession: A90809; B90809; A22769; A20234; A20236  
R:Bothwell, A.L.M.; Paskind, M.; Reth, M.; Imanishi-Kari, T.; Rajewsky, K.; Baltimore, I.  
Cell 24, 625-637, 1981  
A:Title: Heavy chain variable region contribution to the NP(b) family of antibodies: sei  
A:Reference number: A90809; MUID:81234548; PMID:6788376  
A:Accession: A90809  
A:Molecule type: DNA  
A:Residues: 1-139 <B18>  
A:Cross-references: GB:J00529; NID:gi95114; PIDN:AAA38170.1; PID:gi95115  
A:Accession: B90809  
A:Molecule type: DNA  
A:Residues: 1-117 <1862>  
A:Note: the B1-8 mu chain mRNA was cloned from a hybridoma making antibodies to the hap:  
A:Note: the 186-2 germline gene was cloned from a library of C57BL/6 DNA  
R:Dildrop, R.; Bruggemann, M.; Radbruch, A.; Rajewsky, K.; Beyreuther, K.  
EMBO J. 1, 635-640, 1982  
A:Title: Immunoglobulin V region variants in hybridoma cells. II. Recombination between  
A:Reference number: A90971; MUID:84236026; PMID:7188353  
A:Accession: A22769  
A:Molecule type: protein  
A:Residues: 20-139 <D11>  
A:Note: the V region of the B1-8 delta chain, derived as a spontaneous class switch var:  
of the mu chain  
C:Genetics:  
A:Introns: 16/1  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:1-19/Domain: signal sequence #status Predicted <SIG>  
F:20-139/Product: Ig kappa chain V region (B1-8) #status experimental <MAT>  
F:34-117/Domain: immunoglobulin homology <IMW>  
F:118-124/Region: D segment  
F:125-139/Region: J segment (JH2)  
Query Match 74.9%; Score 335.5; DB 1; Length 139;  
Best Local Similarity 58.3%; Pred. No. 6e-26;  
Matches 70; Conservative 11; Mismatches 6; Indels 33; Gaps 3;  
Qy 1 QIQLVQSGGELVKPGASVRVSCKASGYFT-----WVROSPGKGLWEI----- 44

Db 20 QVQLQQPGAEIVKPGASVKLSCKASGYTFSTSYMMHWVKQRPGRGLEWIGRIDPNSGGTKY 79  
QY 45 -----KATLTVDKSTSTAYMELSLRSEDPAVYFCAR-----WGQGTITVTVSS 87  
Db 80 NEKFKSKATLTVDKPSSTAYMQLSLTSEDSAVYICARYDYGSSYFDYWGQGTITVTVSS 139

## RESULT 15

PC4402  
pElB leader/Ig heavy chain anti-NP/linker type 205/alkaline phosphatase fusion protein -  
C:Species: synthetic  
C:Date: 06-Nov-1998 #sequence\_revision 06-Nov-1998 #text\_change 06-Nov-1998  
C:Accession: PC4402  
R:Suzuki, C.; Ueda, H.; Suzuki, E.; Nagamune, T.  
J. Biochem. 122, 322-329, 1997  
A:Title: Construction, bacterial expression, and characterization of hapten-specific sin  
A:Reference number: PC4402  
A:Accession: PC4402  
A:Molecule type: DNA  
A:Residues: 1-287 <SUZ>  
C:Keywords: fusion protein

Query Match 74.9%; Score 335.5; DB 4; Length 287;  
Best Local Similarity 58.3%; Pred. No. 1.2e-25;  
Matches 70; Conservative 11; Mismatches 6; Indels 33; Gaps 3;

QY 1 QIQLVQSGGELVKPGASVVRVSCKASGYST-----WVRQSPGKGLEWIG-----44  
Db 160 QVQLQQPGAEIVKPGASVKLSCKASGYTFSTSYMMHWVKQRPGRGLEWIGRIDPNSGGTKY 219  
QY 45 -----KATLTVDKSTSTAYMELSLRSEDPAVYFCAR-----WGQGTITVTVSS 87  
Db 220 NEKFKSKATLTVDKPSSTAYMQLSLTSEDSAVYICARYDYGSSYFDYWGQGTITVTVSS 279

Search completed: January 13, 2004, 12:44:40  
Job time : 7.30655 secs

GenCore version 5.1.6  
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# OM protein - protein search, using sw model

Run on: January 13, 2004, 12:19:34 ; Search time 3.79913 Seconds  
(without alignments)  
1076.912 Million cell updates/sec

Title: US-09-990-586-90

Perfect score: 448

Sequence: 1 QIQLVQSGGELVKPGASVRV.....DTAVVFCARWGQTTTVSS 87

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	335.5	74.9	139	1 HV07_MOUSE	P01751 mus musculus
2	329.5	73.5	137	1 HV11_MOUSE	P01755 mus musculus
3	329	73.4	117	1 HV12_MOUSE	P01756 mus musculus
4	329	73.4	117	1 HV13_MOUSE	P01757 mus musculus
5	322.5	72.0	118	1 HV51_MOUSE	P06330 mus musculus
6	319	71.2	120	1 HV03_MOUSE	P01747 mus musculus
7	318.5	71.1	120	1 HV50_MOUSE	P06329 mus musculus
8	315	70.3	140	1 HV02_MOUSE	P01746 mus musculus
9	311	69.4	138	1 HV48_MOUSE	P03980 mus musculus
10	305	68.1	121	1 HV01_MOUSE	P01745 mus musculus
11	302.5	67.5	147	1 HV1C_HUMAN	P01749 mus sapien
12	293	65.4	117	1 HV05_MOUSE	P01748 mus musculus
13	293	65.4	117	1 HV14_MOUSE	P01758 mus musculus
14	292	65.2	117	1 HV06_MOUSE	P01750 mus musculus
15	292	65.2	117	1 HV1B_HUMAN	P01743 homo sapien
16	292	65.2	117	1 HV52_MOUSE	P06327 mus musculus
17	289	64.5	117	1 HV09_MOUSE	P01753 mus musculus
18	289	64.5	136	1 HV15_MOUSE	P01759 mus musculus
19	287	64.1	117	1 HV04_MOUSE	P01748 mus musculus
20	286.5	64.0	114	1 HV3B_HUMAN	P01763 homo sapien
21	286	63.8	117	1 HV49_MOUSE	P06328 mus musculus
22	285.5	63.7	114	1 HV00_MOUSE	P01741 mus musculus
23	285	63.6	117	1 HV10_MOUSE	P01754 mus musculus
24	285	63.6	117	1 HV1A_HUMAN	P01742 homo sapien
25	281	62.7	119	1 HV3I_HUMAN	P01781 homo sapien
26	280.5	62.6	116	1 HV3T_HUMAN	P01780 homo sapien
27	280.5	62.6	124	1 HV1D_HUMAN	P23083 homo sapien
28	279	62.3	117	1 HV1G_HUMAN	P23083 homo sapien
29	279	62.3	121	1 HV3J_HUMAN	P01771 homo sapien
30	278.5	62.2	122	1 HV3G_HUMAN	P01768 homo sapien
31	276.5	61.7	122	1 HV3H_HUMAN	P01769 homo sapien
32	271.5	60.6	122	1 HV3A_HUMAN	P01762 homo sapien
33	271.5	60.6	126	1 HV3K_HUMAN	P01772 homo sapien

34	269.5	60.2	119	1 HV38_MOUSE	P01808 mus musculus
35	267.5	59.7	124	1 HV1E_HUMAN	P01761 homo sapien
36	267	59.6	115	1 HV3F_HUMAN	P01767 homo sapien
37	267	59.6	125	1 HV1F_HUMAN	P06326 homo sapien
38	266.5	59.5	119	1 HV37_MOUSE	P01807 mus musculus
39	266.5	59.0	136	1 HV16_MOUSE	P01783 mus musculus
40	263.5	58.8	114	1 HV01_CANFA	P01784 canis famil
41	263	58.7	117	1 HV41_MOUSE	P01811 mus musculus
42	262.5	58.6	119	1 HV40_MOUSE	P01810 mus musculus
43	261.5	58.4	120	1 HV1H_HUMAN	P80421 homo sapien
44	261	58.3	142	1 HV01_RAT	P01805 rattus norv
45	260.5	58.1	122	1 HV21_MOUSE	P01790 mus musculus

## ALIGNMENTS

RESULT 1  
HV07\_MOUSE  
ID HV07\_MOUSE STANDARD; PRT; 139 AA.  
AC P01751; P01752;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Ig heavy chain V region B1-8/186-2 precursor.  
OS Mus musculus (Mouse)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6;  
RX MEDLINE=81234548; PubMed=6788376;  
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,  
RA Baltimore D.;  
RT "Heavy chain variable region contribution to the NPB family of  
RT antibodies: somatic mutation evident in a gamma 2a variable region.";  
RL Cell 24:625-637(1981).  
CC -!- MISCELLANEOUS: THE B1-8 MU CHAIN MRNA WAS CLONED FROM A HYBRIDOMA  
CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL  
CC (NPB ANTIBODIES).  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL; J00529; AAA38170.1; -.  
CC PIR; A90809; MHMS18.  
CC PDB; 1A6U; 27-MAY-98.  
CC PDB; 1A6W; 15-JUL-98.  
CC InterPro; IPR007110; Ig-like.  
CC InterPro; IPR003006; Ig\_MHC.  
CC InterPro; IPR003596; Ig\_V.  
CC Pfam; PF00047; Ig; 1.  
CC SMART; SM00406; IGV; 1.  
CC PROSITE; PS50835; IG LIKE; 1.  
CC Immunoglobulin V region; Signal; 3D-structure.  
CC SIGNAL  
CC 1 19  
CC CHAIN 20 139 IG HEAVY CHAIN V REGION B1-8/186-2.  
CC DOMAIN 20 49 FRAMEWORK-1.  
CC DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.  
CC DOMAIN 55 68 FRAMEWORK-2.  
CC DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.  
CC DOMAIN 86 117 FRAMEWORK-3.  
CC DOMAIN 118 124 D SEGMENT.  
CC DOMAIN 125 139 JH2 SEGMENT.  
CC DISULFID 41 115 BY SIMILARITY.  
CC NON TER 139 139  
CC SEQUENCE 139 AA; 15419 MW; 1B57DD4FD0C9F465 CRC64;

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Query Match      74.9%; Score 335.5; DB 1; Length 139;
Best Local Similarity 58.3%; Pred. No. 2e-31;
Matches 70; Conservative 11; Mismatches 6; Indels 33; Gaps 3;

QY 1 QIOLVQSGGELVKPGASVRVSKASGYSTFT-----WVRQSPGKLEWIG----- 44
Db 20 QVQLQPGAGELVKPGASVKLSCKASGYTFTSYLMMHWVQKQPGKLEWIGRIDPNSGGTTY 79
QY 45 -----KATLTVDKSTAYMELSSLSRSDTAYVFCAR-----WGQTTVTYSS 87
Db 80 NEHFRSKATLTVDKPSSTAYMQLSLTSDSAVYICARYLGRFYDWYFVWGQTTLTIVSS 137

RESULT 2
HV11 MOUSE
ID HV11_MOUSE STANDARD; PRT; 137 AA.
AC P01755;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 943 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81234548; PubMed=6789376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPB family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -|- MISCELLANEOUS: THE GAMMA-2A CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
CC (NPB ANTIBODIES).
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC -----
CC EMBL; J00539; AAA38172.1; -
CC PIR; A02038; G2MS43.
CC HSSP; P01810; 2FBJ.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003006; Ig_MHC.
CC InterPro; IPR003596; Ig_V.
CC Pfam; PF00047; Ig; 1.
CC SMART; SM00406; IGv; 1.
CC PROSITE; PS50835; IG_LIKE; 1.
CC Immunoglobulin V region; Signal.
CC SIGNAL 1 19
CC CHAIN 20 137 IG HEAVY CHAIN V REGION S43.
CC DOMAIN 20 49 FRAMEWORK-1.
CC DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
CC DOMAIN 55 68 FRAMEWORK-2.
CC DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
CC DOMAIN 86 117 FRAMEWORK-3.
CC DOMAIN 118 122 D SEGMENT.
CC DOMAIN 123 137 JH2 SEGMENT.
CC DISULFID 41 115 BY SIMILARITY.
CC NON_TER 137 137
CC SEQUENCE 137 AA; 15200 MW; ADDS881BF44B8EC9 CRC64;

Query Match      73.5%; Score 329.5; DB 1; Length 137;
Best Local Similarity 57.6%; Pred. No. 9.5e-31;
Matches 68; Conservative 11; Mismatches 8; Indels 31; Gaps 3;

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QY 1 QIOLVQSGGELVKPGASVRVSKASGYSTFT-----WVRQSPGKLEWIG----- 44
Db 20 QVQLQPGAGELVKPGASVKLSCKASGYTFTSYLMMHWVQKQPGKLEWIGRIDPNSGGTTY 79
QY 45 -----KATLTVDKSTAYMELSSLSRSDTAYVFCAR-----WGQTTVTYSS 87
Db 80 NEHFRSKATLTVDKPSSTAYMQLSLTSDSAVYICARYLGRFYDWYFVWGQTTLTIVSS 137

RESULT 3
HV12 MOUSE
ID HV12_MOUSE STANDARD; PRT; 117 AA.
AC P01756;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region MOPC 104E.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE, AND CARBOHYDRATE-LINKAGE SITE ASN-55.
RX MEDLINE=83075344; PubMed=6816276;
RA Kehry M.R., Fuhrman J.S., Schilling J.W., Rogers J., Sibley C.H.,
RA Hood L.E.;
RT "Complete amino acid sequence of a mouse mu chain: homology among
RT heavy chain constant region domains.";
RL Biochemistry 21:5415-5424(1982).
CC -|- MISCELLANEOUS: THE SEQUENCE OF THE LIGHT CHAIN OF THIS IGM MYELOMA
CC PROTEIN HAS ALSO BEEN DETERMINED.
CC -|- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
CC -|- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC PIR; A02039; MMS4E.
CC HSSP; P01789; IMCP.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003006; Ig_MHC.
CC InterPro; IPR003596; Ig_V.
CC Pfam; PF00047; Ig; 1.
CC SMART; SM00406; IGv; 1.
CC PROSITE; PS50835; IG_LIKE; 1.
CC Immunoglobulin V region; Glycoprotein.
CC DOMAIN 1 116 IG-LIKE.
CC DISULFID 22 96 BY SIMILARITY.
CC CARBOHYD 55 55 N-LINKED (GLCNAC. .) (COMPLEX).
CC NON_TER 117 117
CC SEQUENCE 117 AA; 12983 MW; 3CF8ACE4B447B41 CRC64;

Query Match      73.4%; Score 329; DB 1; Length 117;
Best Local Similarity 59.8%; Pred. No. 9e-31;
Matches 70; Conservative 11; Mismatches 6; Indels 30; Gaps 3;

QY 1 QIOLVQSGGELVKPGASVRVSKASGYSTFT-----WVRQSPGKLEWIG----- 43
Db 1 EVQLQSGGPELVKPGASVKMSCKASGYTFTDYMMKWVKQSHGKSLKLEWIGDINPNNGGTSY 60
QY 44 -----GKATLTVDKSTAYMELSSLSRSDTAYVFCAR-----WGQTTVTYSS 87
Db 61 NQKFKRATLTVDKSSSTAYMQLNSLTSDSAVYICARYLGRFYDWYFVWGAGTFTIVSS 117

RESULT 4
HV13 MOUSE
ID HV13_MOUSE STANDARD; PRT; 117 AA.
AC P01757;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region J558.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;

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RN SEQUENCE.
RP MEDLINE=80078170; PubMed=6765983;
RA Schilling J., Clevinger B., Davis J.M., Hood L.;
RT "Amino acid sequence of homogeneous antibodies to dextran and DNA
RL Nature 283:35-40(1980).
CC -!- MISCELLANEOUS: THE SEQUENCES OF 10 HYBRIDOMA PROTEINS THAT ALSO
CC BIND DEXTRAN DIFFER FROM THAT SHOWN AT 1-7 POSITIONS, MANY OF
CC WHICH OCCUR IN THE D AND J SEGMENTS.
CC -!- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A26242; MEMSJS.
DR HSSP; P01789; IMCP.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DISULFID 22 96
FT NON TER 117 117
FT SEQUENCE 117 AA; 13024 MW; 292EAF4BE447E41 CRC64;

Query Match 73.4%; Score 329; DB 1; Length 117;
Best Local Similarity 59.8%; Pred. No. 9e-31;
Matches 70; Conservative 11; Mismatches 6; Indels 30; Gaps 3;

QY 1 QIQVQSGGELVKPGASVRVSCKASGYFT-----WVRSQPGKGLEW----- 43
DB 1 EVQLQSGPELVKPGASVKISCKASGYFTDYNNWVKQSHGKSLWIGDINPNNGTSTY 60
QY 44 -----GKATLTVDKSTSTAYMELSLRSEDYAVFCAR-----WGQGTITVTVSS 87
DB 61 NQKPKGKATLTVDKSSSTAYMQLNSLTSEDSAVYCYCARDYVYDVGAGTITVTVSS 117

RESULT 5
HV51 MOUSE
ID HV51 MOUSE STANDARD; PRT; 118 AA.
AC P06330;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region AC38 205.12.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RA Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;
RT "A V region determinant (idiotope) expressed at high frequency in B
RT lymphocytes is encoded by a large set of antibody structural genes.";
RL EMBO J. 3:517-523(1984).
DR PIR; A02040; MEMS38.
DR HSSP; P01789; IMCP.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 98 V SEGMENT.
FT DOMAIN 99 104 D SEGMENT.
FT DOMAIN 105 118 J SEGMENT.
FT DISULFID 22 96
FT NON TER 118 118
FT SEQUENCE 118 AA; 12934 MW; 94F7BEE4C762A018 CRC64;

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Query Match 72.0%; Score 322.5; DB 1; Length 118;
Best Local Similarity 58.5%; Pred. No. 5.1e-30;
Matches 69; Conservative 9; Mismatches 9; Indels 31; Gaps 3;

QY 1 QIQVQSGGELVKPGASVRVSCKASGYFT-----WVRSQPGKGLEW----- 43
DB 1 EVQLQSGPELVKPGASVKISCKASGYFTDYNNWVKQSHGKSLWIGDINPNNGTSTY 60
QY 44 -----GKATLTVDKSTSTAYMELSLRSEDYAVFCAR-----WGQGTITVTVSS 87
DB 61 NQKPKGKATLTVDKSSSTAYMELSLTSEDSAVYCYCARDYVYDVGAGTITVTVSS 118

RESULT 6
HV03 MOUSE
ID HV03 MOUSE STANDARD; PRT; 120 AA.
AC P01747;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region 36-65.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83131846; PubMed=6186498;
RA Siekevitz M., Getter M.L., Brodeur P., Riblet R.,
RA Marshak-Rothstein A.;
RT "The genetic basis of antibody production: the dominant anti-arsonate
RT idiotype response of the strain A mouse.";
RL Eur. J. Immunol. 12:1023-1032(1982).
CC -!- MISCELLANEOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER
CC DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE AUTHORS
CC CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED TO THE SAME J
CC SEGMENT, JH2.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR HSSP; P01789; IMCP.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Hybridoma.
FT DOMAIN 1 111 IG-LIKE.
FT NON TER 120 120
FT SEQUENCE 120 AA; 13307 MW; FF04E4A167B654AF CRC64;

Query Match 71.2%; Score 319; DB 1; Length 120;
Best Local Similarity 55.8%; Pred. No. 1.3e-29;
Matches 67; Conservative 12; Mismatches 7; Indels 34; Gaps 3;

QY 2 QIQVQSGGELVKPGASVRVSCKASGYFT-----WVRSQPGKGLEW----- 43
DB 1 VQLQSGGAEIVRAGSVKMSCKASGYFTSYGINWVKORPGQGLEWIGYINPFGNYTKYN 60
QY 44 -----GKATLTVDKSTSTAYMELSLRSEDYAVFCAR-----WGQGTITVTVSS 87
DB 61 EKFKGKTLTVDKSSSTAYMQLNSLTSEDSAVYFCARVYGGSYFDVWGQGTITVTVSS 120

RESULT 7
HV50 MOUSE
ID HV50 MOUSE STANDARD; PRT; 120 AA.
AC P06329;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region AC38 15.3.
OS Mus musculus (Mouse).

```



OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
SEQUENCE.  
RX MEDLINE=84182519; PubMed=6201362;  
RA Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;  
RT "A V region determinant (idiotope) expressed at high frequency in B  
lymphocytes is encoded by a large set of antibody structural genes.";  
RL ENBO J. 3:517-523(1984).  
DR HSP; P01810; 2FBJ.  
DR InterPro: IPR007110; Ig-like.  
DR InterPro: IPR003006; Ig\_MHC.  
DR InterPro: IPR003596; Ig\_V.  
DR Pfam: PF00047; Ig; 1.  
DR SMART; SMO0406; Ig; 1.  
DR PROSITE; PS0835; IG\_LIKE; 1.  
KW Immunoglobulin V region.  
FT DOMAIN 1 98 V SEGMENT.  
FT DOMAIN 99 105 D SEGMENT.  
FT DOMAIN 106 120 J SEGMENT.  
FT DISULFID 22 96 BY SIMILARITY.  
FT NON\_TER 120 120  
SQ SEQUENCE 120 AA; 13311 MW; 914453P426F09834 CRC64;

Query Match 71.1%; Score 318.5; DB 1; Length 120;  
Best Local Similarity 55.8%; Pred. No. 1.5e-29;  
Matches 67; Conservative 11; Mismatches 9; Indels 33; Gaps 3;

QY 1 QIOLVSGGELVKPGASVRVSKASGYST-----WVROSPGKGLWIG----- 44  
DB 1 QVQLQPGTGLVKPGASVNLSCASGYSTYSVMHWIRQPGGLEWIGINPSNGGNY 60  
QY 45 -----KATLTVDKSTSTAYMELSSRSBDTAVYFCAR-----WGQGTITVTVSS 87  
DB 61 NEKFSGKATLTVDKSSSATYMQLSLTSDSAVYFCARVDYGDYFDVWGQGTITVTVSS 120

RESULT 8  
HV02 MOUSE  
ID HV02 MOUSE STANDARD; PRT; 140 AA.  
AC P01746;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Ig heavy chain V region 93G7 precursor.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
SEQUENCE FROM N.A.  
RP STRAIN=A/J;  
RX MEDLINE=82152818; PubMed=6801765;  
RA Sims J., Rabbitts T.H., Estess P., Slaughter C., Tucker P.W.,  
RA Capra J.D.;  
RT "Somatic mutation in genes for the variable portion of the  
immunoglobulin heavy chain".  
RL Science 216:309-311(1982).  
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch).  
CC -----  
CC EMBL; J00493; AAA38128.1; -.  
DR PIR; A94264; HVMSG7.  
DR HSP; P01810; 2FBJ.

DR InterPro: IPR007110; Ig-like.  
DR InterPro: IPR003006; Ig\_MHC.  
DR InterPro: IPR003596; Ig\_V.  
DR Pfam: PF00047; Ig; 1.  
DR SMART; SMO0406; Ig; 1.  
DR PROSITE; PS0835; IG\_LIKE; 1.  
KW Immunoglobulin V region; Hybridoma; Signal.  
FT SIGNAL 1 19  
FT CHAIN 20 140 IG HEAVY CHAIN V REGION 93G7.  
FT DOMAIN 20 139 IG-LIKE.  
FT NON\_TER 140 140  
SQ SEQUENCE 140 AA; 15514 MW; 25A4CBBE31DA5CE8 CRC64;

Query Match 70.3%; Score 315; DB 1; Length 140;  
Best Local Similarity 54.5%; Pred. No. 4.4e-29;  
Matches 66; Conservative 13; Mismatches 8; Indels 34; Gaps 3;

QY 1 QIOLVSGGELVKPGASVRVSKASGYST-----WVROSPGKGLWIG----- 43  
DB 20 EVQLQSGAELVRAGSSVMSCKASGYTTSVGINVWKQRPQGLEWIGVINGVINY 79  
QY 44 -----GKATLTVDKSTSTAYMELSSRSBDTAVYFCAR-----WGQGTITVTVSS 86  
DB 80 NEKFSGKATLTVDKSSSATYMQLSLTSDSAVYFCARSHYGGSYDFDYWGQGTITVTVSS 139  
QY 87 S 87  
DB 140 S 140

RESULT 9  
HV48 MOUSE  
ID HV48 MOUSE STANDARD; PRT; 138 AA.  
AC P03980;  
DT 23-OCT-1986 (Rel. 02, Created)  
DT 23-OCT-1986 (Rel. 02, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig heavy chain V region TEPC 1017 precursor.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
SEQUENCE FROM N.A.  
RP MEDLINE=84248078; PubMed=6429663;  
RA Gilliam A.C., Shen A., Richards J.E., Blattner F.R., Mushinski J.P.,  
RA Tucker P.W.;  
RT "Illegitimate recombination generates a class switch from C mu to C  
delta in an IgD-secreting plasmacytoma".  
RL Proc. Natl. Acad. Sci. U.S.A. 81:4164-4168(1984).  
DR PIR; A02033; HVMS7.  
DR HSP; P01810; 2FBJ.  
DR InterPro: IPR007110; Ig-like.  
DR InterPro: IPR003006; Ig\_MHC.  
DR InterPro: IPR003596; Ig\_V.  
DR Pfam: PF00047; Ig; 1.  
DR SMART; SMO0406; Ig; 1.  
DR PROSITE; PS0835; IG\_LIKE; 1.  
KW Immunoglobulin V region; Signal.  
FT SIGNAL 1 20  
FT CHAIN 21 138 IG HEAVY CHAIN V REGION TEPC 1017.  
FT DOMAIN 21 49 FRAMEWORK-1.  
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.  
FT DOMAIN 55 68 FRAMEWORK-2.  
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.  
FT DOMAIN 86 117 FRAMEWORK-3.  
FT DOMAIN 118 127 COMPLEMENTARITY-DETERMINING-3.  
FT DOMAIN 128 138 FRAMEWORK-4.  
FT DISULFID 41 115 BY SIMILARITY.  
FT NON\_TER 138 138  
SQ SEQUENCE 138 AA; 15576 MW; 748157E4C6907B8E CRC64;

Query Match 69.4%; Score 311; DB 1; Length 138;

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Best Local Similarity 55.5%; Pred. No. 1.3e-28;
Matches 66; Conservative 12; Mismatches 9; Indels 32; Gaps 3;

QY 1 QIQLVQSGGELVKPGASVRVSKASGYSTFT-----WVRQSPGKGLWIG-----44
DB 20 QVQLQQCAELVKPGASVQLSKASGHTFTNYWHYKQRPQGGLWIGINFDGSRNY 79
QY 45 -----KATLTVDKSTSTAYMELSLRSEDTAIVFCAR-----WGQGTIVTVSS 87
DB 80 NEKPKKATLTVDKSSSTAYMQLSSLTPESFANVYCARSDGYVDWFFYWGQGLTVFSA 138

RESULT 10
ID HV01_MOUSE STANDARD; PRT; 121 AA.
AC P01745;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region MPC 11.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81053741; PubMed=6253904;
RA Zakut R., Cohen J., Givol D.;
RT "Cloning and sequence of the cDNA corresponding to the variable
RT region of immunoglobulin heavy chain MPC11.";
RL Nucleic Acids Res. 8:3591-3601(1980).
RN [2]
RP REVISIONS.
RA Zakut R., Cohen J., Givol D.;
RL Nucleic Acids Res. 8:4839-4840(1980).
CC -!- MISCELLANEOUS: THIS SEQUENCE WAS TRANSLATED FROM AN MRNA ISOLATED
CC FROM A MYELOMA THAT SECRETES IGG2B.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A93708; GVMS11.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 112 IG-LIKE.
FT NON_TER 121 121
SQ SEQUENCE 121 AA; 13135 MW; 227AEF3EC56ED0BF CRC64;

Query Match 68.1%; Score 305; DB 1; Length 121;
Best Local Similarity 52.1%; Pred. No. 5.3e-28;
Matches 63; Conservative 14; Mismatches 10; Indels 34; Gaps 3;

QY 1 QIQLVQSGGELVKPGASVRVSKASGYSTFT-----WVRQSPGKGLWIG-----43
DB 1 EAQVQSSAELVREGTSVKISKAGYFTFTNYWGWKRPGLWIGIYFGGFTNY 60
QY 44 -----GKATLTVDKSTSTAYMELSLRSEDTAIVFCAR-----WGQGTIVTVSS 86
DB 61 NDNLKGTATLADTSSSPAYIQLSLTSSEDSALYHCARGIYNSSPYFDSWGQGTILTVS 120
QY 87 S 87
DB 121 S 121

RESULT 11
ID HV1C_HUMAN STANDARD; PRT; 147 AA.
AC P01744;
DT 21-JUL-1986 (Rel. 01, Created)
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DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-I region ND precursor (Fragments).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83065234; PubMed=6815656;
RA Kenten J.H., Molgaard H.V., Houghton M., Derbyshire R.B., Viney J.,
RA Bell L.O., Gould H.J.;
RT "Cloning and sequence determination of the gene for the human
RT immunoglobulin epsilon chain expressed in a myeloma cell line.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:6661-6665(1982).
RN [2]
RP SEQUENCE OF 20-147.
RA Bernich H.H., Johansson S.G.O., von Bahr-Lindstrom H.;
RL (in) Bach M.K. (eds.);
RL Immediate hypersensitivity: modern concepts and developments, pp.1-36,
RL Marcel Dekker, New York (1978).
CC -!- MISCELLANEOUS: THIS EPSILON CHAIN WAS ISOLATED FROM A MYELOMA
CC PROTEIN.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR HSSP; P01789; 1MCP.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal; Pyrrolidone carboxylic acid.
FT CHAIN 1 19
FT DOMAIN 20 147 IG HEAVY CHAIN V-I REGION ND.
FT MOD_RES 20 20 IG-LIKE.
FT DISULFID 41 115 PYRROLIDONE CARBOXYLIC ACID.
FT CONFLICT 21 21 T -> V (IN REF. 2).
FT CONFLICT 53 54 IH -> HI (IN REF. 2).
FT CONFLICT 67 68 VG -> GV (IN REF. 2).
FT CONFLICT 125 125 MISSING (IN REF. 2).
FT NON_TER 147 147
SQ SEQUENCE 147 AA; 16491 MW; 948F9F72A5366C20 CRC64;

Query Match 67.5%; Score 302.5; DB 1; Length 147;
Best Local Similarity 50.0%; Pred. No. 1.3e-27;
Matches 64; Conservative 13; Mismatches 10; Indels 41; Gaps 3;

QY 1 QIQLVQSGGELVKPGASVRVSKASGYSTFT-----WVRQSPGKGLWIG-----43
DB 20 QIQLVQSGAEVKPKGASVRVSKASGYTFIDSYTHWIRQAQGHGIEWINPNSGCTNY 79
QY 44 -----GKATLTVDKSTSTAYMELSLRSEDTAIVFCAR-----WGQ 79
DB 80 APRFGQRTVMTDASFTAYMDLRSLRSDDSAVFYCAKSDPFWSDYNYFDYSLDVMGQ 139
QY 80 GTTVTVSS 87
DB 140 GTTVTVSS 147

RESULT 12
ID HV05_MOUSE STANDARD; PRT; 117 AA.
AC P01749;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ig heavy chain V region 3 precursor.
OX IGH-VJ558.
```

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OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J.
RX MEDLINE=81234548; PubMed=6789376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPb family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -1- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPb ANTIBODIES.
CC -----
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CC -----
CC EMBL; J00536; AAA38605.1; -.
CC PIR; A02031; HVMS3.
CC HSP; P01810; 2FBJ.
CC MGD; MGI:96486; Igh-VJ558.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003006; Ig_MHC.
CC InterPro; IPR003596; Ig_V.
CC Pfam; PF00047; Ig; 1.
CC SMART; SM00406; IGV; 1.
CC PROSITE; PS50835; IGV LIKE; 1.
CC Immunoglobulin V region; Signal.
FT CHAIN 1
FT DOMAIN 20 117 IG HEAVY CHAIN V REGION 3.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117
FT SEQUENCE 117 AA; 13016 MW; 4270861C53975EDC CRC64;

Query Match 65.4%; Score 293; DB 1; Length 117;
Best Local Similarity 60.2%; Pred. No. 1.2e-26;
Matches 59; Conservative 12; Mismatches 5; Indels 22; Gaps 2;

Qy 1 QIQLVQSGGELVKPGASVRYVSCKASGYFT-----WYRQSPGKLEWIG----- 44
Db 20 QVQLQPGAEIVRGSSVYKLSCKASGYFTSYNDWVYKQPGGLEWIGNIYPSDSETHY 79
Qy 45 -----KATLTVDKSTATYNELSLRSEDSTAYVFCAR 76
Db 80 NQKFKDKATLTVDKSSSTAYNQLSSLTSEDSAVVYCAR 117

RESULT 13
ID HV14 MOUSE STANDARD; PRT; 117 AA.
AC P01758;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region 108A precursor.
GN IGH-VJ558.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]

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RP SEQUENCE FROM N.A.
RX MEDLINE=81245215; PubMed=6789211;
RA Givoli D., Zakut R., Efron K., Rechavi G., Ram D., Cohen J.B.;
RA "Diversity of germ-line immunoglobulin VH genes.";
RL Nature 292:426-430(1981).
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC -----
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CC -----
CC EMBL; J00488; AAA38519.1; -.
CC PIR; A02041; HVMS8A.
CC HSP; P01810; 2FBJ.
CC MGD; MGI:96486; Igh-VJ558.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003006; Ig_MHC.
CC InterPro; IPR003596; Ig_V.
CC Pfam; PF00047; Ig; 1.
CC SMART; SM00406; IGV; 1.
CC PROSITE; PS50835; IGV LIKE; 1.
CC Immunoglobulin V region; Signal.
FT CHAIN 1
FT DOMAIN 20 117 IG HEAVY CHAIN V REGION 108A.
FT DOMAIN 20 >117 IG-LIKE.
FT NON_TER 117
FT SEQUENCE 117 AA; 12972 MW; 428CB44DF25D1BC2 CRC64;

Query Match 65.4%; Score 293; DB 1; Length 117;
Best Local Similarity 62.2%; Pred. No. 1.2e-26;
Matches 61; Conservative 9; Mismatches 6; Indels 22; Gaps 2;

Qy 1 QIQLVQSGGELVKPGASVRYVSCKASGYFT-----WYRQSPGKLEWIG----- 44
Db 20 EVQLQQSGPELVKPGASVKISCKASGYFTFDYNNHWYKQSHGKSLWIGYIYPNGGTGY 79
Qy 45 -----KATLTVDKSTATYNELSLRSEDSTAYVFCAR 76
Db 80 NQKFKSKATLTVDNSSSTAYNELSLTSEDSAVVYCAR 117

RESULT 14
ID HV06 MOUSE STANDARD; PRT; 117 AA.
AC P01750;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 102 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J.
RX MEDLINE=81234548; PubMed=6789376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPb family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -1- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPb ANTIBODIES.
CC -----
CC PIR; A02032; HVMS02.
CC HSP; P01810; 2FBJ.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003006; Ig_MHC.
CC InterPro; IPR003596; Ig_V.

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DR Pfam; PF00047; Ig; 1.
DR SMART; SMO0406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 102.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON TER 117
SQ SEQUENCE 117 AA; 12867 MW; 740A65DD851FCASC CRC64;

Query Match 65.2%; Score 292; DB 1; Length 117;
Best Local Similarity 62.5%; Pred. No. 1.6e-26;
Matches 60; Conservative 9; Mismatches 5; Indels 22; Gaps 2;

QY 2 IQLVQSGGELVKPGASVRSCKASGYSTFT-----WVRQSPGKGLEWNT----- 43
Db 21 VLQLOQPGAELVKPGASVRSCKASGYSTFTSYMHWKVRQPGQGLEWIGRIHPDSDTNYN 80
QY 44 ----GKATLTVDKSTSTAYMELSLRSEDVAVYFCA 75
Db 81 QKFKGKATLTVDKSSSTAYMQLSLTSEDSAVYICA 116

RESULT 15
HVLB HUMAN STANDARD; PRT; 117 AA.
AC P01743;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-I region Hg3 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83144028; PubMed=6298778;
RA Rechavi G., Ram D., Glazer L., Zakut R., Givol D.;
RT "Evolutionary aspects of immunoglobulin heavy chain variable region (VH) gene subgroups.";
RL Proc. Natl. Acad. Sci. U.S.A. 80:855-859(1983).
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC -----
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CC -----
DR EMBL; J00240; AAB52988.1; -.
DR PIR; A02024; HVHUG.
DR HSP; P01772; 2FB4.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SMO0406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1
FT CHAIN 20 117 IG HEAVY CHAIN V-I REGION HG3.
FT DOMAIN 20 >117 IG-LIKE.
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```
FT NON TER 117
SQ SEQUENCE 117 AA; 12946 MW; 2D3F92FC60CD1FE7 CRC64;

Query Match 65.2%; Score 292; DB 1; Length 117;
Best Local Similarity 60.2%; Pred. No. 1.6e-26;
Matches 59; Conservative 10; Mismatches 7; Indels 22; Gaps 2;

QY 1 QIQLVQSGGELVKPGASVRSCKASGYSTFT-----WVRQSPGKGLEWNT----- 43
Db 20 QVQLVQSGAEVKKPGASVKVSCKASGYTFNSYMHVWVRQAPGQGLEWMGIINPSGGSTSY 79
QY 44 ----GKATLTVDKSTSTAYMELSLRSEDVAVYFCA 76
Db 80 AQKFGKATLTVDKSTSTAYMELSLRSEDVAVYCAR 117

Search completed: January 13, 2004, 12:39:26
Job time : 4.79913 secs
```

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 13, 2004, 12:20:44 ; Search time 15.5764 Seconds  
(without alignments)  
1441.318 Million cell updates/sec

Title: US-09-990-586-90  
Perfect score: 448  
Sequence: 1 QIQLVQSGELVPGASVRV.....DTAVYFCARWGQTTVTVSS 87

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

SPTREMBL 23:\*

- 1: sp\_arChaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phase:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_virus:\*
- 16: sp\_bacteriap:\*
- 17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	340	75.9	473	11 Q9D8L4	Q9d8l4 mus musculus
2	339.5	75.8	137	11 Q924R6	Q924r6 mus musculus
3	338	75.4	142	11 Q924Q1	Q924q1 mus musculus
4	337.5	75.3	141	11 Q924Q4	Q924q4 mus musculus
5	337	75.2	140	11 Q924A2	Q924a2 mus musculus
6	335.5	74.9	143	11 Q924R0	Q924r0 mus musculus
7	335.5	74.9	145	11 Q924Q7	Q924q7 mus musculus
8	335	74.8	146	11 Q924R8	Q924r8 mus musculus
9	335	74.8	146	11 Q924Q6	Q924q6 mus musculus
10	334.5	74.7	145	11 Q924Q9	Q924q9 mus musculus
11	334.5	74.7	145	11 Q924R1	Q924r1 mus musculus
12	334.5	74.7	145	11 Q924R4	Q924r4 mus musculus
13	334.5	74.6	146	11 Q924Q3	Q924q3 mus musculus
14	334	74.6	146	11 Q924Q5	Q924q5 mus musculus
15	333.5	74.4	143	11 Q924Q3	Q924q3 mus musculus
16	332.5	74.2	145	11 Q924R3	Q924r3 mus musculus

17	332	74.1	117	11 Q9QXP0	Q9qx0 mus musculus
18	331.5	74.0	482	11 Q8K172	Q8k172 mus musculus
19	331	73.9	117	11 Q9QXE9	Q9qx9 mus musculus
20	330.5	73.8	143	11 Q924R7	Q924r7 mus musculus
21	329	73.4	119	5 Q9GYZ2	Q9gyz2 schistosoma
22	328.5	73.3	143	11 Q924Q0	Q924q0 mus musculus
23	328.5	73.3	145	11 Q924P7	Q924p7 mus musculus
24	328	73.2	481	11 Q91WT1	Q91wt1 mus musculus
25	327.5	73.1	143	11 Q924P9	Q924p9 mus musculus
26	327	73.0	142	11 Q924Q2	Q924q2 mus musculus
27	327	73.0	144	11 Q924P5	Q924p5 mus musculus
28	325.5	72.7	143	11 Q91VA2	Q91va2 mus musculus
29	325	72.5	140	11 Q924P8	Q924p8 mus musculus
30	324.5	72.4	143	11 Q924P6	Q924p6 mus musculus
31	323	72.1	119	4 Q8UL94	Q8ul94 homo sapien
32	323	72.1	123	11 Q8V1U1	Q8v1u1 mus musculus
33	323	72.1	147	11 Q925S3	Q925s3 mus musculus
34	322.5	72.0	124	4 Q8UL92	Q8ul92 homo sapien
35	322.5	72.0	139	11 Q924R5	Q924r5 mus musculus
36	322.5	72.0	463	11 Q99LC4	Q99lc4 mus musculus
37	320.5	71.5	159	4 Q96QS0	Q96qs0 homo sapien
38	320.5	71.1	118	11 Q9Z1C4	Q9z1c4 mus musculus
39	317.5	70.9	143	11 Q91V67	Q91v67 mus musculus
40	316	70.5	474	11 Q8R3H6	Q8r3h6 mus musculus
41	315.5	70.4	488	11 Q8K0F2	Q8k0f2 mus musculus
42	315.5	70.4	500	4 Q8BRV0	Q8brv0 homo sapien
43	315.5	70.4	613	11 Q8VCX7	Q8vcx7 mus musculus
44	314.5	70.2	278	11 Q921K1	Q921k1 mus musculus
45	314	70.1	120	11 Q920E8	Q920e8 mus musculus

#### ALIGNMENTS

#### RESULT 1

Q9D8L4	PRELIMINARY;	PRT; 473 AA.
ID Q9D8L4;		
AC Q9D8L4;		
DT 01-JUN-2001 (TREMBLrel. 17, Created)		
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)		
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)		
DE 1810060009Rik protein.		
GN IGH-1 OR 1810060009Rik.		
OS Mus musculus (Mouse).		
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX NCBI_TaxID=10090;		
RN [1]		
RP SEQUENCE FROM N.A.		
RC STRAIN=C57BL/6J; TISSUE=Pancreas;		
RX MEDLINE=21085650; PubMed=11217851;		
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,		
RA Aizawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,		
RA Kadoya K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,		
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,		
RA Kadoya K., Matsuda H.A., Ashburner M., Batalov S., Cavaant T.,		
RA Fleischmann W., Gaasterland T., Glessi C., King B., Kochiwa H.,		
RA Kuehl P., Lewis S., Matsuo Y., Nikaudo I., Pesole G., Quackenbush J.,		
RA Schirml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,		
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,		
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bernaldo M.F.,		
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,		
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,		
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,		
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,		
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,		
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,		
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S.,		
RA Hayashizaki Y.		
RA "Functional annotation of a full-length mouse cDNA collection."		
RL Nature 409:685-690(2001).		
EMBL: AK007918; BAB25349.1; -		
DR HSSP; P01842; 7FAB.		

DT 01-D:



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DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE VHI86.2-D-J-C mu protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB067781; BAB63266.1; -.
DR InterPro; IPR007110; IG_LIKE.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG_1.
DR SMART; SMO0406; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 146
SQ SEQUENCE 146 AA; 16216 MW; 92460FDF1B7538 CRC64;

Query Match 74.8%; Score 335; DB 11; Length 146;
Best Local Similarity 57.9%; Pred. No. 9.8e-30;
Matches 70; Conservative 11; Mismatches 6; Indels 34; Gaps 3;

QY 1 QIQLVSGGELVKPGASVRVSKASGYST-----WVRQSPKGLEWIG----- 44
DB 1 QVQLQPGAEVLKPGASVKLSCKASGYTFTSYMMHWVKQRPGRGLEWIGRIDPNSGGTKY 60

QY 45 -----KATLTVDKSTAYMELSLRSSEDTAVYFCAR-----WGQGTITVTS 86
DB 61 NEKFKSKATLTVDKPSSTAYMQLSLTSDSAVYCARSTLSHYANDYWGQGTITVTS 120

QY 87 S 87
DB 121 S 121

RESULT 9
Q924Q8 PRELIMINARY; PRT; 146 AA.
ID Q924Q8
AC Q924Q8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE VHI86.2-D-J-C mu protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB067792; BAB63277.1; -.
DR InterPro; IPR007110; IG_LIKE.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 1.
DR SMART; SMO0406; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 146
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SQ SEQUENCE 146 AA; 16023 MW; 4B04959991D49159 CRC64;

Query Match 74.8%; Score 335; DB 11; Length 146;
Best Local Similarity 57.9%; Pred. No. 9.8e-30;
Matches 70; Conservative 11; Mismatches 6; Indels 34; Gaps 3;

QY 1 QIQLVSGGELVKPGASVRVSKASGYST-----WVRQSPKGLEWIG----- 44
DB 1 QVQLQPGAEVLKPGASVKLSCKASGYTFTSYMMHWVKQRPGRGLEWIGRIDPNSGGTKY 60

QY 45 -----KATLTVDKSTAYMELSLRSSEDTAVYFCAR-----WGQGTITVTS 86
DB 61 NEKFKSKATLTVDKPSSTAYMQLSLTSDSAVYCARSTLSHYANDYWGQGTITVTS 120

QY 87 S 87
DB 121 S 121

RESULT 10
Q924Q6 PRELIMINARY; PRT; 145 AA.
ID Q924Q6
AC Q924Q6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE VHI86.2-D-J-C mu protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB067794; BAB63279.1; -.
DR InterPro; IPR007110; IG_LIKE.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 1.
DR SMART; SMO0406; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 145
SQ SEQUENCE 145 AA; 16011 MW; 9BC0846D40DF97EA CRC64;

Query Match 74.7%; Score 334.5; DB 11; Length 145;
Best Local Similarity 58.3%; Pred. No. 1.1e-29;
Matches 70; Conservative 11; Mismatches 6; Indels 33; Gaps 3;

QY 1 QIQLVSGGELVKPGASVRVSKASGYST-----WVRQSPKGLEWIG----- 44
DB 1 QVQLQPGAEVLKPGASVKLSCKASGYTFTSYMMHWVKQRPGRGLEWIGRIDPNSGGTKY 60

QY 45 -----KATLTVDKSTAYMELSLRSSEDTAVYFCAR-----WGQGTITVTS 87
DB 61 NEKFKSKATLTVDKPSSTAYMQLSLTSDSAVYCARSTLSHYANDYWGQGTITVTS 120

RESULT 11
Q924Q9 PRELIMINARY; PRT; 145 AA.
ID Q924Q9
AC Q924Q9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE VHI86.2-D-J-C mu protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6;  
 RA Kozono Y., Kozono H., Azuma T.;  
 RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals  
 RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-  
 RT Hydroxy-3-Nitrophenyl)Acetyl (NP).";  
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB067791; BAB63276.1; -  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR Pfam; PF00047; IG\_1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS00835; IG\_LIKE; 1.  
 DR NON\_TER 1 145  
 FT NON\_TER 145  
 SQ SEQUENCE 145 AA; 16001 MW; 0F409EB09FA333D2 CRC64;  
 Query Match 74.7%; Score 334.5; DB 11; Length 145;  
 Best Local Similarity 58.3%; Pred. No. 1.1e-29;  
 Matches 70; Conservative 11; Mismatches 6; Indels 33; Gaps 3;  
 QY 1 QIQLVQSGGELVPGASVRVSCKASGYFT-----WVRSQPGKLEWIG----- 44  
 DB 1 QVQLQPGAEVLKPGASVKLSCKASGYFTFSYWMHWYKQRPGRGLEWIGRIDPNSGGTKY 60  
 QY 45 -----KATLTVDKSTSTAYMELSSLRSEDTAVYFCAR-----WGQGTIVTVSS 87  
 DB 61 NEKFKSKATLTVDKPSSTAYMQLSSLTSEDSAVYVCARYDGSFPYMDYWGQGTIVTVSS 120

RESULT 12  
 Q924R1  
 ID Q924R1 PRELIMINARY; PRT; 145 AA.  
 AC Q924R1;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE VHI86.2-D-J-C mu protein (Fragment).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6;  
 RA Kozono Y., Kozono H., Azuma T.;  
 RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals  
 RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-  
 RT Hydroxy-3-Nitrophenyl)Acetyl (NP).";  
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB067789; BAB63274.1; -  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR Pfam; PF00047; IG\_1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS00835; IG\_LIKE; 1.  
 DR NON\_TER 1 145  
 FT NON\_TER 145  
 SQ SEQUENCE 145 AA; 15979 MW; 0162D0A26C746C04 CRC64;  
 Query Match 74.7%; Score 334.5; DB 11; Length 145;  
 Best Local Similarity 58.3%; Pred. No. 1.1e-29;  
 Matches 70; Conservative 11; Mismatches 6; Indels 33; Gaps 3;  
 QY 1 QIQLVQSGGELVPGASVRVSCKASGYFT-----WVRSQPGKLEWIG----- 44  
 DB 1 QVQLQPGAEVLKPGASVKLSCKASGYFTFSYWMHWYKQRPGRGLEWIGRIDPNSGGTKY 60

QY 45 -----KATLTVDKSTSTAYMELSSLRSEDTAVYFCAR-----WGQGTIVTVSS 87  
 DB 61 NEKFKSKATLTVDKPSSTAYMQLSSLTSEDSAVYVCARYDGSFPYMDYWGQGTIVTVSS 120

QY 45 -----KATLTVDKSTSTAYMELSSLRSEDTAVYFCAR-----WGQGTIVTVSS 87  
 DB 61 NEKFKSKATLTVDKPSSTAYMQLSSLTSEDSAVYVCARYDGSFPYMDYWGQGTIVTVSS 120

RESULT 13  
 Q924R4  
 ID Q924R4 PRELIMINARY; PRT; 145 AA.  
 AC Q924R4;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE VHI86.2-D-J-C mu protein (Fragment).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6;  
 RA Kozono Y., Kozono H., Azuma T.;  
 RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals  
 RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-  
 RT Hydroxy-3-Nitrophenyl)Acetyl (NP).";  
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB067785; BAB63270.1; -  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR Pfam; PF00047; IG\_1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS00835; IG\_LIKE; 1.  
 DR NON\_TER 1 145  
 FT NON\_TER 145  
 SQ SEQUENCE 145 AA; 16081 MW; ECDBLA135E05B8AA CRC64;  
 Query Match 74.7%; Score 334.5; DB 11; Length 145;  
 Best Local Similarity 58.3%; Pred. No. 1.1e-29;  
 Matches 70; Conservative 11; Mismatches 6; Indels 33; Gaps 3;  
 QY 1 QIQLVQSGGELVPGASVRVSCKASGYFT-----WVRSQPGKLEWIG----- 44  
 DB 1 QVQLQPGAEVLKPGASVKLSCKASGYFTFSYWMHWYKQRPGRGLEWIGRIDPNSGGTKY 60  
 QY 45 -----KATLTVDKSTSTAYMELSSLRSEDTAVYFCAR-----WGQGTIVTVSS 87  
 DB 61 NEKFKSKATLTVDKPSSTAYMQLSSLTSEDSAVYVCARYDGSFPYMDYWGQGTIVTVSS 120

RESULT 14  
 Q924Q3  
 ID Q924Q3 PRELIMINARY; PRT; 146 AA.  
 AC Q924Q3;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE VHI86.2-D-J-C mu protein (Fragment).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6;  
 RA Kozono Y., Kozono H., Azuma T.;  
 RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals  
 RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-  
 RT Hydroxy-3-Nitrophenyl)Acetyl (NP).";  
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB067797; BAB63282.1; -  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR NON\_TER 1 146  
 FT NON\_TER 146  
 SQ SEQUENCE 146 AA; 16081 MW; ECDBLA135E05B8AA CRC64;  
 Query Match 74.7%; Score 334.5; DB 11; Length 145;  
 Best Local Similarity 58.3%; Pred. No. 1.1e-29;  
 Matches 70; Conservative 11; Mismatches 6; Indels 33; Gaps 3;  
 QY 1 QIQLVQSGGELVPGASVRVSCKASGYFT-----WVRSQPGKLEWIG----- 44  
 DB 1 QVQLQPGAEVLKPGASVKLSCKASGYFTFSYWMHWYKQRPGRGLEWIGRIDPNSGGTKY 60  
 QY 45 -----KATLTVDKSTSTAYMELSSLRSEDTAVYFCAR-----WGQGTIVTVSS 87  
 DB 61 NEKFKSKATLTVDKPSSTAYMQLSSLTSEDSAVYVCARYDGSFPYMDYWGQGTIVTVSS 120

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DR Pfam, PF00047; ig, 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
DR FT 1
DR NON_TER 1
FT 146
FT 146
SQ SEQUENCE 145 AA; 16136 MW; CEA8DD6E1955807F CRC64;

Query Match 74.6%; Score 334; DB 11; Length 146;
Best Local Similarity 57.9%; Pred. No. 1.3e-29;
Matches 70; Conservative 11; Mismatches 6; Indels 34; Gaps 3

QY 1 QIQLVQSGGELVKPGASVRVSKASGYSFT-----WVRQSPGKGLEWIG----- 44
Db 1 QVQLQPGAEVLKPGASVKLSCKASGYTFTSYNHWVKQRPGRGLEWIGRIDPNSGGTKY 60

QY 45 -----KATLTVDKSTSTAYMELSSLSRSEDATVYFCAR-----WQGGTTVTVVS 86
Db 61 NEKFSKATLTVDKPSSTAYMQLSLTSEDASVYCARSLYDGYANDYWGQGTSTVTS 120

QY 87 S 87
Db 121 S 121

RESULT 15
Q924Q5 PRELIMINARY; PRT; 143 AA.
AC Q924Q5
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Vhl86.2-D-J-C mu protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_Taxid=10090;
RN [1]
SQ SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB067795; BAB63280.1; -.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
DR NON_TER 1
FT 143
FT 143
SQ SEQUENCE 143 AA; 15908 MW; 55A2372870F0D568 CRC64;

Query Match 74.4%; Score 333.5; DB 11; Length 143;
Best Local Similarity 59.3%; Pred. No. 1.4e-29;
Matches 70; Conservative 10; Mismatches 7; Indels 31; Gaps 3

QY 1 QIQLVQSGGELVKPGASVRVSKASGYSFT-----WVRQSPGKGLEWIG----- 44
Db 1 QVQLQPGAEVLKPGASVKLSCKASGYTFTSYNHWVKQRPGRGLEWIGRIDPNSGGTKY 60

QY 45 -----KATLTVDKSTSTAYMELSSLSRSEDATVYFCAR-----WQGGTTVTVVS 87
Db 61 NEKFSKATLTVDKPSSTAYMQLSLTSEDASVYCARSLYDGYANDYWGQGTSTVTS 118

```

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 13, 2004, 12:18:44 ; Search time 20.2873 Seconds  
(without alignments)  
680.681 Million cell updates/sec

Title: US-09-990-586-90

Perfect score: 448

Sequence: 1 QIQLVSGGELVKPGASRV.....DTAVFYCARWGQGTWTVSS 87

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_19Jun03:\*

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- 2: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:\*
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- 21: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:\*
- 22: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:\*
- 23: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:\*
- 24: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	376	83.9	87	17 AAR92991	Homologous sequenc
2	370	82.6	87	24 AAG74721	Murine humanised M
3	367	81.9	115	21 AAB12168	Humanised HBV pre-
4	366	81.7	177	17 AAR33003	Homologous sequenc
5	365	81.5	117	20 AAW84097	Humanised anti-alp
6	360.5	80.5	135	21 AAB07965	A heavy chain vari
7	360	80.4	136	17 AAW06442	HuMc3 VH region.
8	356	79.5	121	13 AAR28744	Heavy chain variab
9	356	79.5	136	21 AAY71548	Humanised antibody

10	354	79.0	470	21	AAW90935	Humanised anti-Fas
11	354	79.0	470	23	ABB74904	Mouse humanised an
12	353.5	78.9	116	17	AAR92218	Humanised LL2 MAB
13	353.5	78.9	116	18	AAW27698	Variable heavy cha
14	353.5	78.9	135	13	AAR29017	pUC-RVh-1220d. Sy
15	353.5	78.9	139	19	AAW65773	Anti-human HMI.24
16	353.5	78.9	139	19	AAW65774	Anti-human HMI.24
17	353.5	78.9	139	19	AAW62205	Humanised anti-HMI
18	353.5	78.9	139	19	AAW62206	Humanised anti-HMI
19	353.5	78.9	139	20	AAV32770	Anti-HMI.24 antibo
20	353.5	78.9	139	20	AAV32771	Anti-HMI.24 antibo
21	353.5	78.9	139	20	AAV02575	Humanised H chain
22	353.5	78.9	139	20	AAV02572	Humanised H chain
23	353.5	78.9	139	20	AAV05486	H chain V region o
24	353.5	78.9	139	23	AAW52354	H chain V region o
25	353.5	78.9	139	23	AAW52355	H chain V region v
26	353.5	78.9	139	23	AAW52355	H chain V region v
27	353.5	78.9	139	24	ABG71946	Human reshaped ant
28	353.5	78.9	140	19	AAW77294	HMI.24 antibody he
29	352.5	78.7	115	18	AAW22418	Reshaped human AUK
30	352.5	78.7	135	13	AAR29016	PUC-RVh-1220b. Sy
31	352.5	78.7	139	19	AAW62212	Humanised anti-HMI
32	352.5	78.7	139	20	AAV02564	Humanised H chain
33	352.5	78.7	139	20	AAV02558	Humanised H chain
34	352.5	78.7	448	23	AAW49203	Humanised monoclon
35	351	78.3	121	23	AAE27819	Mouse 425 antibody
36	351	78.3	121	23	ABG32691	Murine anti-EGFR a
37	351	78.3	470	21	AAW50933	Humanised anti-Fas
38	351	78.3	470	23	ABB74902	Humanised anti-Fas
39	350.5	78.2	116	14	AAR38617	Modified (prop) he
40	350.5	78.2	116	19	AAW58510	Protein SEQ ID NO:
41	350	78.1	119	19	AAW49813	Amino acid sequenc
42	350	78.1	222	14	AAR39267	Humanised C4G1 Ig
43	350	78.1	222	19	AAW49817	Fragment of humani
44	350	78.1	235	14	AAR39268	Humanised C4G1 Ig
45	350	78.1	235	19	AAW49818	Amino acid sequenc

#### ALIGNMENTS

RESULT 1  
AAR92991  
ID AAR92991 standard; Protein; 87 AA.  
XX  
AC AAR92991;  
XX  
DT 25-MAR-2003 (updated)  
DT 18-MAY-1996 (first entry)  
XX  
DE Homologous sequences to antibody IOR-R3 variable region heavy chain.  
XX  
KW IOR-R3; monoclonal antibody; human; mouse; heavy chain; homology;  
KW variable region; epidermal growth factor receptor; hybridoma;  
KW framework; cloning; computer; algorithm; immunogenicity;  
KW site-directed mutagenesis; T-lymphocyte epitope; tertiary structure;  
KW point mutation; antibody engineering; protein engineering;  
KW humanised antibody; antitumour; cancer; therapy.  
XX  
OS Homo sapiens.

Key	Location/Qualifiers
Region	26..30
Region	/note= "Amino acids involved in tertiary structure"
Region	76
Region	/note= "Amino acid involved in tertiary structure"

EP699755-A2.

06-MAR-1996.

27-JUN-1995; 95EP-0201752.

XX



```

PI Hong HJ, Ryu CJ, Hur H;
XX
XX WPI; 2000-400048/34.
XX N-PSDB; AAR62118.
XX
XX Humanized antibody specific for hepatitis B virus surface antigen
XX pre-S1, containing humanized heavy and light chain regions, useful for
XX preventing hepatitis B virus (HBV) infection and for treating chronic
XX hepatitis B.
XX
XX Claim 2; Fig 1; 61pp; English.
XX
XX Hepatitis B virus (HBV) is responsible for hepatitis infection in
XX humans, which may progress to liver cirrhosis or cancer. One of HBV's
XX surface antigens is pre-S1. Monoclonal antibodies specific for pre-S1
XX antigen may efficiently neutralise HBV. The present invention relates to
XX humanised antibodies specific for HBV surface antigen pre-S1. The
XX humanised antibodies are useful for preventing HBV infection and for
XX treating chronic hepatitis B. The Complementarity Determining Regions of
XX mouse pre-S1 antibody KR127 were grafted onto human antibody to produce
XX the humanised antibodies of the present invention. The present sequence
XX is the humanised pre-S1 antibody HRR127HC(I) heavy chain variable region
XX (VH). The coding sequence for the present sequence was produced from the
XX coding sequence of the mouse pre-S1 antibody VH sequence (AAA62115).
XX
XX Sequence 115 AA;
SQ
Query Match 81.9%; Score 367; DB 21; Length 115;
Best Local Similarity 67.0%; Pred. No. 3.9e-27;
Matches 77; Conservative 7; Mismatches 3; Indels 28; Gaps 3;
QY 1 QIQLVQSGGELVKPGASVRSCKASGYST-----WVRSQPGKLEW----- 43
DB 1 QVQLVQSGAEVVKPGASVRSCKASGYAFSSSMNWRQAPGQGLEWIGRIYVPGDNTY 60
QY 44 -----QKATLVDSKSTAYMELSLRSEDYVYFCAR-----WQGGTVTVSS 87
DB 61 AQKFGKATLTADKSTAYMELSLRSEDYVYFCAREYDAYWQGGTLTVSS 115
RESULT 4
AAR93003
ID AAR93003 standard; Protein; 87 AA.
XX
XX AAR93003;
XX
XX 25-MAR-2003 (updated)
XX 18-MAY-1996 (first entry)
XX
XX Homologous sequences to antibody IOR-CEA-1 variable region heavy chain.
XX IOR-CEA-1; monoclonal antibody; human; mouse; heavy chain; homology;
XX variable region; framework; cloning; computer; algorithm;
XX immunogenicity; site-directed mutagenesis; T-lymphocyte epitope;
XX tertiary structure; point mutation; antibody engineering;
XX protein engineering; humanised antibody; antitumour; cancer; therapy.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Region 26..30
XX /note= "Amino acid involved in tertiary structure"
XX Region 50
XX /note= "Amino acid involved in tertiary structure"
XX Region 76
XX /note= "Amino acid involved in tertiary structure"
XX
XX EP699755-A2.
XX
XX 06-MAR-1996.
XX
XX 27-JUN-1995; 95EP-0201752.
XX

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PR 30-JUN-1994; 94CU-0000080.
XX (IMMU-) CENT IMMUNOLOGIA MOLECULAR.
XX
XX Rodriguez RP, Valladares JL, Mateo De Acosta Del Rio CM;
XX WPI; 1996-130770/14.
XX
XX Identifying interspecies differences in amino acid sequence of Ig
XX T-cell epitopes - by sequence comparison, also humanised antibodies
XX contg. altered T-cell epitopes, retaining antigen specificity but
XX not immunogenicity, esp. for tumour treatment
XX
XX Claim 22; Fig 9; 33pp; English.
XX
XX The sequence represents residues from a human immunoglobulin with
XX homology to the heavy chain variable region from mouse monoclonal
XX antibody IOR-CEA-1 (AAR93002). The sequence is partial, and
XX complementarity determining regions are omitted. The sequence is
XX isolated by comparison of human and mouse immunoglobulins and
XX analysis for T-lymphocyte antigenic sequences using a computer
XX algorithm. Residues not within a complementarity determining region,
XX canonical structure or Vernier zone may be modified to reduce
XX immunogenicity in humans (e.g. in sequence AAR93004). This method,
XX which involves the introduction of only a few point mutations into
XX T-cell epitope coding regions, is generally applicable in humanisation
XX of mouse antibodies. The resulting humanised antibodies may be used
XX e.g. as antitumour agents. They retain the antigen recognition of the
XX original antibody, but are not immunogenic in humans.
XX (Updated on 25-MAR-2003 to correct PI field.)
XX
XX Sequence 87 AA;
Query Match 81.7%; Score 366; DB 17; Length 87;
Best Local Similarity 77.0%; Pred. No. 3.7e-27;
Matches 67; Conservative 12; Mismatches 8; Indels 0; Gaps 0;
QY 1 QIQLVQSGGELVKPGASVRSCKASGYSTFWRSQPGKLEWIKATLVDSKSTAYME 60
DB 1 QVQLVQSGAEVVKPGASVRSCKASGYTFWRSQPGKLEWIGRVTITRDSASTAYME 60
QY 61 LSSLRSEDYVYFCARWQGGTVTVSS 87
DB 61 LSSLRSEDYVYFCARWQGGTVTVSS 87
RESULT 5
AAR84097
ID AAR84097 standard; Protein; 117 AA.
XX
XX AAR84097;
XX
XX 15-MAR-1999 (first entry)
XX
XX Humanised anti-alpha-v beta-3 MAB D12H2HC 1-0 VH.
XX
XX Humanised antibody; monoclonal antibody; MAb; antibody engineering;
XX mouse; human; vitronectin; alpha-v beta-3; receptor; restenosis;
XX cancer; metastasis; rheumatoid arthritis; atherosclerosis;
XX angiogenesis; diabetic retinopathy; inflammation;
XX macular degeneration; osteoporosis; Paget's disease;
XX hyperparathyroidism; hypercalcaemia; therapy; immunotherapy;
XX D12H2HC-10.
XX
XX Homo sapiens.
XX Synthetic.
XX
XX Key Location/Qualifiers
XX Region 31..35
XX /label= CDR1
XX Region 50..66
XX /label= CDR2
XX Region 99..106

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FT  /label= CDR3
XX WO9840488-A1.
XX 17-SEP-1998.
XX 12-MAR-1998; 98WO-US04987.
XX 12-MAR-1997; 97US-0039609.
XX (SMK ) SMITHKLINE BEECHAM CORP.
XX Johanson KO, Jonak ZL, Taylor AH;
XX WPI; 1999-034590/03.
XX N-PSDB; AAV71799.
XX New anti alpha v beta_3 vitronectin receptor antibodies - used for
XX immunotherapeutic treatment of e.g. diabetic retinopathy,
XX inflammatory disorders, atherosclerosis, restenosis, cancers or
XX osteoporosis
XX Claim 1; Page 58; 97pp; English.
XX This is the amino acid sequence of the heavy chain variable region
XX (VH) of humanised anti-alpha-v beta-3 vitronectin receptor
XX monoclonal antibody D12H2C 1-0. It is based on the VH sequence
XX (see AAW84095) of human Kabat subgroup I VH, with complementarity
XX determining regions (CDRs) from the murine anti-human alpha-v
XX beta-3 vitronectin receptor monoclonal antibody D12 (see AAW84093).
XX 7 Murine framework residues (24, 48, 67, 68, 70, 72 and 74)
XX are retained. The humanised heavy chain can be expressed in host
XX cells using nucleic acid molecules (see AAV71799) of the invention.
XX Humanised D12 VL is also provided (see AAW84098)). The humanised
XX antibodies can be used for passive immunotherapy of disorders
XX mediated by the alpha-v beta-3 receptor, e.g. cardiovascular or
XX angiogenic-related disorders, such as angiogenesis associated
XX with diabetic retinopathy, atherosclerosis and restenosis, chronic
XX inflammatory disorders, macular degeneration, rheumatoid arthritis
XX and cancer, e.g. solid tumour metastasis, and diseases where bone
XX resorption is associated with pathology such as osteoporosis,
XX hyperparathyroidism, Paget's disease, hypercalcaemia of malignancy,
XX osteolytic lesions produced by bone metastasis, bone loss due to
XX immobilisation or sex hormone deficiency. They can also be used for
XX targeted drug therapy, and for detection and diagnosis.
XX
XX Sequence 117 AA;
XX Query Match 81.5%; Score 365; DB 20; Length 117;
XX Best Local Similarity 65.8%; Pred. NO. 6.2e-27;
XX Matches 77; Conservative 7; Mismatches 3; Indels 30; Gaps 3;
XX
XX 1 QIQLVSGGELVKPGASVRSCKASGYST-----WVRQSPGKGLEW----- 43
XX 1 QVQLVSGAEVVKPGASVKSCASGYFTSYMTWRVRAQPGGLEWIGYDPYNGDTFF 60
XX
XX 44 -----GKATLTVDKSTAYMELSLRSEDITAVYFCAR-----WQGGTTVTVSS 87
XX 61 NQFKGKATLTVDKSTAYMELSLRSEDITAVYFCARQNYGSFYAWGQGLTLTVSS 117
XX
RESULT 6
AAB07965
ID AAB07965 standard; Protein; 135 AA.
XX AC AAB07965;
XX 14-NOV-2000 (first entry)
XX A heavy chain variable region of humanised 3S1 antibody.
XX Antibody 3D1; B7 molecule; B7; humanised immunoglobulin;
XX autoimmune disease; infectious disease; inflammatory disorder;

```

Db 80 NQKFKGKATWVDKSTSTAYMELSSLRSEDTAVYVCARAAMTYMDYWGQGLTVTVSS 135

RESULT 7  
AAW06442  
ID ID AAW06442 standard; Protein; 136 AA.  
XX AC AAW06442;  
XX 04-FEB-1997 (first entry)  
XX HuMc3 VH region.  
XX Humanised antibody; variable heavy region; buried residue modification;  
KW VH; HuMc3 VH; BA46 antigen; human; milk fat globule; HMF; lactation;  
KW fat globule membrane; murine; mammary; epithelial cell; breast cancer;  
KW breast membrane glycoprotein; therapy; immunotherapy.  
XX Synthetic.  
XX WO9608565-A2.  
XX 21-MAR-1996.  
XX 14-SEP-1995; 95WO-US11683.  
XX 07-JUN-1995; 95US-0487598.  
XX 16-SEP-1994; 94US-0307868.  
XX (CANC-) CANCER RES FUND CONTRA COSTA.  
XX Ceriani RI, Do Couto FJR, Peterson JA;  
XX WPI; 1996-179941/19.  
XX N-PSDB; AAT42717.  
XX Recombinant Mc3 antibody which binds BA46 antigen of HMF -  
PT comprises a modified heavy or light chain variable region, useful in  
PT the diagnosis and therapy of breast cancer  
XX Claim 13; Fig 18; 91pp; English.  
XX This sequence represents the variable heavy (VH) chain of the humanised  
CC murine antibody HuMc3 VH. The Mc3 VH sequence was humanised using the  
CC buried residue modification technique, where important non-human  
CC framework residues are unaffected. The Mc3 antibody binds to the BA46  
CC antigen of the human milk fat globule (HMF). The milk fat globule  
CC membrane is derived from the apical surface of the mammalian epithelial  
CC cell during lactation, and therefore is a source for breast membrane  
CC glycoproteins. The antibody can be used in an in vitro method to detect  
CC a HMF antigen (or antigen fragment), and to diagnose the presence of the  
CC antigen in a subject. The antibody can also be used to deliver an agent  
CC to a target (within a subject's body), containing a HMF antigen. The  
CC antibodies can also be used for diagnosis, prognosis, and therapeutic  
CC applications of breast cancer. As the humanised antibodies retain their  
CC high affinity binding to the antigen, they are useful for  
CC immunodiagnostic and immunotherapeutic applications in humans.  
XX SQ Sequence 136 AA;  
Query Match 80.4%; Score 360; DB 17; Length 136;  
Best Local Similarity 65.8%; Pred. No. 2.1e-26;  
Matches 77; Conservative 5; Mismatches 5; Indels 30; Gaps 3;  
QY 1 QIQLVQSGGELVKGASVYKSCASGYSTFT-----WYQSPGKGLWIG----- 44  
Db 20 EVQLVQSGAEVKGASVYKSCASGYSTFTGTYTHHWKQSPGNLEWIGLIPYNGGTY 79  
QY 45 -----KATLTVDKSTSTAYMELSSLRSEDTAVYFCAR-----WGQGLTVTVSS 87  
Db 80 NQKFDKATLTVDKSTSTAYMELSSLRSEDTAVYFCARRWRYTMDYWGQGLTVTVSS 136

RESULT 8  
AAR28744  
ID AAR28744 standard; Protein; 121 AA.  
XX AC AAR28744;  
XX 25-MAR-2003 (updated)  
XX 11-JAN-1993 (first entry)  
XX Heavy chain variable domain of GEU humanised CDR grafted Ab.  
XX monoclonal antibody; humanised; chimeric; CDR; neoplastic therapy;  
KW shock; antilymphocyte therapy; endotoxin shock; septic shock;  
KW sepsis; cardiovascular shock; tumour necrosis factor alpha;  
KW multi-organ failure.  
XX Chimeric.  
XX WO9211383-A1.  
XX 09-JUL-1992.  
XX 20-DEC-1991; 91WO-GB02300.  
XX 21-DEC-1990; 90WO-GB02017.  
XX 03-MAY-1991; 91GB-0009645.  
XX (CLLT) CELLTech LTD.  
XX Adair JR, Athwal DS, Bodmer MW, Entage JS;  
XX WPI; 1992-250102/30.  
XX Recombinant antibody specific for human TNF-alpha - for treatment  
PT of shock and immunoregulatory and inflammatory disorders, also  
PT used in diagnosis  
XX Example 1; Fig 1; 57pp; English.  
XX This sequence is that of the heavy chain variable domain of a chimeric  
CC antibody to an epitope of human tumour necrosis factor. It is also known  
CC as hTNF1. Mouse CDRs were used at positions 26-35 (CDR1),  
CC 50-65 (CDR2), and 95-102 (CDR3). In addition mouse residues were used  
CC in the frameworks at positions 48, 67, 69, 71, 73, 76, 89, 91, 94 and 108.  
CC Comparison of the hTNF1 mouse and EU human heavy chain residues  
CC reveals that these are identical at positions 23, 24, 29, and 78.  
CC (Updated on 25-MAR-2003 to correct PN field.)  
XX SQ Sequence 121 AA;  
Query Match 79.5%; Score 356; DB 13; Length 121;  
Best Local Similarity 61.2%; Pred. No. 4.5e-26;  
Matches 74; Conservative 10; Mismatches 3; Indels 34; Gaps 3;  
QY 1 QIQLVQSGGELVKGASVYKSCASGYSTFT-----WYQSPGKGLWIG----- 43  
Db 1 QVQLVQSGAEVYKPGSSVYKSCASGYSTFTDYNDVYKQAPGQGLWIGINPNNGGTY 60  
QY 44 -----KATLTVDKSTSTAYMELSSLRSEDTAVYFCAR-----WGQGLTVTVSS 86  
Db 61 NQKFKGKGLTVDKSTSTAYMELSSLRSEDTAVYVCARSAFYNNYEFYDVGQGLTVTVSS 120  
QY 87 S 87  
Db 121 S 121  
RESULT 9  
AA71548  
ID AA71548 standard; Protein; 136 AA.  
XX AC AA71548;  
XX





Query Match 79.5%; Score 356; DB 21; Length 136;  
 Best Local Similarity 64.1%; Pred. No. 5e-26;  
 Matches 75; Conservative 8; Mismatches 4; Indels 30; Gaps 3;

QY 1 QIQLVQSGGELVKPGASVRVSKASGYST-----WVRQSPGKGLWGT----- 44  
 DB 20 QVQLVQSGAELKPGSSVKVSKASGYIFTSMINWVKQAPGQGLEWIGRIDPSGEVHY 79  
 QY 45 -----KATLTVDKSTAYMELSSLRSEDTAVYFCAR-----WQGTITVTSS 87  
 DB 80 NQPKFKATLTVDKSTNTAYMELSSLRSEDTAVYFCARGLFWFADWQGTITVTSS 136

RESULT 10  
 AAW90935  
 ID AAW90935 standard; Protein; 470 AA.  
 XX  
 AC AAW90935;  
 XX  
 DT 08-AUG-2000 (first entry)  
 XX  
 DE Humanised anti-Fas designed heavy chain Heu 3 protein.  
 XX  
 KW Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;  
 KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiant;  
 KW dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;  
 KW nephrotropic; antinfertility; neuroprotective; antiarteriosclerotic;  
 KW hepatocytic; humanized; apoptosis; systemic lupus erythematosus;  
 KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;  
 KW Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;  
 KW Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;  
 KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;  
 KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;  
 KW cardiomyopathy; Glomerulonephritis; hepatitis; transplant rejection.  
 XX  
 OS Synthetic.  
 XX  
 XX EP990663-A2.  
 XX  
 PD 05-APR-2000.  
 XX  
 XX 29-SEP-1999; 99EP-0307711.  
 XX  
 XX 30-SEP-1998; 98JP-0276881.  
 XX  
 XX 30-SEP-1998; 98JP-0276882.  
 XX  
 XX (SANY ) SANKYO CO LTD.  
 XX  
 XX Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;  
 XX  
 XX WPI; 2000-258930/23.  
 XX  
 XX N-PSDB; AAA11646.  
 XX  
 XX New humanized anti-Fas antibody, useful for treating or preventing e.g.  
 XX inflammatory or autoimmune disease, induces apoptosis selectively in  
 XX cells with abnormal Fas-Fas ligand systems -  
 XX  
 XX Claim 2; Page 180-182; 263pp; English.  
 XX  
 XX This invention describes a novel humanized anti-Fas antibody-like  
 XX molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas  
 XX ligand system, by binding to Fas on the cell surface, and prevents  
 XX apoptosis in cells with a normal system, by inhibiting binding between  
 XX Fas and its ligand. The products of the invention have anti-inflammatory,  
 XX anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,  
 XX immunomodulatory, dermatological, immunosuppressive, thyromimetic,  
 XX antirheumatic, nephrotropic, antinfertility, neuroprotective,  
 XX antiarteriosclerotic, cardiant and hepatropic activity. (I) induce  
 XX apoptosis by binding to cell surface Fas or inhibit it by competitive  
 XX inhibition of ligand binding. (I) are used to treat and/or prevent  
 XX diseases associated with the Fas/Fas ligand system, especially systemic  
 XX lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft  
 XX versus host disease, Sjorgen's syndrome, pernicious or hypoplastic

CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's  
 CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,  
 CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin  
 CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,  
 CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral  
 CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively  
 CC inhibit apoptosis in normal cells but selectively induce it in abnormal  
 CC cells. They bind to both human and murine Fas, so can be evaluated in  
 CC murine disease models. (I) act on the active site of Fas, i.e. they mimic  
 CC the native ligand, do not induce liver disease, and have reduced risk of  
 CC inducing a human anti-murine antibody response. This sequence represents  
 CC a humanised anti-Fas antibody heavy chain construct designated Heu 3  
 CC which is described in the method of the invention.

XX SQ Sequence 470 AA;

Query Match 79.0%; Score 354; DB 21; Length 470;  
 Best Local Similarity 62.0%; Pred. No. 2.6e-25;  
 Matches 75; Conservative 8; Mismatches 4; Indels 34; Gaps 3;

QY 1 QIQLVQSGGELVKPGASVRVSKASGYST-----WVRQSPGKGLWGT----- 43  
 DB 20 QVQLVQSGAELKPGSSVKVSKASGYFTFTSYMWVVRQAPGQGLEWIGRIDPSDVTNY 79  
 QY 44 -----GKATLTVDKSTAYMELSSLRSEDTAVYFCAR-----WQGTITVTSS 86  
 DB 80 NQPKFKATLTVDKSTNTAYMELSSLRSEDTAVYFCARGLFWFADWQGTITVTSS 139  
 QY 87 S 87  
 DB 140 S 140

RESULT 11

ABW74904  
 ID ABE74904 standard; Protein; 470 AA.

XX AC ABB74904;

XX DT 26-APR-2002 (first entry)

XX DE Mouse humanised anti-Fas antibody related protein SEQ ID NO 9.

XX KW Human; mouse; humanised anti-Fas antibody; Fas/Fas ligand;  
 XX light chain subunit; apoptosis; immunosuppressive; antiallergic;  
 XX autoimmune disease; allergy; atopic.

XX OS Mus musculus.

XX PN JP2001342148-A.

XX PD 11-DEC-2001.

XX PF 28-MAR-2001; 2001JP-0093106.

XX PR 29-MAR-2000; 2000JP-0090918.

XX PA (SANY ) SANKYO CO LTD.

XX WPI; 2002-1451113/19.

XX DR N-PSDB; ABL45926.

XX PT Drug containing humanised anti-Fas antibody, used for preventing and  
 XX treating autoimmune diseases, allergy, and atopy -

XX PS Example 4 (Preparatory); Page 79-80; 194pp; Japanese.

XX CC The invention relates to a preventive or treating agent for diseases  
 XX caused by abnormality in Fas/Fas ligand system containing as the active  
 XX component an antibody having as the light chain subunit a polypeptide  
 XX containing residues 1-218 of one of 3, 239 residue amino acid sequences,  
 XX or residues 1-451 of one of 3, 470 residue amino acid sequences, all  
 XX fully defined in the specification and having an activity of combining

CC The complementarity determining regions (CDRs) of mouse monoclonal  
CC antibody (Mab) LL2 VK (AAR92215) and VH (AAR92216) regions were  
CC recombinantly linked to the framework sequences of human VK and VH  
CC regions, respectively, to give humanised LL2 VK (AAR92217) and VH  
CC regions, respectively.

The present sequence is the variable heavy chain of the B cell specific monoclonal antibody (MAB) hLL2. hLL2 is a highly specific anti-B cell lymphoma and anti-lymphocytic leukaemia cell humanised murine MAB. The MAB can be used to diagnose or treat B

CC cell malignancies, e.g. non-Hodgkins lymphoma or chronic  
 CC lymphocytic leukaemia.

SQ Sequence 116 AA;

Query Match 78.9%; Score 353.5; DB 18; Length 116;

Best Local Similarity 62.9%; Pred. No. 7.3e-26;  
 Matches 73; Conservative 10; Mismatches 4; Indels 29; Gaps 3;

QY 1 QIQLVSGGELVKPGASVRVSKASGYST-----WVROSPGKGLWIG----- 44

DB 1 QVQLVSGAEVKKPGSSVKVSKASGYTTSYHLHWVRQAPGQGLEWIGYINPRNDYTEY 60

QY 45 -----KATLTVDKSTSTAYMELSSLRSEDTAYFCAR-----WGQGTFTVTVSS 87

DB 61 NQNFKDKATITADESTNTAYMELSSLRSEDTAFYFCARDITTFYWGQGTFTVTVSS 116

#### RESULT 14

AAR29017  
 ID AAR29017 standard; Protein; 135 AA.

XX

AC AAR29017;

DT 25-MAR-2003 (updated)

DT 30-MAR-1993 (first entry)

XX pUC-RVh-1220d.

XX Human; antibody; interleukin-6; receptor; IL-6R; CDR; PCR; mouse;  
 KW complementarity determining region; monoclonal; hybridoma; PCR;  
 KW plasmid; polymerase chain reaction; amplify.

OS Synthetic.

XX Key Location/Qualifiers

FT Peptide 1..19

FT /note= "Leader peptide"

FT Region 20..49

FT /label= FR1

FT Region 50..54

FT /label= CDR1

FT Region 55..68

FT /label= FR2

FT Region 69..85

FT /label= CDR2

FT Region 86..117

FT /label= FR3

FT Region 118..124

FT /label= CDR3

FT Region 125..135

FT /label= FR4

XX WO9219759-A1.

PN

XX

PD 12-NOV-1992.

XX

PF 24-APR-1992; 92WO-JP00544.

XX

PR 25-APR-1991; 91JP-0095476.

PR 19-FEB-1992; 92JP-0032084.

XX

XX (CHUS ) CHUGAI SEIYAKU KK.

PA

XX Bendig MM, Jones ST, Saldanha JW, Sato K, Teuchiya M;

PI

XX WPI; 1992-398882/48.

XX N-PSDB; AAQ31391.

DR

XX Reconstituted human antibody to human interleukin-6 receptor -

PT has low antigenicity and contains mouse V-region complementarity

PT determining regions

XX

PS Disclosure; Page 159-60; 207pp; Japanese.

XX The sequences given in AAR29016-17 are portions of monoclonal antibodies  
 CC which were encoded by plasmids contained within the mouse hybridoma,  
 CC AUK12-20. The DNA encoding the complementarity determining regions  
 CC (CDR's) was isolated by polymerase chain reaction. These antibodies  
 CC recognise human interleukin-6 receptor (IL-6R). The hybridoma cells  
 CC were transformed with plasmids containing fragments of the antibody  
 CC gene which caused the production of the antibody from the hybridoma  
 CC cell line.  
 CC (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 135 AA;

QY Query Match 78.9%; Score 353.5; DB 13; Length 135;

Best Local Similarity 63.8%; Pred. No. 8.5e-26;

Matches 74; Conservative 8; Mismatches 5; Indels 29; Gaps 3;

QY 1 QIQLVSGGELVKPGASVRVSKASGYST-----WVROSPGKGLWIG----- 43

DB 20 QVQLVSGAEVKKPGASVRVSKASGYSTSYIHWVRQAPGQGLEWIGYIDPFNGGTSY 79

QY 44 -----GKATLTVDKSTSTAYMELSSLRSEDTAYFCAR-----WGQGTFTVTVSS 87

DB 80 NQKFKGKVTMTVDTSINTAYMELSSLRSEDTAVVYCARGGNRFAYWGQGLTVTVSS 135

#### RESULT 15

AAW65773

ID AAW65773 standard; Protein; 139 AA.

XX

AC AAW65773;

DT 16-NOV-1998 (first entry)

XX Anti-human HM1.24 antibody heavy chain variable region r.

DE Cytotoxic antibody; anti-human HM1.24; lymphocytic tumours;  
 KW pre-B lymphoma; Burkitt's lymphoma; T-cell tumour; B-cell tumour.

XX Synthetic.

XX Key Location/Qualifiers

FT Peptide 1..19

FT /note= "Signal peptide"

FT Peptide 20..139

FT /note= "Mature peptide"

XX WO9835698-A1.

PN

XX

PD 20-AUG-1998.

XX

PF 12-FEB-1998; 98WO-JP00568.

XX

PR 12-FEB-1997; 97JP-0041410.

XX

PA (CHUS ) CHUGAI SEIYAKU KK.

XX Koishihara Y, Yoshimura Y;

PI

XX WPI; 1998-456869/39.

DR N-PSDB; AAV07581.

XX

PT Treatment of lymphocytic tumours using cytotoxic antibody - binding  
 PT to specific antigen such as HM1.24 and effective against T-cell  
 PT tumours and B-cell tumours other than myeloma

XX Disclosure; Page 47-48; 82pp; Japanese.

XX The anti-human HM1.24 antibody is the preferred cytotoxic antibody to be

CC used in the treatment of lymphocytic tumours, including T-cell tumours  
 CC and B-cell tumours other than myeloma. The antibody is preferably  
 CC monoclonal and has ADCC or CDC type cytotoxicity. It may be chimeric or

CC humanised, and preferably contains a human antibody constant region C  
CC gamma (such as C gamma 1 or C gamma 3). A preferred antibody is an  
CC anti-human Hm1.24 antibody or an antibody which binds to an epitope  
CC recognising anti-human Hm1.24 antibody. The cytotoxic antibody is useful  
CC in the treatment of lymphocytic tumours such as acute or chronic B  
CC lymphocytic leukaemia, pre-B lymphoma, Burkitt's lymphoma, or acute or  
CC chronic T lymphocytic leukaemia.

XX  
SQ Sequence 139 AA;

Query Match 78.9%; Score 353.5; DB 19; Length 139;  
Best Local Similarity 60.8%; Pred. No. 8.8e-26;  
Matches 73; Conservative 10; Mismatches 4; Indels 33; Gaps 3;

QY 1 QIQLVQSGGELVKPGASVRSCKASGYST-----WVRQSPCKGLEW----- 43  
DB 20 QVQLVQSGAEVKKPGASVKVCKASGYTFTPYWMQWVRQAPQGLEWNGSIFPGDGDTRY 79  
QY 44 -----GKATLTVDKSTSTAYMELSLRSEDTAIFYCAR-----WQGGTIVTVSS 87  
DB 80 SQKFKGRVTMTADKSTSTAYMELSLRSEDTAIFYCARLRRGGYFDYWGQGTIVTVSS 139

Search completed: January 13, 2004, 12:38:24  
Job time : 21.2873 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 13, 2004, 12:43:20 ; Search time 13.9048 Seconds  
(without alignments)  
1260.812 Million cell updates/sec

Title: US-09-990-586-90

Perfect score: 448

Sequence: 1 QIQLVQSGGELVKPGASVRV.....DTAVYFCARWGQGTIVTVSS 87

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747907 seqs, 201509753 residues

Total number of hits satisfying chosen parameters: 747907

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*  
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2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*  
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5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*  
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7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*  
8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep.\*  
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10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep.\*  
11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep.\*  
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15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep.\*  
16: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*  
17: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*  
18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	448	100.0	87	11	US-09-990-586-90
2	448	100.0	87	12	US-10-230-880-90
3	440	98.2	87	12	US-09-990-586-95
4	440	98.2	87	12	US-10-230-880-95
5	439	98.0	87	11	US-09-990-586-89
6	439	98.0	87	11	US-09-990-586-91
7	439	98.0	87	11	US-09-990-586-92
8	439	98.0	87	12	US-10-230-880-91
9	439	98.0	87	12	US-10-230-880-92
10	439	98.0	87	11	US-09-990-586-96
11	437	97.5	87	12	US-10-230-880-96
12	437	97.5	87	11	US-09-990-586-94
13	434	96.9	87	11	US-10-230-880-94
14	434	96.9	87	12	US-10-230-880-94
15	431	96.2	87	11	US-09-990-586-93

16	431	96.2	87	12	US-10-230-880-93	Sequence 93, Appl
17	426	95.1	87	11	US-09-990-586-88	Sequence 88, Appl
18	426	95.1	87	12	US-10-230-880-88	Sequence 88, Appl
19	415	92.6	87	11	US-09-990-586-87	Sequence 87, Appl
20	415	92.6	87	12	US-10-230-880-87	Sequence 87, Appl
21	407	90.8	87	11	US-09-990-586-86	Sequence 86, Appl
22	407	90.8	87	12	US-10-230-880-86	Sequence 86, Appl
23	405	90.4	87	12	US-10-230-880-166	Sequence 166, App
24	405	90.4	87	12	US-10-230-880-172	Sequence 172, App
25	394	87.9	87	11	US-09-990-586-85	Sequence 85, Appl
26	394	87.9	87	12	US-10-230-880-85	Sequence 168, App
27	390	87.1	87	12	US-10-230-880-168	Sequence 167, App
28	387	86.4	87	12	US-10-230-880-167	Sequence 167, App
29	382	85.3	87	11	US-09-509-098-200	Sequence 200, App
30	380	84.8	87	12	US-10-230-880-159	Sequence 159, App
31	380	84.8	87	12	US-10-230-880-171	Sequence 171, App
32	379	84.6	87	11	US-09-990-586-84	Sequence 84, Appl
33	379	84.6	87	12	US-10-230-880-84	Sequence 157, App
34	377	84.2	87	12	US-10-230-880-157	Sequence 160, App
35	377	84.2	87	12	US-10-230-880-160	Sequence 7, Appl
36	377	84.2	87	12	US-10-412-703A-7	Sequence 83, Appl
37	373	83.3	87	11	US-09-990-586-83	Sequence 83, Appl
38	373	83.3	87	12	US-10-230-880-83	Sequence 83, Appl
39	367	81.9	87	12	US-10-230-880-165	Sequence 5, Appl
40	365	81.5	117	12	US-10-223-880-5	Sequence 6, Appl
41	360.5	80.5	135	10	US-09-249-011A-6	Sequence 24, Appl
42	360.5	80.5	461	10	US-09-249-011A-24	Sequence 78, Appl
43	360	80.4	117	10	US-09-556-206A-78	Sequence 63, Appl
44	360	80.4	136	10	US-09-556-206A-63	Sequence 199, App
45	356	79.5	87	11	US-09-509-098-199	

ALIGNMENTS

RESULT 1  
US-09-990-586-90  
; Sequence 90, Application US/0990586  
; Publication No. US20030109680A1  
; GENERAL INFORMATION:  
; APPLICANT: JIAO, JIN-AN  
; APPLICANT: WONG, HING C  
; TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD COAGULATION AND METHODS  
; TITLE OF INVENTION: OF USE THEREOF  
; FILE REFERENCE: 71758/46943-CIP2  
; CURRENT APPLICATION NUMBER: US/09/990,586  
; CURRENT FILING DATE: 2001-11-21  
; PRIOR APPLICATION NUMBER: 09/293,854  
; PRIOR FILING DATE: 1999-04-16  
; NUMBER OF SEQ ID NOS: 102  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 90  
; LENGTH: 87  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-990-586-90

Query Match	100.0%	Score 448	DB 11	Length 87
Best Local Similarity	100.0%	Pred. No. 2.9e-37		
Matches	87	Conservative	0	Mismatches 0
				Indels 0
				Gaps 0
QY	1	QIQLVQSGGELVKPGASVRVSKAGSYFTVVRQSPGKLEWIGKATLTVDKSTSTAYME	60	
DB	1	QIQLVQSGGELVKPGASVRVSKAGSYFTVVRQSPGKLEWIGKATLTVDKSTSTAYME	60	
QY	61	LSLSRSEDATVYFCARWGQGTIVTVSS	87	
DB	61	LSLSRSEDATVYFCARWGQGTIVTVSS	87	
RESULT 2				
US-10-230-880-90				
				; Sequence 90, Application US/10230880

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; Publication No. US20030190705A1
; GENERAL INFORMATION:
; APPLICANT: WONG, HING C.
; APPLICANT: STINSON, JEFFREY L.
; APPLICANT: MOSQUERA, LUIS A.
; TITLE OF INVENTION: METHOD OF HUMANIZING IMMUNE SYSTEM MOLECULES
; FILE REFERENCE: 71758/58066
; CURRENT APPLICATION NUMBER: US/10/230,880
; CURRENT FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: 09/990,586
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/343,306
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/293,854
; PRIOR FILING DATE: 1999-04-16
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 90
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-230-880-90

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Query Match 100.0%; Score 448; DB 12; Length 87;
Best Local Similarity 100.0%; Pred. No. 2.9e-37;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QIQLVQSGGELVKPGASVRVSCKASGYSTWVRQSPGKGLWIGKATLTVDKSTSTAYME 60
DB 1 QIQLVQSGGELVKPGASVRVSCKASGYSTWVRQSPGKGLWIGKATLTVDKSTSTAYME 60

QY 61 LSSLRSEDATVYFCARWGQGTIVTVSS 87
DB 61 LSSLRSEDATVYFCARWGQGTIVTVSS 87

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RESULT 3
US-09-990-586-95
; Sequence 95, Application US/09990586
; Publication No. US20030109680A1
; GENERAL INFORMATION:
; APPLICANT: WONG, HING C.
; APPLICANT: JIAO, JIN-AN
; TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD COAGULATION AND METHODS
; TITLE OF INVENTION: OF USE THEREOF
; FILE REFERENCE: 71758/46943-CIP2
; CURRENT APPLICATION NUMBER: US/09/990,586
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 09/293,854
; PRIOR FILING DATE: 1999-04-16
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 95
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-990-586-95

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Query Match 98.2%; Score 440; DB 11; Length 87;
Best Local Similarity 98.9%; Pred. No. 1.8e-36;
Matches 86; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QIQLVQSGGELVKPGASVRVSCKASGYSTWVRQSPGKGLWIGKATLTVDKSTSTAYME 60
DB 1 QIQLVQSGGELVKPGASVRVSCKASGYSTWVRQSPGKGLWIGKATLTVDKSTSTAYME 60

QY 61 LSSLRSEDATVYFCARWGQGTIVTVSS 87
DB 61 LSSLRSEDATVYFCARWGQGTIVTVSS 87

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RESULT 4
US-10-230-880-95

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; Sequence 95, Application US/10230880
; Publication No. US20030190705A1
; GENERAL INFORMATION:
; APPLICANT: WONG, HING C.
; APPLICANT: STINSON, JEFFREY L.
; APPLICANT: MOSQUERA, LUIS A.
; TITLE OF INVENTION: METHOD OF HUMANIZING IMMUNE SYSTEM MOLECULES
; FILE REFERENCE: 71758/58066
; CURRENT APPLICATION NUMBER: US/10/230,880
; CURRENT FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: 09/990,586
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/343,306
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/293,854
; PRIOR FILING DATE: 1999-04-16
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 95
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-230-880-95

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Query Match 98.2%; Score 440; DB 12; Length 87;
Best Local Similarity 98.9%; Pred. No. 1.8e-36;
Matches 86; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QIQLVQSGGELVKPGASVRVSCKASGYSTWVRQSPGKGLWIGKATLTVDKSTSTAYME 60
DB 1 QIQLVQSGGELVKPGASVRVSCKASGYSTWVRQSPGKGLWIGKATLTVDKSTSTAYME 60

QY 61 LSSLRSEDATVYFCARWGQGTIVTVSS 87
DB 61 LSSLRSEDATVYFCARWGQGTIVTVSS 87

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RESULT 5
US-09-990-586-89
; Sequence 89, Application US/09990586
; Publication No. US20030109680A1
; GENERAL INFORMATION:
; APPLICANT: JIAO, JIN-AN
; APPLICANT: WONG, HING C.
; TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD COAGULATION AND METHODS
; TITLE OF INVENTION: OF USE THEREOF
; FILE REFERENCE: 71758/46943-CIP2
; CURRENT APPLICATION NUMBER: US/09/990,586
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 09/293,854
; PRIOR FILING DATE: 1999-04-16
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 89
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-990-586-89

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```

Query Match 98.0%; Score 439; DB 11; Length 87;
Best Local Similarity 97.7%; Pred. No. 2.3e-36;
Matches 85; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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DB 1 QMQLQSGGELVKPGASVRVSCKASGYSTWVRQSPGKGLWIGKATLTVDKSTSTAYME 60

QY 61 LSSLRSEDATVYFCARWGQGTIVTVSS 87
DB 61 LSSLRSEDATVYFCARWGQGTIVTVSS 87

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RESULT 6

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US-09-990-586-91
; Sequence 91, Application US/09990586
; Publication No. US20030109680A1
; GENERAL INFORMATION:
; APPLICANT: JIAO, JIN-AN
; TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD COAGULATION AND METHODS
; TITLE OF INVENTION: OF USE THEREOF
; FILE REFERENCE: 71758/46943-CIP2
; CURRENT APPLICATION NUMBER: US/09/990,586
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 09/293,854
; PRIOR FILING DATE: 1999-04-16
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 91
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-990-586-91

Query Match      98.0%; Score 439; DB 11; Length 87;
Best Local Similarity 97.7%; Pred. No. 2.3e-36;
Matches 85; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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DB 1 QIQLVQSGGEVKPGASVRVSCKASGYSTFTWVRQSPGKGLEWIGKATLTVDKSTSTAYME 60

QY 61 LSSLRSEDTAVYFCARWGQGTITVSS 87
DB 61 LSSLRSEDTAVYFCARWGQGTITVSS 87

RESULT 7
US-09-990-586-92
; Sequence 92, Application US/09990586
; Publication No. US20030109680A1
; GENERAL INFORMATION:
; APPLICANT: JIAO, JIN-AN
; TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD COAGULATION AND METHODS
; TITLE OF INVENTION: OF USE THEREOF
; FILE REFERENCE: 71758/46943-CIP2
; CURRENT APPLICATION NUMBER: US/09/990,586
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 09/293,854
; PRIOR FILING DATE: 1999-04-16
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 92
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-990-586-92

Query Match      98.0%; Score 439; DB 11; Length 87;
Best Local Similarity 97.7%; Pred. No. 2.3e-36;
Matches 85; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QIQLVQSGGELVKPGASVRVSCKASGYSTFTWVRQSPGKGLEWIGKATLTVDKSTSTAYME 60
DB 1 QIQLVQSGGEVKPGASVRVSCKASGYSTFTWVRQSPGKGLEWIGKATLTVDKSTSTAYME 60

QY 61 LSSLRSEDTAVYFCARWGQGTITVSS 87
DB 61 LSSLRSEDTAVYFCARWGQGTITVSS 87

RESULT 8
US-10-230-880-89
; Sequence 89, Application US/10230880
; Publication No. US20030190705A1
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; GENERAL INFORMATION:
; APPLICANT: WONG, HING C.
; APPLICANT: STINSON, JEFFREY L.
; APPLICANT: MOSQUERA, LUIS A.
; TITLE OF INVENTION: METHOD OF HUMANIZING IMMUNE SYSTEM MOLECULES
; FILE REFERENCE: 71758/58066
; CURRENT APPLICATION NUMBER: US/10/230,880
; CURRENT FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: 09/990,586
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/343,306
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/293,854
; PRIOR FILING DATE: 1999-04-16
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 89
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-230-880-89

Query Match      98.0%; Score 439; DB 12; Length 87;
Best Local Similarity 97.7%; Pred. No. 2.3e-36;
Matches 85; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QIQLVQSGGELVKPGASVRVSCKASGYSTFTWVRQSPGKGLEWIGKATLTVDKSTSTAYME 60
DB 1 QIQLVQSGGELVKPGASVRVSCKASGYSTFTWVRQSPGKGLEWIGKATLTVDKSTSTAYME 60

QY 61 LSSLRSEDTAVYFCARWGQGTITVSS 87
DB 61 LSSLRSEDTAVYFCARWGQGTITVSS 87

RESULT 9
US-10-230-880-91
; Sequence 91, Application US/10230880
; Publication No. US20030190705A1
; GENERAL INFORMATION:
; APPLICANT: WONG, HING C.
; APPLICANT: STINSON, JEFFREY L.
; APPLICANT: MOSQUERA, LUIS A.
; TITLE OF INVENTION: METHOD OF HUMANIZING IMMUNE SYSTEM MOLECULES
; FILE REFERENCE: 71758/58066
; CURRENT APPLICATION NUMBER: US/10/230,880
; CURRENT FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: 09/990,586
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/343,306
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/293,854
; PRIOR FILING DATE: 1999-04-16
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 91
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-230-880-91

Query Match      98.0%; Score 439; DB 12; Length 87;
Best Local Similarity 97.7%; Pred. No. 2.3e-36;
Matches 85; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QIQLVQSGGELVKPGASVRVSCKASGYSTFTWVRQSPGKGLEWIGKATLTVDKSTSTAYME 60
DB 1 QIQLVQSGGEVKPGASVRVSCKASGYSTFTWVRQSPGKGLEWIGKATLTVDKSTSTAYME 60

QY 61 LSSLRSEDTAVYFCARWGQGTITVSS 87
DB 61 LSSLRSEDTAVYFCARWGQGTITVSS 87
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## RESULT 10

US-10-230-880-92  
; Sequence 92, Application US/10230880  
; Publication No. US20030190705A1  
; GENERAL INFORMATION:  
; APPLICANT: WONG, HING C.  
; APPLICANT: STINSON, JEFFREY L.  
; APPLICANT: MOSQUERA, LUIS A.  
; TITLE OF INVENTION: METHOD OF HUMANIZING IMMUNE SYSTEM MOLECULES  
; FILE REFERENCE: 71758/58066  
; CURRENT APPLICATION NUMBER: US/10/230,880  
; CURRENT FILING DATE: 2002-12-23  
; PRIOR APPLICATION NUMBER: 09/990,586  
; PRIOR FILING DATE: 2001-11-21  
; PRIOR APPLICATION NUMBER: 60/343,306  
; PRIOR FILING DATE: 2001-10-29  
; PRIOR APPLICATION NUMBER: 09/293,854  
; PRIOR FILING DATE: 1999-04-16  
; NUMBER OF SEQ ID NOS: 174  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 92  
; LENGTH: 87  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-230-880-92

Query Match 98.0%; Score 439; DB 12; Length 87;  
Best Local Similarity 97.7%; Pred. No. 2.3e-36;  
Matches 85; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QIQLVSGGELVKPGASVRVSCASGYSTWVRQSPGKLEWIGKATLTVDKSTSTAYME 60  
DB 1 QIQLVSGGEVVKPGASVRVSCASGYSTWVRQSPGKLEWIGKATLTVDKSTSTAYME 60  
QY 61 LSSLRSEDATVYFCARWGQTTVTSS 87  
DB 61 LSSLRSEDATVYFCARWGQTTVTSS 87

## RESULT 11

US-09-990-586-96  
; Sequence 96, Application US/09990586  
; Publication No. US20030109680A1  
; GENERAL INFORMATION:  
; APPLICANT: JIAO, JIN-AN  
; APPLICANT: WONG, HING C.  
; TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD COAGULATION AND METHODS  
; TITLE OF INVENTION: OF USE THEREOF  
; FILE REFERENCE: 71758/46943-CIP2  
; CURRENT APPLICATION NUMBER: US/09/990,586  
; CURRENT FILING DATE: 2001-11-21  
; PRIOR APPLICATION NUMBER: 09/293,854  
; PRIOR FILING DATE: 1999-04-16  
; NUMBER OF SEQ ID NOS: 102  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 96  
; LENGTH: 87  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-990-586-96

Query Match 97.5%; Score 437; DB 11; Length 87;  
Best Local Similarity 97.7%; Pred. No. 3.6e-36;  
Matches 85; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QIQLVSGGELVKPGASVRVSCASGYSTWVRQSPGKLEWIGKATLTVDKSTSTAYME 60  
DB 1 QIQLVSGGEVVKPGASVRVSCASGYSTWVRQSPGKLEWIGKATLTVDKSTSTAYME 60  
QY 61 LSSLRSEDATVYFCARWGQTTVTSS 87  
DB 61 LSSLRSEDATVYFCARWGQTTVTSS 87

## RESULT 12

US-10-230-880-96  
; Sequence 96, Application US/10230880  
; Publication No. US20030190705A1  
; GENERAL INFORMATION:  
; APPLICANT: WONG, HING C.  
; APPLICANT: STINSON, JEFFREY L.  
; APPLICANT: MOSQUERA, LUIS A.  
; TITLE OF INVENTION: METHOD OF HUMANIZING IMMUNE SYSTEM MOLECULES  
; FILE REFERENCE: 71758/58066  
; CURRENT APPLICATION NUMBER: US/10/230,880  
; CURRENT FILING DATE: 2002-12-23  
; PRIOR APPLICATION NUMBER: 09/990,586  
; PRIOR FILING DATE: 2001-11-21  
; PRIOR APPLICATION NUMBER: 60/343,306  
; PRIOR FILING DATE: 2001-10-29  
; PRIOR APPLICATION NUMBER: 09/293,854  
; PRIOR FILING DATE: 1999-04-16  
; NUMBER OF SEQ ID NOS: 174  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 96  
; LENGTH: 87  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-230-880-96

Query Match 97.5%; Score 437; DB 12; Length 87;  
Best Local Similarity 97.7%; Pred. No. 3.6e-36;  
Matches 85; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QIQLVSGGELVKPGASVRVSCASGYSTWVRQSPGKLEWIGKATLTVDKSTSTAYME 60  
DB 1 QIQLVSGGEVVKPGASVRVSCASGYSTWVRQSPGKLEWIGKATLTVDKSTSTAYME 60  
QY 61 LSSLRSEDATVYFCARWGQTTVTSS 87  
DB 61 LSSLRSEDATVYFCARWGQTTVTSS 87

## RESULT 13

US-09-990-586-94  
; Sequence 94, Application US/09990586  
; Publication No. US20030109680A1  
; GENERAL INFORMATION:  
; APPLICANT: JIAO, JIN-AN  
; APPLICANT: WONG, HING C.  
; TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD COAGULATION AND METHODS  
; TITLE OF INVENTION: OF USE THEREOF  
; FILE REFERENCE: 71758/46943-CIP2  
; CURRENT APPLICATION NUMBER: US/09/990,586  
; CURRENT FILING DATE: 2001-11-21  
; PRIOR APPLICATION NUMBER: 09/293,854  
; PRIOR FILING DATE: 1999-04-16  
; NUMBER OF SEQ ID NOS: 102  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 94  
; LENGTH: 87  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-990-586-94

Query Match 96.9%; Score 434; DB 11; Length 87;  
Best Local Similarity 97.7%; Pred. No. 7.2e-36;  
Matches 85; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QIQLVSGGELVKPGASVRVSCASGYSTWVRQSPGKLEWIGKATLTVDKSTSTAYME 60  
DB 1 QIQLVSGGEVVKPGASVRVSCASGYSTWVRQSPGKLEWIGKATLTVDKSTSTAYME 60  
QY 61 LSSLRSEDATVYFCARWGQTTVTSS 87



Db 61 LSSLRSEDVAVFCARWGQGTTVTVSS 87

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Job time : 13.9048 secs

Db 61 LSSLRSEDVAVFCARWGQGTTVTVSS 87

## RESULT 14

US-10-230-880-94  
; Sequence 94, Application US/10230880  
; Publication No. US20030190705A1  
; GENERAL INFORMATION:  
; APPLICANT: WONG, HING C.  
; APPLICANT: STINSON, JEFFREY L.  
; APPLICANT: MOSQUERA, LUIS A.  
; TITLE OF INVENTION: METHOD OF HUMANIZING IMMUNE SYSTEM MOLECULES  
; FILE REFERENCE: 71758/58066  
; CURRENT APPLICATION NUMBER: US/10/230,880  
; CURRENT FILING DATE: 2002-12-23  
; PRIOR APPLICATION NUMBER: 09/990,586  
; PRIOR FILING DATE: 2001-11-21  
; PRIOR APPLICATION NUMBER: 60/343,306  
; PRIOR FILING DATE: 2001-10-29  
; PRIOR APPLICATION NUMBER: 09/293,854  
; PRIOR FILING DATE: 1999-04-16  
; NUMBER OF SEQ ID NOS: 174  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 94  
; LENGTH: 87  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-230-880-94

Query Match 96.9%; Score 434; DB 12; Length 87;  
Best Local Similarity 97.7%; Pred. No. 7.2e-36;  
Matches 85; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 QIQLVQSGGELVPGASVRVSCKASGYSTFWRQSPGKGLEWIGKATLTVDKSTSTAYME 60  
DB 1 QIQLVQSGGELVPGASVRVSCKASGYSTFWRQSPGKGLEWIGKATLTVDKSTSTAYME 60  
QY 61 LSSLRSEDVAVFCARWGQGTTVTVSS 87  
DB 61 LSSLRSEDVAVFCARWGQGTTVTVSS 87

## RESULT 15

US-09-990-586-93  
; Sequence 93, Application US/09990586  
; Publication No. US20030109680A1  
; GENERAL INFORMATION:  
; APPLICANT: JIAO, JIN-AN  
; APPLICANT: WONG, HING C.  
; TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD COAGULATION AND METHODS  
; FILE REFERENCE: 71758/46943-CIP2  
; CURRENT APPLICATION NUMBER: US/09/990,586  
; CURRENT FILING DATE: 2001-11-21  
; PRIOR APPLICATION NUMBER: 09/293,854  
; PRIOR FILING DATE: 1999-04-16  
; NUMBER OF SEQ ID NOS: 102  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 93  
; LENGTH: 87  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-990-586-93

Query Match 96.2%; Score 431; DB 11; Length 87;  
Best Local Similarity 96.6%; Pred. No. 1.4e-35;  
Matches 84; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
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DB 1 QIQLVQSGGELVPGASVRVSCKASGYSTFWRQSPGKGLEWIGKATLTVDKSTSTAYME 60  
QY 61 LSSLRSEDVAVFCARWGQGTTVTVSS 87

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OM protein - protein search, using sw model

Run on: January 13, 2004, 12:33:50 ; Search time 7.52227 Seconds  
(without alignments)  
489.353 Million cell updates/sec

Title: US-09-990-586-90

Perfect score: 448

Sequence: 1 Q1QLVSGGLVKGASVRV.....DTAVYFCARWGQTTVTWSS 87

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: Issued Patents AA:\*
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- 3: /cgn2\_6/ptodata/1/iaa/5B COMB.pep.\*
- 4: /cgn2\_6/ptodata/1/iaa/6A COMB.pep.\*
- 5: /cgn2\_6/ptodata/1/iaa/6B COMB.pep.\*
- 6: /cgn2\_6/ptodata/1/iaa/PCTUS COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	376	83.9	87	1	US-08-497-312-16
2	360	80.4	117	4	US-08-525-539A-78
3	360	80.4	136	4	US-08-525-539A-63
4	356	79.5	136	4	US-08-450-520A-8
5	354.5	79.1	86	1	US-08-497-312-27
6	353.5	78.9	116	1	US-08-690-102A-8
7	353.5	78.9	116	3	US-08-127-902-8
8	353.5	78.9	116	3	US-08-135-107-8
9	353.5	78.9	116	5	PCT-US95-09641-8
10	353.5	78.9	135	1	US-08-137-117D-102
11	353.5	78.9	135	2	US-08-436-717-102
12	353.5	78.9	139	4	US-09-335-925-7
13	353.5	78.9	139	4	US-09-335-925-8
14	352.5	78.7	116	2	US-08-561-521-41
15	352.5	78.7	116	5	PCT-US95-01219-41
16	350.5	78.2	116	1	US-08-488-113B-168
17	350.5	78.2	116	1	US-08-477-484B-168
18	350.5	78.2	116	1	US-08-107-669D-54
19	350.5	78.2	116	1	US-08-472-788A-54
20	350.5	78.2	116	2	US-08-477-531B-54
21	350.5	78.2	116	2	US-08-646-360-168
22	350.5	78.2	116	2	US-08-082-842A-54
23	350.5	78.2	116	2	US-08-839-765-168
24	350.5	78.2	116	3	US-09-136-389-168
25	350.5	78.2	116	4	US-09-610-838-168
26	350	78.1	119	1	US-08-458-516-10
27	350	78.1	222	1	US-08-458-516-22

28	350	78.1	235	1	US-08-458-516-23
29	350	78.1	449	1	US-08-458-516-13
30	349.5	78.0	116	1	US-07-634-278-5
31	349.5	78.0	116	1	US-07-634-278-57
32	349.5	78.0	116	1	US-07-634-278-73
33	349.5	78.0	116	1	US-08-477-728-5
34	349.5	78.0	116	1	US-08-477-728-57
35	349.5	78.0	116	1	US-08-477-728-73
36	349.5	78.0	116	1	US-08-474-040-5
37	349.5	78.0	116	1	US-08-474-040-57
38	349.5	78.0	116	1	US-08-474-040-73
39	349.5	78.0	116	1	US-08-487-200-5
40	349.5	78.0	116	1	US-08-487-200-57
41	349.5	78.0	116	1	US-08-487-200-73
42	349.5	78.0	116	1	US-08-488-113B-169
43	349.5	78.0	116	1	US-08-477-484B-169
44	349.5	78.0	116	1	US-08-107-669D-55
45	349.5	78.0	116	1	US-08-472-788A-86

#### ALIGNMENTS

#### RESULT 1

US-08-497-312-16  
; Sequence 16, Application US/08497312  
; Patent No. 5712120

#### GENERAL INFORMATION:

APPLICANT:  
TITLE OF INVENTION: Method for obtaining modified immunoglobulins with reduced immunogenicity of murine antibody variable domains, compositions containing them.  
TITLE OF INVENTION: antibody variable domains, compositions containing them.  
NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CENTRO DE INMUNOLOGIA MOLECULAR  
STREET: 215 Y 15, ATABEY PLAYA  
CITY: HAVANA  
STATE:  
COUNTRY: CUBA  
ZIP: 11600

#### COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/497,312  
FILING DATE: 30-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: CU 80/94  
FILING DATE: 30-JUN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: BOND, LAURENCE B.  
REGISTRATION NUMBER: 30,549  
REFERENCE/DOCKET NUMBER: 2629US  
TELEPHONE: 801/532-1922  
TELEFAX: 801/531-9168  
TELEX: 388961 LPMO4UT  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 87 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO

Query Match 83.9%; Score 376; DB 1; Length 87;  
Best Local Similarity 79.3%; Pred. No. 1e-31;  
Matches 69; Conservative 10; Mismatches 8; Indels 0; Gaps 0;

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QY 1 QIQLVQSGGELVKPGASVRSCKASGYSTWVRQSPGKGLWIGKATLVDSKSTAYME 60
Db 1 QVQLVQSGAEVKPGASVRSCKASGYSTWVRQSPGKGLWIGKATLVDSKSTAYME 60
QY 61 LSSLRSSEDTAVYFCARWGQGTIVTVSS 87
Db 61 LSSLRSSEDTAVYFCARWGQGTIVTVSS 87

RESULT 2
US-08-525-539A-78
; Sequence 78, Application US/08525539A
; Patent No. 6309636
; GENERAL INFORMATION:
; APPLICANT: DO COUTO, FERNANDO J.R.
; APPLICANT: CERIANI, ROBERTO L.
; APPLICANT: PETERSON, JERRY A.
; TITLE OF INVENTION: RECOMBINANT PEPTIDES DERIVED FROM THE
; TITLE OF INVENTION: MC3 ANTI-BA46 ANTIBODY, METHODS OF USE THEREOF, AND
; TITLE OF INVENTION: METHODS OF HUMANIZING ANTIBODY PEPTIDES
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/525,539A
; FILING DATE: 14-SEP-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: DYLAN, TYLER
; REGISTRATION NUMBER: 37,612
; REFERENCE/DOCKET NUMBER: 27633-20001.21
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 78:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-525-539A-78

Query Match 80.4%; Score 360; DB 4; Length 117;
Best Local Similarity 65.8%; Pred. No. 6.1e-30;
Matches 77; Conservative 5; Mismatches 5; Indels 30; Gaps 3;

QY 1 QIQLVQSGGELVKPGASVRSCKASGYSTWVRQSPGKGLWIGKATLVDSKSTAYME 60
Db 1 EVQLVQSGAEVKPGASVRSCKASGYSTGTYTMHWKQSPGMNLEWIGLINFYNGTIV 60
QY 45 -----KATLVDSKSTAYMELSSLRSEDTAVYFCAR-----WGQGTIVTVSS 87
Db 61 NQKFDKATLVDSKSTAYMELSSLRSEDTAVYFCARRWRYTMDYWGQGTIVTVSS 117

RESULT 3
US-08-525-539A-63
; Sequence 63, Application US/08525539A
; Patent No. 6309636
; GENERAL INFORMATION:
; APPLICANT: DO COUTO, FERNANDO J.R.
; APPLICANT: CERIANI, ROBERTO L.

```

```

; APPLICANT: PETERSON, JERRY A.
; TITLE OF INVENTION: RECOMBINANT PEPTIDES DERIVED FROM THE
; TITLE OF INVENTION: MC3 ANTI-BA46 ANTIBODY, METHODS OF USE THEREOF, AND
; TITLE OF INVENTION: METHODS OF HUMANIZING ANTIBODY PEPTIDES
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/525,539A
; FILING DATE: 14-SEP-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: DYLAN, TYLER
; REGISTRATION NUMBER: 37,612
; REFERENCE/DOCKET NUMBER: 27633-20001.21
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 63:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 136 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-525-539A-63

Query Match 80.4%; Score 360; DB 4; Length 136;
Best Local Similarity 65.8%; Pred. No. 7.2e-30;
Matches 77; Conservative 5; Mismatches 5; Indels 30; Gaps 3;

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Db 20 EVQLVQSGAEVKPGASVRSCKASGYSTGTYTMHWKQSPGMNLEWIGLINFYNGTIV 79
QY 45 -----KATLVDSKSTAYMELSSLRSEDTAVYFCAR-----WGQGTIVTVSS 87
Db 80 NQKFDKATLVDSKSTAYMELSSLRSEDTAVYFCARRWRYTMDYWGQGTIVTVSS 136

RESULT 4
US-09-450-520A-8
; Sequence 8, Application US/09450520A
; Patent No. 6329511
; GENERAL INFORMATION:
; APPLICANT: Vasquez, Maximiliano
; APPLICANT: Landolfi, Nicholas F.
; APPLICANT: Tsurushita, Naoya
; APPLICANT: Queen, Cary L.
; APPLICANT: Protein Design Labs, Inc.
; TITLE OF INVENTION: Humanized Antibodies To Gamma-Interferon
; FILE REFERENCE: 011823-008110US
; CURRENT APPLICATION NUMBER: US/09/450,520A
; CURRENT FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 60/110,523
; PRIOR FILING DATE: 1998-12-01
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

```

OTHER INFORMATION: Description of Artificial Sequence: human-mouse  
OTHER INFORMATION: transgenic construct HuZAF VH  
US-09-450-520A-8

Query Match 79.5%; Score 356; DB 4; Length 136;  
Best Local Similarity 64.1%; Pred. No. 1.8e-23;  
Matches 75; Conservative 8; Mismatches 4; Indels 30; Gaps 3;

QY 1 QIQLVSGGELVKPGASVRVSKASGYSFT-----WVROSPGKGLWIG-----44  
DB 20 QVQLVSGAELKPGSSVKVSKASGYITSSINWVWKAAPGGLEWIGRIDPSDEVHY 79  
QY 45 -----KATLTVDKSTSTAYMELSLRSEDATVYFCAR-----WGQGTIVTVSS 87  
DB 80 NQDFPKDKATLTVDKSTNTAYMELSLRSEDATVYFCARGLPWFADWGQGTIVTVSS 136

RESULT 5  
US-08-497-312-27  
; Sequence 27, Application US/08497312  
; Patent No. 5712120  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: Method for obtaining modified  
; TITLE OF INVENTION: immunoglobulins with reduced immunogenicity of murine  
; NUMBER OF SEQUENCES: 31  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CENTRO DE INMUNOLOGIA MOLECULAR  
; STREET: 215 Y 15, ATABEY PLAYA  
; CITY: HAVANA  
; STATE:  
; COUNTRY: CUBA  
; ZIP: 11600  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/497,312  
; FILING DATE: 30-JUN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: CU 80/94  
; FILING DATE: 30-JUN-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BOND, LAURENCE B.  
; REGISTRATION NUMBER: 30,549  
; REFERENCE/DOCKET NUMBER: 2629US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 801/532-1922  
; TELEFAX: 801/531-9168  
; TELEX: 388961 1PMO4UT  
; INFORMATION FOR SEQ ID NO: 27:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 86 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: protein  
; HYPOTHEICAL: NO  
US-08-497-312-27

Query Match 79.1%; Score 354.5; DB 1; Length 86;  
Best Local Similarity 77.0%; Pred. No. 1.6e-29;  
Matches 67; Conservative 11; Mismatches 8; Indels 1; Gaps 1;

QY 1 QIQLVSGGELVKPGASVRVSKASGYSFTWVROSPGKGLWIGKATLTVDKSTSTAYME 60  
DB 1 QVQLVSGAELKPGSSVKVSKASGY-FTWVRAQPGRLWGMGRVITRDTSTAYME 59  
QY 61 LSSLRSEDATVYFCARWGQGTIVTVSS 87

DB 60 LSSLRSEDATVYFCARWGQGTIVTVSS 86

## RESULT 6

US-08-690-102A-8  
; Sequence 8, Application US/08690102A  
; Patent No. 5789554  
; GENERAL INFORMATION:  
; APPLICANT: LEUNG, Shui-on  
; APPLICANT: HANSEN, Hans  
; TITLE OF INVENTION: IMMUNOCONJUGATES AND HUMANIZED  
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR B-CELL LYMPHOMA AND LEUKEMIA CELLS  
; NUMBER OF SEQUENCES: 21  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington, D.C.  
; COUNTRY: USA  
; ZIP: 20007-5109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/690,102A  
; FILING DATE: 01-JUL-1996  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/289,576  
; FILING DATE: 12-AUG-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: SAXE, Bernhard D.  
; REGISTRATION NUMBER: 28,665  
; REFERENCE/DOCKET NUMBER: 18733/453/IMIN  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 672-5300  
; TELEFAX: (202) 672-5399  
; TELEX: 904136  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 116 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-690-102A-8

Query Match 78.9%; Score 353.5; DB 1; Length 116;  
Best Local Similarity 62.9%; Pred. No. 2.8e-29;  
Matches 73; Conservative 10; Mismatches 4; Indels 29; Gaps 3;

QY 1 QIQLVSGGELVKPGASVRVSKASGYSFT-----WVROSPGKGLWIG-----44  
DB 1 QVQLVSGAELKPGSSVKVSKASGYTFTSYWLHWVRAQPGGLEWIGYINPRNDYTEY 60  
QY 45 -----KATLTVDKSTSTAYMELSLRSEDATVYFCAR-----WGQGTIVTVSS 87  
DB 61 NQDFPKDKATITADESTNTAYMELSLRSEDATVYFCARDITTFYWGQGTIVTVSS 116

## RESULT 7

US-09-127-902-8  
; Sequence 8, Application US/09127902  
; Patent No. 6187287  
; GENERAL INFORMATION:  
; APPLICANT: LEUNG, Shui-on  
; APPLICANT: HANSEN, Hans  
; TITLE OF INVENTION: IMMUNOCONJUGATES AND HUMANIZED  
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR B-CELL LYMPHOMA AND LEUKEMIA CELLS  
; NUMBER OF SEQUENCES: 21  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 3000 K Street, N.W., Suite 500

```
/ CITY: Washington, D.C.
/ COUNTRY: USA
/ ZIP: 20007-5109
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/127,902
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/690,102
/ FILING DATE: 01-JUL-1996
/ APPLICATION NUMBER: US 08/289,576
/ FILING DATE: 12-AUG-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: SAXE, Bernhard D.
/ REGISTRATION NUMBER: 28,665
/ REFERENCE/DOCKET NUMBER: 18733/463/IMIN
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (202)672-5300
/ TELEFAX: (202)672-5399
/ TELEX: 904136
/ INFORMATION FOR SEQ ID NO: 8:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 116 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-09-127-902-8

Query Match      78.9%; Score 353.5; DB 3; Length 116;
Best Local Similarity 62.9%; Pred. No. 2.8e-29;
Matches 73; Conservative 10; Mismatches 4; Indels 29; Gaps 3;

QY 1 QIQLVSGGELVPGASVRVSKASGYSTFT-----WROSPGKGLEWIG----- 44
Db 1 QVQLVSGAEVKPGSSVKVSKASGYTFTSYWLHWVRQAPGGGLEWIGYINPRNDYTEY 60
QY 45 -----KATLTVDKSTSTAYMELSSLSRSEDTAVYFCAR-----WQGGTTVTVSS 87
Db 61 NQNFKDKATITADESTINATMELSSLSRSEDTAFYFCARRDITTFYWGQGTITVTVSS 116

RESULT 8
US-09-155-107-8
; Sequence 8, Application US/09155107
; Patent No. 6254868
; GENERAL INFORMATION:
; APPLICANT: LEUNG, Shui-on
; APPLICANT: HANSEN, Hans
; APPLICANT: QU, Zhengxing
; TITLE OF INVENTION: GLYCOSYLATED HUMANIZED B-CELL SPECIFIC ANTIBODIES
; FILE REFERENCE: 018733/0879
; CURRENT APPLICATION NUMBER: US/09/155,107
; CURRENT FILING DATE: 1998-11-17
; EARLIER APPLICATION NUMBER: WO PCT/US97/04196
; EARLIER FILING DATE: 1997-03-19
; EARLIER APPLICATION NUMBER: US 60/013,709
; EARLIER FILING DATE: 1996-03-20
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo sapiens
/ US-09-155-107-8

Query Match      78.9%; Score 353.5; DB 3; Length 116;
Best Local Similarity 62.9%; Pred. No. 2.8e-29;
Matches 73; Conservative 10; Mismatches 4; Indels 29; Gaps 3;
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QY 1 QIQLVSGGELVPGASVRVSKASGYSTFT-----WROSPGKGLEWIG----- 44
Db 1 QVQLVSGAEVKPGSSVKVSKASGYTFTSYWLHWVRQAPGGGLEWIGYINPRNDYTEY 60
QY 45 -----KATLTVDKSTSTAYMELSSLSRSEDTAVYFCAR-----WQGGTTVTVSS 87
Db 61 NQNFKDKATITADESTINATMELSSLSRSEDTAFYFCARRDITTFYWGQGTITVTVSS 116

RESULT 9
PCT-US95-09641-8
; Sequence 8, Application PC/TUS9509641
; GENERAL INFORMATION:
; APPLICANT: IMMUNOCONJUGATES AND HUMANIZED
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR B-CELL LYMPHOMA AND LEUKEMIA CELLS
; NUMBER OF SEQUENCES: 21
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/09641
; FILING DATE: 11-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/289,576
; FILING DATE: 12-AUG-1994
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 116 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
/ PCT-US95-09641-8

Query Match      78.9%; Score 353.5; DB 5; Length 116;
Best Local Similarity 62.9%; Pred. No. 2.8e-29;
Matches 73; Conservative 10; Mismatches 4; Indels 29; Gaps 3;

QY 1 QIQLVSGGELVPGASVRVSKASGYSTFT-----WROSPGKGLEWIG----- 44
Db 1 QVQLVSGAEVKPGSSVKVSKASGYTFTSYWLHWVRQAPGGGLEWIGYINPRNDYTEY 60
QY 45 -----KATLTVDKSTSTAYMELSSLSRSEDTAVYFCAR-----WQGGTTVTVSS 87
Db 61 NQNFKDKATITADESTINATMELSSLSRSEDTAFYFCARRDITTFYWGQGTITVTVSS 116

RESULT 10
US-08-137-117D-102
; Sequence 102, Application US/08137117D
; Patent No. 5793965
; GENERAL INFORMATION:
; APPLICANT: TSUCHIYA, Masayuki
; APPLICANT: SATO, Koh
; APPLICANT: BENDIG, Mary
; APPLICANT: JONES, Steven
; APPLICANT: SALDANHA, Jose
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
; INTERLEUKIN-6 RECEPTOR
; NUMBER OF SEQUENCES: 158
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
```

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/137,117D  
FILING DATE: 20-DEC-1993  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/JP92/00544  
FILING DATE: 24-APR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 4-32084  
FILING DATE: 19-FEB-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 3-95476  
FILING DATE: 25-APR-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: WEGNER, Harold C.  
REGISTRATION NUMBER: 25,259  
REFERENCE/DOCKET NUMBER: 53466/126/RAOK  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 102:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 135 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-137-117D-102

Query Match 78.9%; Score 353.5; DB 1; Length 135;  
Best Local Similarity 63.8%; Pred. No. 3.3e-29;  
Matches 74; Conservative 8; Mismatches 5; Indels 29; Gaps 3;

QY 1 QIQLVQSGGELVKPGASVRSCKASGYSFT-----WVRQSPGKGLEWI----- 43  
Db 20 QVQLVQSGAEVKKPGASVKVSKASGYSFTSYIHWVRQAPGQGLEWIGYIDPFNGGTSY 79

QY 44 -----GKATLVDSKSTAYNELSLRSEDNAVYFCAR-----WGQGTTVTVSS 87  
Db 80 NQKFKGKVTMTVDSTNTAYNELSLRSEDNAVYFCARGNRFAYWGQGLTLTVSS 135

RESULT 11  
US-08-436-717-102  
Sequence 102, Application US/08436717  
Patent No. 5817790  
GENERAL INFORMATION:  
APPLICANT: TSUCHIYA, Masayuki  
APPLICANT: SATO, Koh  
APPLICANT: BENDIG, Mary  
APPLICANT: JONES, Steven  
APPLICANT: SALDANHA, Jose  
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN  
TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR  
NUMBER OF SEQUENCES: 158  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/436,717  
FILING DATE:  
CLASSIFICATION: 536

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/137,117  
FILING DATE: 20-DEC-1993  
APPLICATION NUMBER: WO PCT/JP92/00544  
FILING DATE: 24-APR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 4-32084  
FILING DATE: 19-FEB-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 3-95476  
FILING DATE: 25-APR-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: WEGNER, Harold C.  
REGISTRATION NUMBER: 25,258  
REFERENCE/DOCKET NUMBER: 53466/126/RAOK  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 102:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 135 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-436-717-102

Query Match 78.9%; Score 353.5; DB 2; Length 135;  
Best Local Similarity 63.8%; Pred. No. 3.3e-29;  
Matches 74; Conservative 8; Mismatches 5; Indels 29; Gaps 3;

QY 1 QIQLVQSGGELVKPGASVRSCKASGYSFT-----WVRQSPGKGLEWI----- 43  
Db 20 QVQLVQSGAEVKKPGASVKVSKASGYSFTSYIHWVRQAPGQGLEWIGYIDPFNGGTSY 79

QY 44 -----GKATLVDSKSTAYNELSLRSEDNAVYFCAR-----WGQGTTVTVSS 87  
Db 80 NQKFKGKVTMTVDSTNTAYNELSLRSEDNAVYFCARGNRFAYWGQGLTLTVSS 135

RESULT 12  
US-09-355-925-7  
Sequence 7, Application US/09355925  
Patent No. 6503510  
GENERAL INFORMATION:  
APPLICANT: KOISHIHARA, YASUO  
APPLICANT: YOSHIMURA, YASUO  
TITLE OF INVENTION: THERAPEUTIC AGENT FOR LYMPHATIC TUMORS  
FILE REFERENCE: 053466/0255  
CURRENT APPLICATION NUMBER: US/09/355,925  
CURRENT FILING DATE: 1999-08-11  
PRIOR APPLICATION NUMBER: PCT/JP98/00568  
PRIOR FILING DATE: 1998-02-12  
PRIOR APPLICATION NUMBER: JP 9-41410  
PRIOR FILING DATE: 1997-02-12  
NUMBER OF SEQ ID NOS: 8  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 7  
LENGTH: 139  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Amino acid  
OTHER INFORMATION: sequence of H chain V region version r of  
OTHER INFORMATION: humanized anti-HM1.24 antibody  
US-09-355-925-7

Query Match 78.9%; Score 353.5; DB 4; Length 139;  
Best Local Similarity 60.8%; Pred. No. 3.4e-29;  
Matches 73; Conservative 10; Mismatches 4; Indels 33; Gaps 3;

QY 1 QIQLVQSGGELVKPGASVRSCKASGYSFT-----WVRQSPGKGLEWI----- 43  
Db 80 NQKFKGKVTMTVDSTNTAYNELSLRSEDNAVYFCARGNRFAYWGQGLTLTVSS 135

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Db 20 QVQLVQSGAEVKKPGASVKVSCKASGYTFPTFYMWMQVRCAPQGLEWNGSIFPGDGT 79
QY 44 -----GKATLTVDKSTAYMELSLRSEDATVYFCAR-----WGQGTITVTVSS 87
Db 80 SQKFQGRVTMTADKSTAYMELSLRSEDATVYVCARGLRGGYFDYWGQGTITVTVSS 139

RESULT 13
US-09-355-925-8
; Sequence 8, Application US/093555925
; Patent No. 6503510
; GENERAL INFORMATION:
; APPLICANT: KOISHIHARA, YASUO
; TITLE OF INVENTION: THERAPEUTIC AGENT FOR LYMPHATIC TUMORS
; FILE REFERENCE: 053465/0255
; CURRENT APPLICATION NUMBER: US/09/355,925
; CURRENT FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: PCT/JP98/00568
; PRIOR FILING DATE: 1998-02-12
; PRIOR APPLICATION NUMBER: JP 9-41410
; PRIOR FILING DATE: 1997-02-12
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 8
; LENGTH: 139
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Amino acid
; OTHER INFORMATION: sequence H chain V region version 8 of
; OTHER INFORMATION: anti-HM1.24 antibody
; US-09-355-925-8

Query Match 78.9%; Score 353.5; DB 4; Length 139;
Best Local Similarity 60.8%; Pred. No. 3.4e-29;
Matches 73; Conservative 10; Mismatches 4; Indels 3; Gaps 3;

QY 1 QIQLVQSGGELVKPGASVRSVCKASGYST-----WVRSPPGKLEWI-----43
Db 20 QVQLVQSGAEVKKPGASVKVSCKASGYTFPTFYMWMQVRCAPQGLEWNGSIFPGDGT 79
QY 44 -----GKATLTVDKSTAYMELSLRSEDATVYFCAR-----WGQGTITVTVSS 87
Db 80 SQKFQGRVTMTADKSTAYMELSLRSEDATVYVCARGLRGGYFDYWGQGTITVTVSS 139

RESULT 14
US-08-561-521-41
; Sequence 41, Application US/08561521
; Patent No. 5840299
; GENERAL INFORMATION:
; APPLICANT: Bendig, Mary M.
; APPLICANT: Leger, Olivier J.
; APPLICANT: Saldanha, Jose
; APPLICANT: Jones, S. Tarran
; TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
; TITLE OF INVENTION: Adhesion Molecule VLA-4
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/561,521
; FILING DATE: 25-JAN-1995
; CLASSIFICATION:
; PRIOR APPLICATION NUMBER: US 08/186,269
; FILING DATE: 25-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William L.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15270-14
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-543-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; US-08-561-521-41
```

```
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/186,269A
; FILING DATE: 25-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William L.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15270-14
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-543-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 116 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-561-521-41

Query Match 78.7%; Score 352.5; DB 2; Length 116;
Best Local Similarity 62.9%; Pred. No. 3.5e-29;
Matches 73; Conservative 9; Mismatches 5; Indels 29; Gaps 3;

QY 1 QIQLVQSGGELVKPGASVRSVCKASGYST-----WVRSPPGKLEWI-----43
Db 1 QVQLVQSGAEVKKPGASVKVSCKASGYSTFYIHWVRQAPGQGLEWVYIDPFNGGTSY 60
QY 44 -----GKATLTVDKSTAYMELSLRSEDATVYFCAR-----WGQGTITVTVSS 87
Db 61 NQKFQGRVTMTADKSTAYMELSLRSEDATVYVCARGNRFPAYWGQGTITVTVSS 116

RESULT 15
PCT-US95-01219-41
; Sequence 41, Application PC/TUS9501219
; GENERAL INFORMATION:
; APPLICANT: Bendig, Mary M.
; APPLICANT: Leger, Olivier J.
; APPLICANT: Saldanha, Jose
; APPLICANT: Jones, S. Tarran
; TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
; TITLE OF INVENTION: Adhesion Molecule VLA-4
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/01219
; FILING DATE: 25-JAN-1995
; CLASSIFICATION:
; PRIOR APPLICATION NUMBER: US 08/186,269
; FILING DATE: 25-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William L.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15270-14
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-543-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; US-08-561-521-41
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; LENGTH: 116 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-01219-41

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Query Match      78.7%  Score 352.5;  DB 5;  Length 116;
Best Local Similarity  52.9%  Pred. No. 3.5e-29;
Matches 73;  Conservative 9;  Mismatches 5;  Indels 29;  Gaps 3;

Qy  1 QIQLVQSGGELVXPGASRVVSCXASGYST-----WVRSFGKGLWFI----- 43
Db  1 QVQLVQSGAEVKKFGASVKVSCXASGYSTSYIHWVRQAPGQGLEWVGVIDPFNGGTSY 60
Qy  44 -----GKATLTVDKSTSTAYMELSSLSRSEDYVYFCAR-----WGQGTITVTVSS 87
Db  61 NQKFKGVTVTVDTSTNTAYMELSSLSRSEDYVYFCARGNRFAYWGQGLTVTVSS 116

```

Search completed: January 13, 2004, 12:46:32  
Job time : 7.52227 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 13, 2004, 12:22:35 ; Search time 6.30655 Seconds  
(without alignments)  
1326.664 Million cell updates/sec

Title: US-09-990-586-91

Perfect score: 449

Sequence: 1 QIQLVQSGGVKPGASVRV.....DTAVFCARWGQTTVTYSS 87

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR 76.\*

2: PIR1.\*

3: PIR2.\*

4: PIR3.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	347	77.3	119	2 PH0961	Ig heavy chain V r
2	345.5	76.3	122	2 PH0958	Ig heavy chain V r
3	344.5	76.7	118	2 S36265	Ig heavy chain V r
4	342.5	76.3	116	2 PH0959	Ig heavy chain V r
5	342.5	76.3	136	2 PH0960	Ig heavy chain V r
6	341	75.9	142	2 A32483	Ig heavy chain V r
7	340.5	75.8	120	2 PH0962	Ig heavy chain V r
8	340.5	75.8	128	2 PH0952	Ig heavy chain V r
9	340.5	75.8	132	2 PH0954	Ig heavy chain V r
10	339	75.5	127	2 PH0955	Ig heavy chain V r
11	337	75.1	133	2 C33548	Ig heavy chain V-1
12	337	75.1	627	2 S14682	Ig mu chain precuor
13	336.5	74.9	119	2 A24672	Ig heavy chain pre
14	336.5	74.9	126	2 B33548	Ig heavy chain V-1
15	336.5	74.9	135	2 S49330	anti-Sm antibody V
16	336	74.8	129	2 A33548	Ig heavy chain V-1
17	335	74.6	121	2 S20783	Ig heavy chain V r
18	335	74.6	129	2 S36260	Ig heavy chain V r
19	334.5	74.5	469	2 S37483	Ig gamma-2a chain
20	334	74.4	125	2 PH0957	Ig heavy chain V r
21	333.5	74.3	124	2 S19665	Ig heavy chain V r
22	332	73.9	138	2 S21810	Ig heavy chain V r
23	331	73.7	246	2 S38950	Ig gamma chain - m
24	331	73.7	446	2 S40295	Ig gamma-2a chain
25	330.5	73.6	132	2 S46394	Ig heavy chain V r
26	330.5	73.6	137	2 H32513	Ig heavy chain pre
27	329.5	73.4	135	2 B32274	Ig heavy chain pre
28	329	73.3	127	2 S34014	Ig heavy chain V r
29	328.5	73.2	120	2 B22769	Ig heavy chain V r

ALIGNMENTS

RESULT 1

PH0961

Ig heavy chain V region (G6+ T-L33) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 16-Aug-1996

C:Accession: PH0961

R:Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.

J. Exp. Med. 175, 983-991, 1992

A:Title: Evidence for somatic selection of natural autoantibodies.

A:Reference number: PH0952; MUID:92202880; PMID:1552291

A:Accession: PH0961

A:Status: nucleic acid sequence not shown

A:Molecule type: DNA

A:Residues: 1-119 <MAR>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-30/Region: framework 1

F:15-98/Domain: immunoglobulin homology <IMM>

F:31-35/Region: complementarity-determining 1

F:36-50/Region: complementarity-determining 2

F:51-67/Region: complementarity-determining 2

F:68-98/Region: framework 3

F:99-107/Region: complementarity-determining 3

Query Match 77.3%; Score 347; DB 2; Length 119;

Best Local Similarity 59.7%; Pred. No. 4.3e-27; Mismatches 12; Indels 32; Gaps 3;

Matches 71; Conservative 71; Mismatches 12; Indels 32; Gaps 3;

QY 1 QIQLVQSGGVKPGASVRVSKASG-----YSTWVRQSPFGKLEWI----- 43

Db 1 QVQLVQSGAEVKKPGSSVKVSKASGGTFFSSYALSWVRQAPGQGLEWMGGIPIFGTANY 60

QY 44 -----GKATLVDSKSTAYNELSLRSEDPAVYFCAR-----WGQGTIVTVYSS 87

Db 61 AQKFGQRTIITADESTAYNELSLRSEDPAVYFCAR-----WGQGTIVTVYSS 119

RESULT 2

PH0958

Ig heavy chain V region (G6+ CLL-HUR) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 16-Aug-1996

C:Accession: PH0958

R:Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.

J. Exp. Med. 175, 983-991, 1992

A:Title: Evidence for somatic selection of natural autoantibodies.

A:Reference number: PH0952; MUID:92202880; PMID:1552291

A:Accession: PH0958

A:Status: nucleic acid sequence not shown

A:Molecule type: DNA

A:Residues: 1-122 <MAR>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotrimer; immunoglobulin  
F;1-30/Region: framework 1  
F;15-98/Domain: immunoglobulin homology <IMW>  
F;31-35/Region: complementarity-determining 1  
F;36-50/Region: framework 2  
F;51-67/Region: complementarity-determining 2  
F;68-98/Region: framework 3  
F;99-110/Region: complementarity-determining 3

Query Match 76.9%; Score 345.5; DB 2; Length 122;  
Best Local Similarity 58.2%; Pred. No. 6.2e-27;  
Matches 71; Conservative 12; Mismatches 4; Indels 35; Gaps 3;  
  
QY 1 QIQLVSGGEVKKPGASVRVSKASG-----YSFTWRQSPGKGLW----- 43  
DB 1 QVQLVSGAEVKKPGSSVKVSKASGCTFSSVAISWVRQAPQGQLEWMGGIPIFGTANY 60  
  
QY 44 -----GKATLVDSKSTAYMELSLRSRSDTAVYFCAR-----WGQGTITVSS 85  
DB 61 AQKFGQGVITADESTAYMELSLRSRSDTAVYFCARVNPFPFAVGMDVWGQGTITV 120  
  
QY 86 SS 87  
DB 121 SS 122

## RESULT 3

S36265  
Ig heavy chain V region (clone alpha-MUC1-1) - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 23-Jul-1999  
C;Accession: S36265  
R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.  
EMBO J. 12, 725-734, 1993  
A;Title: Human anti-self antibodies with high specificity from phage display libraries.  
A;Reference number: S36265; MUID:93178448; PMID:7679990  
A;Accession: S36265  
A;Status: preliminary; nucleic acid sequence not shown  
A;Molecule type: mRNA  
A;Residues: 1-118 <GRI>  
A;Cross-references: EMBL:Z18846; NID:G33121; PID:G939900  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotrimer; immunoglobulin  
F;15-98/Domain: immunoglobulin homology <IMW>

Query Match 76.7%; Score 344.5; DB 2; Length 118;  
Best Local Similarity 61.0%; Pred. No. 7.6e-27;  
Matches 72; Conservative 9; Mismatches 6; Indels 31; Gaps 3;  
  
QY 1 QIQLVSGGEVKKPGASVRVSKASGYST-----VWRQSPGKGLW----- 43  
DB 1 QVQLVSGAEVKKPGASVKVSKASGYTPTGYMHVVRQAPQGQLEWMGWINPNSGGTNY 60  
  
QY 44 -----GKATLVDSKSTAYMELSLRSRSDTAVYFCAR-----WGQGTITVSS 87  
DB 61 AQKFGQGVITRDTASTAYMELSLRSRSDTAVYFCARFLSGYLDYWGQGTITVSS 118

## RESULT 4

PH0959  
Ig heavy chain V region (G6+ T-L26) - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 16-Aug-1996  
C;Accession: PH0959  
R;Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.  
J. Exp. Med. 175, 983-991, 1992  
A;Title: Evidence for somatic selection of natural autoantibodies.  
A;Reference number: PH0952; MUID:92202880; PMID:1152291  
A;Accession: PH0959  
A;Status: nucleic acid sequence not shown  
A;Molecule type: DNA  
A;Residues: 1-116 <MAR>  
C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotrimer; immunoglobulin  
F;1-30/Region: framework 1  
F;15-98/Domain: immunoglobulin homology <IMW>  
F;31-35/Region: complementarity-determining 1  
F;36-50/Region: framework 2  
F;51-67/Region: complementarity-determining 2  
F;68-98/Region: framework 3  
F;99-104/Region: complementarity-determining 3

Query Match 76.3%; Score 342.5; DB 2; Length 116;  
Best Local Similarity 60.3%; Pred. No. 1.2e-26;  
Matches 70; Conservative 12; Mismatches 5; Indels 29; Gaps 3;  
  
QY 1 QIQLVSGGEVKKPGASVRVSKASG-----YSFTWRQSPGKGLW----- 43  
DB 1 QVQLVSGAEVKKPGSSVKVSKASGCTFSSVAISWVRQAPQGQLEWMGGIPIFGTANY 60  
  
QY 44 -----GKATLVDSKSTAYMELSLRSRSDTAVYFCAR-----WGQGTITVSS 87  
DB 61 AQKFGQGVITADESTAYMELSLRSRSDTAVYFCARNDWFDPMGQGTITVSS 116

## RESULT 5

PH0960  
Ig heavy chain V region (G6+ T-L30) - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 16-Aug-1996  
C;Accession: PH0960  
R;Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.  
J. Exp. Med. 175, 983-991, 1992  
A;Title: Evidence for somatic selection of natural autoantibodies.  
A;Reference number: PH0952; MUID:92202880; PMID:1152291  
A;Accession: PH0960  
A;Status: nucleic acid sequence not shown  
A;Molecule type: DNA  
A;Residues: 1-136 <MAR>

C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotrimer; immunoglobulin  
F;1-30/Region: framework 1  
F;15-98/Domain: immunoglobulin homology <IMW>  
F;31-35/Region: complementarity-determining 1  
F;36-50/Region: framework 2  
F;51-67/Region: complementarity-determining 2  
F;68-98/Region: framework 3  
F;99-124/Region: complementarity-determining 3

Query Match 76.3%; Score 342.5; DB 2; Length 136;  
Best Local Similarity 52.9%; Pred. No. 1.4e-26;  
Matches 72; Conservative 11; Mismatches 4; Indels 49; Gaps 3;  
  
QY 1 QIQLVSGGEVKKPGASVRVSKASG-----YSFTWRQSPGKGLW----- 43  
DB 1 QVQLVSGAEVKKPGSSVKVSKASGCTFSSVAISWVRQAPQGQLEWMGGIPIFGTANY 60  
  
QY 44 -----GKATLVDSKSTAYMELSLRSRSDTAVYFCAR----- 76  
DB 61 AQKFGQGVITADKSTAYMELSLRSRSDTAVYFCARVSVSTLYDSSGYIDFSY 120  
  
QY 77 -----WGQGTITVSS 87  
DB 121 YGMDVWGQGTITVSS 136

## RESULT 6

A32483  
Ig heavy chain V region - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 12-Oct-1989 #sequence\_revision 12-Oct-1989 #text\_change 16-Aug-1996  
C;Accession: A32483  
R;Larrick, J.W.; Danielsson, L.; Brenner, C.A.; Abrahamson, M.; Fry, K.E.; Borrebaeck, C.  
Biochem. Biophys. Res. Commun. 160, 1250-1256, 1989  
A;Title: Rapid cloning of rearranged immunoglobulin genes from human hybridoma cells us:  
A;Reference number: A32483; MUID:89273586; PMID:2499327

A:Accession: A32483

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-142 <LAR>

C:Cross-references: GB:W26463

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:25-108/Domain: immunoglobulin homology <IMM>

Query Match 75.9%; Score 341; DB 2; Length 142;

Best Local Similarity 56.7%; Pred. No. 2e-26;

Matches 72; Conservative 9; Mismatches 6; Indels 40; Gaps 3;

QY 1 QIQLVQSGGEVKKPGASVRVSCKASGVSFT-----YRQSPGKGLWLI----- 43

DB 11 QVQLVQSGAEVKKPGASVKVSCKASGYTFNYYMHVWVQAPGQGLEWMGIINPFGNNTNY 70

QY 44 -----GKATLTVDKSTSTAYMELSLRSEDVAVYFCAR-----WGQG 80

DB 71 AQKFGQGVTTITADKSTSTAYMELSLRSEDVAVYFCAREKLATIFGVLIITGMDYWGQ 130

QY 81 TTVTVSS 87

DB 131 TTVTVSS 137

RESULT 7

PH0962

Ig heavy chain V region (G6+ T-L42) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 16-Aug-1996

A:Accession: PH0962

R:Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.

J. Exp. Med. 175, 983-991, 1992

A:Title: Evidence for somatic selection of natural autoantibodies.

A:Reference number: PH0952; MUID:92202880; PMID:1552291

A:Accession: PH0962

A:Status: nucleic acid sequence not shown

A:Molecule type: DNA

A:Residues: 1-120 <MAR>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-30/Region: framework 1

F:15-98/Domain: immunoglobulin homology <IMM>

F:31-35/Region: complementarity-determining 1

F:36-50/Region: framework 2

F:51-67/Region: complementarity-determining 2

F:68-98/Region: framework 3

F:99-108/Region: complementarity-determining 3

Query Match 75.8%; Score 340.5; DB 2; Length 120;

Best Local Similarity 58.3%; Pred. No. 1.9e-26;

Matches 70; Conservative 12; Mismatches 5; Indels 33; Gaps 3;

QY 1 QIQLVQSGGEVKKPGASVRVSCKASG-----YSTWVRQSPGKGLWLI----- 43

DB 1 QVQLVQSGAEVKKPGASVKVSCKASGGTFSSYALSWVRQAPGQGLEWMGIIPIFGTANY 60

QY 44 -----GKATLTVDKSTSTAYMELSLRSEDVAVYFCAR-----WGQGTITVTVSS 87

DB 61 AQKFGQGVTTITADKSTSTAYMELSLRSEDVAVYFCARGGVAGRPFDYWGQGLTVTVSS 120

RESULT 8

PH0952

Ig heavy chain V region (G6+ CLL-SMI) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 16-Aug-1996

A:Accession: PH0952

R:Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.

J. Exp. Med. 175, 983-991, 1992

A:Title: Evidence for somatic selection of natural autoantibodies.

A:Reference number: PH0952; MUID:92202880; PMID:1552291

A:Accession: PH0952

A:Status: nucleic acid sequence not shown

A:Molecule type: DNA

A:Residues: 1-128 <MAR>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-30/Region: framework 1

F:15-98/Domain: immunoglobulin homology <IMM>

F:31-35/Region: complementarity-determining 1

F:36-50/Region: framework 2

F:51-67/Region: complementarity-determining 2

F:68-98/Region: framework 3

F:99-116/Region: complementarity-determining 3

Query Match 75.8%; Score 340.5; DB 2; Length 128;

Best Local Similarity 55.5%; Pred. No. 2e-26;

Matches 71; Conservative 11; Mismatches 5; Indels 41; Gaps 3;

QY 1 QIQLVQSGGEVKKPGASVRVSCKASG-----YSTWVRQSPGKGLWLI----- 43

DB 1 QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYALSWVRQAPGQGLEWMGGIPIFGTANY 60

QY 44 -----GKATLTVDKSTSTAYMELSLRSEDVAVYFCAR-----WGQ 79

DB 61 AQKFGQGVTTITADKSTSTAYMELSLRSEDVAVYFCARGGNYDIWGSYRSDAFDIWGQ 120

QY 80 GTTVTVSS 87

DB 121 GIMTVTVSS 128

RESULT 9

PH0954

Ig heavy chain V region (G6+ CLL-HEN) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 16-Aug-1996

A:Accession: PH0954

R:Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.

J. Exp. Med. 175, 983-991, 1992

A:Title: Evidence for somatic selection of natural autoantibodies.

A:Reference number: PH0952; MUID:92202880; PMID:1552291

A:Accession: PH0954

A:Status: nucleic acid sequence not shown

A:Molecule type: DNA

A:Residues: 1-132 <MAR>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-30/Region: framework 1

F:15-98/Domain: immunoglobulin homology <IMM>

F:31-35/Region: complementarity-determining 1

F:36-50/Region: framework 2

F:51-67/Region: complementarity-determining 2

F:68-98/Region: framework 3

F:99-120/Region: complementarity-determining 3

Query Match 75.8%; Score 340.5; DB 2; Length 132;

Best Local Similarity 53.8%; Pred. No. 2.1e-26;

Matches 71; Conservative 12; Mismatches 4; Indels 45; Gaps 3;

QY 1 QIQLVQSGGEVKKPGASVRVSCKASG-----YSTWVRQSPGKGLWLI----- 43

DB 1 QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYALSWVRQAPGQGLEWMGGIPIFGTANY 60

QY 44 -----GKATLTVDKSTSTAYMELSLRSEDVAVYFCAR----- 76

DB 61 AQKFGQGVTTITADKSTSTAYMELSLRSEDVAVYFCARPHASIDDFWISGYPNYYGMD 120

QY 77 -WGQGTITVTVSS 87

DB 121 VWGQGTITVTVSS 132

RESULT 10

PH0955  
IG heavy chain V region (G6+ CLL-AND) - human (fragment)  
C:Species: Homo sapiens (man)  
C>Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 16-Aug-1996  
C:Accession: PH0955  
R:Martin, T.; Duffy, S.F.; Carson, D.A.; Kippes, T.J.  
J. Exp. Med. 175, 983-991, 1992  
A:Title: Evidence for somatic selection of natural autoantibodies.  
A:Reference number: PH0952; MUID:92202880; PMID:1552291  
A:Accession: PH0955  
A>Status: nucleic acid sequence not shown  
A:Molecule type: DNA  
A:Residues: 1-127 <MAR>  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
F:1-30/Region: framework 1  
F:15-98/Domain: immunoglobulin homology <IMM>  
F:31-35/Region: complementarity-determining 1  
F:36-50/Region: framework 2  
F:51-67/Region: complementarity-determining 2  
F:68-98/Region: framework 3  
F:99-115/Region: complementarity-determining 3

Query Match 75.1%; Score 339; DB 2; Length 127;  
Best Local Similarity 55.1%; Pred. No. 2.8e-26;  
Matches 70; Conservative 13; Mismatches 4; Indels 40; Gaps 3;

Qy 1 QIQLVQSGGEVKKPGASVRVSKASG-----YSFTWVRQSPGKGLEWI----- 43  
Db 1 QVQLVQSGAEVKKPGSSVKVSKASGDTFSSVAISWVRQAPGQGLEWMGGIPIFGTANY 60  
Qy 44 -----GKATLTVDKSTSTAYMELSSLRSEDTAVYFCAR-----WGQG 80  
Db 61 AQRFGQGVITADESTSTAYMELSSLRSEDTAVYFCARVGVQVQHYHYTYMDVWGKG 120  
Qy 81 TTVTVSS 87  
Db 121 TTVTVSS 127

RESULT 11  
C33548  
IG heavy chain V-1 region (783) - human  
C:Species: Homo sapiens (man)  
C>Date: 17-Jan-1990 #sequence\_revision 17-Jan-1990 #text\_change 16-Aug-1996  
C:Accession: C33548  
R:Kippes, T.J.; Tomhave, E.; Pratt, L.F.; Duffy, S.; Chen, P.P.; Carson, D.A.  
Proc. Natl. Acad. Sci. U.S.A. 86, 5913-5917, 1989  
A:Title: Developmentally restricted immunoglobulin heavy chain variable region gene expression in the developing mouse.  
A:Reference number: A33548; MUID:89345575; PMID:2503826  
A:Accession: C33548  
A>Status: preliminary; nucleic acid sequence not shown; not compared with conceptual translation  
A:Molecule type: DNA  
A:Residues: 1-133 <KIP>  
A:Experimental source: the sequence was determined from the differentiated gene  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 75.1%; Score 337; DB 2; Length 133;  
Best Local Similarity 52.6%; Pred. No. 4.6e-26;  
Matches 70; Conservative 13; Mismatches 4; Indels 46; Gaps 3;

Qy 1 QIQLVQSGGEVKKPGASVRVSKASG-----YSFTWVRQSPGKGLEWI----- 43  
Db 1 QVQLVQSGAEVKKPGSSVKVSKASGDTFSSVAISWVRQAPGQGLEWMGGIPIFGTANY 60  
Qy 44 -----GKATLTVDKSTSTAYMELSSLRSEDTAVYFCAR----- 76  
Db 61 AQRFGQGVITADESTSTAYMELSSLRSEDTAVYFCARVGVQVQHYHYTYMDVWGKG 120  
Qy 77 --WGQGTITVTVSS 87  
Db 121 TTVTVSS 127

RESULT 12  
S14683  
IG mu chain precursor, membrane-bound (clone 201) - human  
C:Species: Homo sapiens (man)  
C>Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 23-Jul-1999  
C:Accession: S14683; S08047  
R:Friedlander, R.M.; Nussenzweig, M.C.; Leder, P.  
Nucleic Acids Res. 18, 4278, 1990  
A:Title: Complete nucleotide sequence of the membrane form of the human IgM heavy chain  
A:Reference number: S14683; MUID:90332450; PMID:2115996  
A:Accession: S14683  
A:Molecule type: mRNA  
A:Residues: 1-627 <FRI>  
A:Cross-references: EMBL:X17115; NID:933450; PIDN:CAA34971.1; PID:g933451  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: immunoglobulin; membrane protein  
F:1-15/Domain: signal sequence #status predicted <SIG>  
F:16-627/Product: Ig mu chain #status predicted <MAT>  
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 75.1%; Score 337; DB 2; Length 627;  
Best Local Similarity 52.6%; Pred. No. 2.1e-25;  
Matches 70; Conservative 13; Mismatches 4; Indels 46; Gaps 3;

Qy 1 QIQLVQSGGEVKKPGASVRVSKASG-----YSFTWVRQSPGKGLEWI----- 43  
Db 20 QVQLVQSGAEVKKPGSSVKVSKASGDTFSSVAISWVRQAPGQGLEWMGGIPIFGTANY 79  
Qy 44 -----GKATLTVDKSTSTAYMELSSLRSEDTAVYFCAR----- 76  
Db 80 AQRFGQGVITADESTSTAYMELSSLRSEDTAVYFCARVGVQVQHYHYTYMDVWGKG 139  
Qy 77 --WGQGTITVTVSS 87  
Db 140 DVWGQGTITVTVSS 152

RESULT 13  
A24672  
IG heavy chain precursor V region (VMU-3.2) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C>Date: 19-Nov-1988 #sequence\_revision 19-Nov-1988 #text\_change 23-Jul-1999  
C:Accession: A24672  
R:Winter, E.; Radbruch, A.; Krawinkel, U.  
EMBO J. 4, 2861-2867, 1985  
A:Reference number: A91022; MUID:86055722; PMID:2998759  
A:Accession: A24672  
A:Molecule type: DNA  
A:Residues: 1-119 <WIN>  
A:Cross-references: GB:X03088; NID:952378; PIDN:CAA26881.1; PID:g773578  
A:Note: This sequence was determined from the germline gene  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:4-119/Product: Ig heavy chain V region VMU-3.2 #status predicted <MAT>  
F:18-101/Domain: immunoglobulin homology <IMM>

Query Match 74.9%; Score 336.5; DB 2; Length 119;  
Best Local Similarity 60.3%; Pred. No. 4.6e-26;  
Matches 70; Conservative 11; Mismatches 6; Indels 29; Gaps 3;

Qy 1 QIQLVQSGGEVKKPGASVRVSKASGYSFT-----YWRQSPGKGLEWI----- 43  
Db 4 QVQLVQSGPELVKPGASVKISCKASGYAFSSWMNWKQRPKGLEWIGRIYFGDGTNY 63  
Qy 44 -----GKATLTVDKSTSTAYMELSSLRSEDTAVYFCAR-----WGQGTITVTVSS 87  
Db 64 NGKFKGKATLTADKSSSTAYMQLSLTSDSAVYFCARDYVGSYDWGQGTITVTVSS 119

RESULT 14

PH0955  
IG heavy chain V region (G6+ CLL-AND) - human (fragment)  
C:Species: Homo sapiens (man)  
C>Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 16-Aug-1996  
C:Accession: PH0955  
R:Martin, T.; Duffy, S.F.; Carson, D.A.; Kippes, T.J.  
J. Exp. Med. 175, 983-991, 1992  
A:Title: Evidence for somatic selection of natural autoantibodies.  
A:Reference number: PH0952; MUID:92202880; PMID:1552291  
A:Accession: PH0955  
A>Status: nucleic acid sequence not shown  
A:Molecule type: DNA  
A:Residues: 1-127 <MAR>  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
F:1-30/Region: framework 1  
F:15-98/Domain: immunoglobulin homology <IMM>  
F:31-35/Region: complementarity-determining 1  
F:36-50/Region: framework 2  
F:51-67/Region: complementarity-determining 2  
F:68-98/Region: framework 3  
F:99-115/Region: complementarity-determining 3

Query Match 75.5%; Score 339; DB 2; Length 127;  
Best Local Similarity 55.1%; Pred. No. 2.8e-26;  
Matches 70; Conservative 13; Mismatches 4; Indels 40; Gaps 3;

Qy 1 QIQLVQSGGEVKKPGASVRVSKASG-----YSFTWVRQSPGKGLEWI----- 43  
Db 1 QVQLVQSGAEVKKPGSSVKVSKASGDTFSSVAISWVRQAPGQGLEWMGGIPIFGTANY 60  
Qy 44 -----GKATLTVDKSTSTAYMELSSLRSEDTAVYFCAR-----WGQG 80  
Db 61 AQRFGQGVITADESTSTAYMELSSLRSEDTAVYFCARVGVQVQHYHYTYMDVWGKG 120  
Qy 81 TTVTVSS 87  
Db 121 TTVTVSS 127

RESULT 11  
C33548  
IG heavy chain V-1 region (783) - human  
C:Species: Homo sapiens (man)  
C>Date: 17-Jan-1990 #sequence\_revision 17-Jan-1990 #text\_change 16-Aug-1996  
C:Accession: C33548  
R:Kippes, T.J.; Tomhave, E.; Pratt, L.F.; Duffy, S.; Chen, P.P.; Carson, D.A.  
Proc. Natl. Acad. Sci. U.S.A. 86, 5913-5917, 1989  
A:Title: Developmentally restricted immunoglobulin heavy chain variable region gene expression in the developing mouse.  
A:Reference number: A33548; MUID:89345575; PMID:2503826  
A:Accession: C33548  
A>Status: preliminary; nucleic acid sequence not shown; not compared with conceptual translation  
A:Molecule type: DNA  
A:Residues: 1-133 <KIP>  
A:Experimental source: the sequence was determined from the differentiated gene  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 75.1%; Score 337; DB 2; Length 133;  
Best Local Similarity 52.6%; Pred. No. 4.6e-26;  
Matches 70; Conservative 13; Mismatches 4; Indels 46; Gaps 3;

Qy 1 QIQLVQSGGEVKKPGASVRVSKASG-----YSFTWVRQSPGKGLEWI----- 43  
Db 1 QVQLVQSGAEVKKPGSSVKVSKASGDTFSSVAISWVRQAPGQGLEWMGGIPIFGTANY 60  
Qy 44 -----GKATLTVDKSTSTAYMELSSLRSEDTAVYFCAR----- 76  
Db 61 AQRFGQGVITADESTSTAYMELSSLRSEDTAVYFCARVGVQVQHYHYTYMDVWGKG 120  
Qy 77 --WGQGTITVTVSS 87  
Db 121 TTVTVSS 127

RESULT 12  
S14683  
IG mu chain precursor, membrane-bound (clone 201) - human  
C:Species: Homo sapiens (man)  
C>Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 23-Jul-1999  
C:Accession: S14683; S08047  
R:Friedlander, R.M.; Nussenzweig, M.C.; Leder, P.  
Nucleic Acids Res. 18, 4278, 1990  
A:Title: Complete nucleotide sequence of the membrane form of the human IgM heavy chain  
A:Reference number: S14683; MUID:90332450; PMID:2115996  
A:Accession: S14683  
A:Molecule type: mRNA  
A:Residues: 1-627 <FRI>  
A:Cross-references: EMBL:X17115; NID:933450; PIDN:CAA34971.1; PID:g933451  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: immunoglobulin; membrane protein  
F:1-15/Domain: signal sequence #status predicted <SIG>  
F:16-627/Product: Ig mu chain #status predicted <MAT>  
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 75.1%; Score 337; DB 2; Length 627;  
Best Local Similarity 52.6%; Pred. No. 2.1e-25;  
Matches 70; Conservative 13; Mismatches 4; Indels 46; Gaps 3;

Qy 1 QIQLVQSGGEVKKPGASVRVSKASG-----YSFTWVRQSPGKGLEWI----- 43  
Db 20 QVQLVQSGAEVKKPGSSVKVSKASGDTFSSVAISWVRQAPGQGLEWMGGIPIFGTANY 79  
Qy 44 -----GKATLTVDKSTSTAYMELSSLRSEDTAVYFCAR----- 76  
Db 80 AQRFGQGVITADESTSTAYMELSSLRSEDTAVYFCARVGVQVQHYHYTYMDVWGKG 139  
Qy 77 --WGQGTITVTVSS 87  
Db 140 DVWGQGTITVTVSS 152

RESULT 13  
A24672  
IG heavy chain precursor V region (VMU-3.2) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C>Date: 19-Nov-1988 #sequence\_revision 19-Nov-1988 #text\_change 23-Jul-1999  
C:Accession: A24672  
R:Winter, E.; Radbruch, A.; Krawinkel, U.  
EMBO J. 4, 2861-2867, 1985  
A:Reference number: A91022; MUID:86055722; PMID:2998759  
A:Accession: A24672  
A:Molecule type: DNA  
A:Residues: 1-119 <WIN>  
A:Cross-references: GB:X03088; NID:952378; PIDN:CAA26881.1; PID:g773578  
A:Note: This sequence was determined from the germline gene  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:4-119/Product: Ig heavy chain V region VMU-3.2 #status predicted <MAT>  
F:18-101/Domain: immunoglobulin homology <IMM>

Query Match 74.9%; Score 336.5; DB 2; Length 119;  
Best Local Similarity 60.3%; Pred. No. 4.6e-26;  
Matches 70; Conservative 11; Mismatches 6; Indels 29; Gaps 3;

Qy 1 QIQLVQSGGEVKKPGASVRVSKASGYSFT-----YWRQSPGKGLEWI----- 43  
Db 4 QVQLVQSGPELVKPGASVKISCKASGYAFSSWMNWKQRPKGLEWIGRIYFGDGTNY 63  
Qy 44 -----GKATLTVDKSTSTAYMELSSLRSEDTAVYFCAR-----WGQGTITVTVSS 87  
Db 64 NGKFKGKATLTADKSSSTAYMQLSLTSDSAVYFCARDYVGSYDWGQGTITVTVSS 119

RESULT 14

B33548  
Ig heavy chain V-1 region (AND) - human  
C:Species: Homo sapiens (man)  
C>Date: 17-Jan-1990 #sequence\_revision 17-Jan-1990 #text\_change 16-Aug-1996  
C:Accession: B33548  
R:Kippes, T.J.; Tomhave, E.; Pratt, L.F.; Duffy, S.; Chen, P.P.; Carson, D.A.  
Proc. Natl. Acad. Sci. U.S.A. 86, 5913-5917, 1989  
A:Title: Developmentally restricted immunoglobulin heavy chain variable region gene expression  
A:Reference number: A33548; MUID:99345575; PMID:2503826  
A:Accession: B33548  
A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual translation  
A:Molecule type: DNA  
A:Residues: 1-126 <KIP>  
A:Experimental source: the sequence was determined from the differentiated gene  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 74.9%; Score 336.5; DB 2; Length 126;  
Best Local Similarity 55.6%; Pred. No. 4.9e-26;  
Matches 70; Conservative 12; Mismatches 5; Indels 39; Gaps 3;

QY 1 QIQLVQSGGEVKKPGASVRSCKASG-----YSFTVTRQSPGKGLEWI----- 43  
Db 1 QVQLVQSGAEVKKPQSSVKPSCKASGTFSSYALISWRQAPGQGLEWMGGIIIFGTANY 60  
QY 44 -----GKATLTVDKSTAYMELSLRSEDVAVYFCAR-----WGQGT 81  
Db 61 AQKFGQGRVTITADESSTAYMELSLRSEDVAVYCARVIFGVQHYHYMYMDVMVGLGT 120  
QY 82 TTVTVSS 87  
Db 121 TTVTVSS 126

RESULT 15  
S49530  
anti-Sm antibody VH chain (VH1/DK1 or DM1/JH4b) - human  
C:Species: Homo sapiens (man)  
C>Date: 01-Feb-1995 #sequence\_revision 12-May-1995 #text\_change 23-Jul-1999  
C:Accession: S49530  
R:Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.  
submitted to the EMBL Data Library, October 1994  
A:Description: Molecular characterization of natural human anti-Sm autoantibodies.  
A:Reference number: S48797  
A:Accession: S49530  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-135 <MAH>  
A:Cross-references: EMBL:Z46348; NID:G560839; PIDN:CAAB6467.1; PID:G560840  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 74.9%; Score 336.5; DB 2; Length 135;  
Best Local Similarity 60.3%; Pred. No. 5.2e-26;  
Matches 70; Conservative 10; Mismatches 7; Indels 29; Gaps 3;

QY 1 QIQLVQSGGEVKKPGASVRSCKASGYSFT-----WTRQSPGKGLEWI----- 43  
Db 20 QVQLVQSGAEVKKPQASVKPSCKASGYTFGYMHWRQAPGQGLEWMGWINFNSGGTNY 79  
QY 44 -----GKATLTVDKSTAYMELSLRSEDVAVYFCAR-----WGQGTITVTVSS 87  
Db 80 AQKFGQGRVTITADESSTAYMELSLRSDDTAVYICARATGYNYWGQGTITVTVSS 135

Search completed: January 13, 2004, 12:44:41  
Job time : 7.30655 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 13, 2004, 12:19:34 ; Search time 3.79913 Seconds  
(without alignments)  
1076.912 Million cell updates/sec

Title: US-09-990-586-91

Perfect score: 449

Sequence: 1 QIQVQSGGVKKPGASVRV.....DTAVYFCARWGQTTTVSS 87

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	326.5	72.7	139	1 HV07_MOUSE	P01751 mus musculu
2	322.5	71.8	137	1 HV11_MOUSE	P01755 mus musculu
3	320	71.3	117	1 HV12_MOUSE	P01756 mus musculu
4	320	71.3	117	1 HV13_MOUSE	P01757 mus musculu
5	313.5	69.8	118	1 HV51_MOUSE	P06330 mus musculu
6	310.5	69.2	147	1 HV1C_HUMAN	P01744 homo sapien
7	310	68.0	120	1 HV03_MOUSE	P01747 mus musculu
8	309.5	68.9	120	1 HV50_MOUSE	P06329 mus musculu
9	306	68.2	140	1 HV02_MOUSE	P01746 mus musculu
10	302	67.3	117	1 HV1B_HUMAN	P01743 homo sapien
11	302	67.3	138	1 HV48_MOUSE	P03980 mus musculu
12	296	65.9	121	1 HV01_MOUSE	P01745 mus musculu
13	295	65.7	117	1 HV1A_HUMAN	P01742 homo sapien
14	290.5	64.7	124	1 HV1D_HUMAN	P01760 homo sapien
15	289	64.4	117	1 HV1G_HUMAN	P23083 homo sapien
16	286	63.7	136	1 HV15_MOUSE	P01759 mus musculu
17	284	63.3	117	1 HV05_MOUSE	P01749 mus musculu
18	284	63.3	117	1 HV14_MOUSE	P01758 mus musculu
19	283	63.0	117	1 HV06_MOUSE	P01750 mus musculu
20	283	63.0	117	1 HV52_MOUSE	P06327 mus musculu
21	280	62.4	117	1 HV09_MOUSE	P01753 mus musculu
22	278	61.9	117	1 HV04_MOUSE	P01748 mus musculu
23	278	61.9	119	1 HV31_HUMAN	P01770 homo sapien
24	277.5	61.8	114	1 HV3B_HUMAN	P01763 homo sapien
25	277.5	61.8	124	1 HV1E_HUMAN	P01761 homo sapien
26	277	61.7	117	1 HV49_MOUSE	P06328 mus musculu
27	277	61.7	125	1 HV1F_HUMAN	P06326 homo sapien
28	276.5	61.6	114	1 HV00_MOUSE	P01741 mus musculu
29	276	61.5	117	1 HV10_MOUSE	P01754 mus musculu
30	276	61.5	121	1 HV3J_HUMAN	P01771 homo sapien
31	275.5	61.4	122	1 HV3G_HUMAN	P01768 homo sapien
32	271.5	60.5	116	1 HV3T_HUMAN	P01781 homo sapien
33	271.5	60.5	122	1 HV3H_HUMAN	P01769 homo sapien

#### ALIGNMENTS

##### RESULT 1

HV07\_MOUSE STANDARD; PRT; 139 AA.

AC P01751; P01752; 126 1 HV3K\_HUMAN  
 DT 21-JUL-1986 (Rel. 01, Created) 120 1 HV1H\_HUMAN  
 DT 21-JUL-1986 (Rel. 01, Last sequence update) 122 1 HV3A\_HUMAN  
 DT 15-SEP-2003 (Rel. 42, Last annotation update) 119 1 HV38\_MOUSE  
 DE Ig heavy chain V region B1-8/186-2 precursor. 115 1 HV3F\_HUMAN  
 OS Mus musculus (Mouse). 115 1 HV3F\_MOUSE  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; 119 1 HV37\_MOUSE  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 136 1 HV16\_MOUSE  
 OX NCBI\_TaxID=10090; 114 1 HV01\_CANFA  
 RN [1] 114 1 HV41\_MOUSE  
 RP SEQUENCE FROM N.A. 117 1 HV40\_MOUSE  
 RC STRAIN=C57BL/6; 119 1 HV01\_RAT  
 RX MEDLINE=81234548; PubMed=6788376; 122 1 HV21\_MOUSE  
 RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,  
 Baltimore D.;  
 RT "Heavy chain variable region contribution to the NPb family of  
 antibodies: somatic mutation evident in a gamma 2a variable region.";  
 RL Cell 24:625-637(1981).  
 CC -!- MISCELLANEOUS: THE B1-8 MU CHAIN MRNA WAS CLONED FROM A HYBRIDOMA  
 MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL  
 (NPB ANTIBODIES).  
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P01772 homo sapien  
 P0421 homo sapien  
 P01762 homo sapien  
 P01808 mus musculu  
 P01767 homo sapien  
 P01807 mus musculu  
 P01783 mus musculu  
 P01784 canis famil  
 P01811 mus musculu  
 P01810 mus musculu  
 P01805 rattus norv  
 P01790 mus musculu

```

Query Match      72.7%; Score 325.5; DB 1; Length 139;
Best Local Similarity 56.7%; Pred. No. 1.1e-30;
Matches 68; Conservative 12; Mismatches 7; Indels 33; Gaps 3;

QY 1 QIQLVQSGGEVKKPGASVRVSKASGYST-----WVRQSPGKGLWIG----- 44
DB 20 QVQLQPGAEVFKPGASVKLSCKASGYTFTSYLHMWVNRQPGKGLWIGRIDPNSGGTTY 79

QY 1 QIQLVQSGGEVKKPGASVRVSKASGYST-----WVRQSPGKGLWIG----- 44
DB 20 QVQLQPGAEVFKPGASVKLSCKASGYTFTSYLHMWVNRQPGKGLWIGRIDPNSGGTKY 79

QY 45 -----KATLVTKSTAYMELSSLSRSDTAVYFCAR-----WGQTTVTYSS 87
DB 80 NEHFRSKATLTDKPSSTAYMQLSSLTSDSAVYCYARYLGRFYDWGQTTVTYSS 139

RESULT 2
HV11_MOUSE
ID HV11_MOUSE STANDARD; PRT; 137 AA.
AC P01755;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region S43 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.; variable region contribution to the NPb family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -1- MISCELLANEOUS: THE GAMMA-2A CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
CC (NPB ANTIBODIES).
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; J00539; AAA38172.1; -
DR PIR; A02038; G2MS43.
DR HSP; P01810; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR Immunoglobulin V region; Signal.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 137 IG HEAVY CHAIN V REGION S43.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DOMAIN 118 122 D SEGMENT.
FT DOMAIN 123 137 JH2 SEGMENT.
FT DISULFID 41 115 BY SIMILARITY.
FT NON TER 137 137
FT SEQUENCE 137 AA; 15200 MW; ADD5881BF44B8EC9 CRC64;

Query Match      71.8%; Score 322.5; DB 1; Length 137;
Best Local Similarity 56.8%; Pred. No. 3.1e-30;
Matches 67; Conservative 11; Mismatches 9; Indels 31; Gaps 3;

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QY 1 QIQLVQSGGEVKKPGASVRVSKASGYST-----WVRQSPGKGLWIG----- 44
DB 20 QVQLQPGAEVFKPGASVKLSCKASGYTFTSYLHMWVNRQPGKGLWIGRIDPNSGGTTY 79

QY 45 -----KATLVTKSTAYMELSSLSRSDTAVYFCAR-----WGQTTVTYSS 87
DB 80 NEHFRSKATLTDKPSSTAYMQLSSLTSDSAVYCYARYLGRFYDWGQTTVTYSS 139

RESULT 3
HV12_MOUSE
ID HV12_MOUSE STANDARD; PRT; 117 AA.
AC P01756;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region MOPC 104E.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE, AND CARBOHYDRATE-LINKAGE SITE ASN-55.
RX MEDLINE=83075344; PubMed=6816276;
RA Kehry M.R., Fuhrman J.S., Schilling J.W., Rogers J., Sibley C.H.,
RA Hood L.E.; amino acid sequence of a mouse mu chain: homology among
RT heavy chain constant region domains.";
RL Biochemistry 21:5415-5424(1982).
CC -1- MISCELLANEOUS: THE SEQUENCE OF THE LIGHT CHAIN OF THIS IGM MYELOMA
CC PROTEIN HAS ALSO BEEN DETERMINED.
CC -1- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC PIR; A02039; MMS4E.
DR HSP; P01789; IMCP.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR Immunoglobulin V region; Glycoprotein.
FT DOMAIN 1 116 IG-LIKE.
FT DISULFID 22 96 BY SIMILARITY.
FT CARBOHYD 55 55 N-LINKED (GLCNAC. .) (COMPLEX).
FT NON TER 117 117
FT SEQUENCE 117 AA; 12983 MW; 3CF8ACE4BE447E41 CRC64;

Query Match      71.3%; Score 320; DB 1; Length 117;
Best Local Similarity 55.1%; Pred. No. 5.1e-30;
Matches 68; Conservative 12; Mismatches 7; Indels 30; Gaps 3;

QY 1 QIQLVQSGGEVKKPGASVRVSKASGYST-----WVRQSPGKGLWIG----- 43
DB 1 EVQLQQSGPELVKPGASVKMSCKASGYTFTDYMKWKQSHGKSLWIGIDNPNGGTSY 60

QY 44 -----GKATLVTKSTAYMELSSLSRSDTAVYFCAR-----WGQTTVTYSS 87
DB 61 NQKFKGKATLVTKSSSTAYMQLNSLTSDSAVYCYARYLGRFYDWGAGTTVTYSS 117

RESULT 4
HV13_MOUSE
ID HV13_MOUSE STANDARD; PRT; 117 AA.
AC P01757;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region J558.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;

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RN  SEQUENCE.
RP  MEDLINE=80078170; PubMed=6765983;
RX  Schilling J., Clevinger B., Davie J.M., Hood L.;
RA  "Amino acid sequence of homogeneous antibodies to dextran and DNA
RT  rearrangements in heavy chain V-region gene segments.";
RL  Nature 283:35-40(1980).
CC  -1- MISCELLANEOUS: THE SEQUENCES OF 10 HYBRIDOMA PROTEINS THAT ALSO
CC  BIND DEXTRAN DIFFER FROM THAT SHOWN AT 1-7 POSITIONS, MANY OF
CC  WHICH OCCUR IN THE D AND J SEGMENTS.
CC  -1- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
CC  -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR  PIR; A26242; MHMSJ5.
DR  HSSP; P01789; IMCP.
DR  InterPro; IPR007110; Ig-like.
DR  InterPro; IPR003006; Ig_MHC.
DR  InterPro; IPR003596; Ig_V.
DR  Pfam; PF00047; Ig; 1.
DR  SMART; SM00406; IGV; 1.
DR  PROSITE; PS50835; IG LIKE; 1.
KW  Immunoglobulin V region.
FT  DOMAIN 1 116 IG-LIKE.
FT  DISULFID 22 96 BY SIMILARITY.
FT  NON_TER 117 117
SQ  SEQUENCE 117 AA; 13024 MW; 292E2AF4BE447E41 CRC64;

Query Match 71.3%; Score 320; DB 1; Length 117;
Best Local Similarity 58.1%; Pred. No. 5.1e-30; Indels 30; Gaps 3;
Matches 68; Conservative 12; Mismatches 7;

QY 1 QIQLVQSGGEVKKPGASVRVSKASGYSTFT-----WVRQSPGKGLWEI----- 43
DB 1 EVQLQSGPELVKPGASVKMSCKASGYTFDYMKWVKQSHGKSLWIGDINPNNGTSTY 60
QY 44 -----GKATLTVDKSTSTAYNELSLRSEDATVYFCAR-----WQGGTTVTVSS 87
DB 61 NQKFKGKATLTVDKSSSTAYNELSLTSDSAVYCARGYDPPDVMGTGTTVTVSS 117
61 NQKFKGKATLTVDKSSSTAYNELSLTSDSAVYCARGYDPPDVMGTGTTVTVSS 117

RESULT 5
HV51_MOUSE STANDARD; PRT; 118 AA.
AC P06330;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region AC38 205.12.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=84182519; PubMed=6201362;
RA Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;
RT "A V region determinant (idiotope) expressed at high frequency in B
RT lymphocytes is encoded by a large set of antibody structural genes.";
RL EMBO J. 3:517-523(1984).
DR PIR; A02040; MHMS38.
DR HSSP; P01789; IMCP.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 98 V SEGMENT.
FT DOMAIN 99 104 D SEGMENT.
FT DOMAIN 105 118 J SEGMENT.
FT DISULFID 22 96 BY SIMILARITY.
FT NON_TER 118 118
SQ SEQUENCE 118 AA; 12934 MW; 94F7BEE4C762A018 CRC64;

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Query Match 69.8%; Score 313.5; DB 1; Length 118;
Best Local Similarity 56.8%; Pred. No. 2.9e-29; Indels 31; Gaps 3;
Matches 67; Conservative 10; Mismatches 10;

QY 1 QIQLVQSGGEVKKPGASVRVSKASGYSTFT-----WVRQSPGKGLWEI----- 43
DB 1 EVQLQSGPELVKPGASVKMSCKASGYTFDYMKWVKQSHGKSLWIGDINPNNGTSTY 60
QY 44 -----GKATLTVDKSTSTAYNELSLRSEDATVYFCAR-----WQGGTTVTVSS 87
DB 61 NQKFKGKATLTVDKSSSTAYNELSLTSDSAVYCARGYDPPDVMGTGTTVTVSS 118
61 NQKFKGKATLTVDKSSSTAYNELSLTSDSAVYCARGYDPPDVMGTGTTVTVSS 118

RESULT 6
HV1C_HUMAN STANDARD; PRT; 147 AA.
ID P01744;
AC P01744;
DT 21-JUL-1986 (Rel. 01, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-I region ND precursor (Fragments).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83065234; PubMed=6815656;
RA Kenten J.H., Molgaard H.V., Houghton M., Derbyshire R.B., Viney J.,
RA Bell L.O., Gould H.J.;
RT "Cloning and sequence determination of the gene for the human
RT immunoglobulin epsilon chain expressed in a myeloma cell line.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:6661-6665(1982).
RN [2]
RP SEQUENCE OF 20-147.
RA Bennich H.H., Johansson S.G.O., von Bahr-Lindstrom H.;
RL (in) Bach M.K. (eds.);
RL Immediate hypersensitivity: modern concepts and developments, pp.1-36,
RL Marcel Dekker, New York (1978).
CC -1- MISCELLANEOUS: THIS EPSILON CHAIN WAS ISOLATED FROM A MYELOMA
CC PROTEIN.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR HSSP; P01789; IMCP.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Signal; Pyrrolidone carboxylic acid.
FT SIGNAL 1 19
FT CHAIN 20 147 IG HEAVY CHAIN V-I REGION ND.
FT DOMAIN 20 131 IG-LIKE.
FT MOD_RES 20 20 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 41 115
FT CONFLICT 21 21 T -> V (IN REF. 2).
FT CONFLICT 53 54 IH -> HI (IN REF. 2).
FT CONFLICT 67 68 VG -> GV (IN REF. 2).
FT CONFLICT 125 125 MISSING (IN REF. 2).
FT NON_TER 147 147
SQ SEQUENCE 147 AA; 16491 MW; 948F9F72A5366C20 CRC64;

Query Match 69.2%; Score 310.5; DB 1; Length 147;
Best Local Similarity 50.8%; Pred. No. 8.2e-29; Indels 41; Gaps 3;
Matches 65; Conservative 13; Mismatches 9;

QY 1 QIQLVQSGGEVKKPGASVRVSKASGYSTFT-----WVRQSPGKGLWEI----- 43
DB 20 QTQLVQSGAEVRKPGASVRVSKASGYTFIDSYIHWIRQAPGHLEWGVGNPNPNSGGTNY 79
20 QTQLVQSGAEVRKPGASVRVSKASGYTFIDSYIHWIRQAPGHLEWGVGNPNPNSGGTNY 79

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QY 44 -----GKATLVTKSTAYMELSLRSEDVAVFCAR-----WGO 79
DB 80 APRQGRVMTDRDASPTAYMDLRSLRSDSAVFCARSDPFWSDYFNDYSYTLTDWGO 139
QY 80 GTTIVTSS 87
DB 140 GTTIVTSS 147

RESULT 7
HV03_MOUSE
ID HV03_MOUSE STANDARD; PRT; 120 AA.
AC P01747;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region 36-65.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8313846; PubMed=6186498;
RA Siekevitz M., Geffer M.L., Brodeur P., Riblet R.,
RA Marshak-Rothstein A.;
RT "The genetic basis of the strain A mouse.";
RT idiotypic response of the strain A mouse.";
RL Eur. J. Immunol. 12:1023-1032(1982).
CC -1- MISCELLANEOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER
CC DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE AUTHORS
CC CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED TO THE SAME J
CC SEGMENT, JH2.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR HSP; P01789; IMCP.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
KW Immunoglobulin V region; Hybridoma.
FT DOMAIN 1 111 IG-LIKE.
FT NON_TER 120 120
SQ SEQUENCE 120 AA; 13307 MW; PF04E4A167B654AF CRC64;

Query Match 69.0%; Score 310; DB 1; Length 120;
Best Local Similarity 54.2%; Pred. No. 7.5e-29;
Matches 65; Conservative 13; Mismatches 8; Indels 34; Gaps 3;

QY 2 IQLVQSGEVKPKGASVRVSCASGYSTFT-----WVRQSPGKLEWI-----43
DB 1 VQLQSGAEVLVRAGSSVVMKSCASGYTFTSYGNWVKRQPGQGLEWIGVINGVTKYN 60
QY 44 -----GKATLVTKSTAYMELSLRSEDVAVFCAR-----WGO 79
DB 61 EKFKGKTLTVTKSSSTAYMQLSLRSLSDSAVFCARSVYGGSYFYDVGQGTILTSS 120

RESULT 8
HV50_MOUSE
ID HV50_MOUSE STANDARD; PRT; 120 AA.
AC P06329;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUN-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region AC38 15.3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]

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RP SEQUENCE.
RX MEDLINE=84182519; PubMed=6201362;
RA Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;
RA "A V region determinant (idiotope) expressed at high frequency in B
RT lymphocytes is encoded by a large set of antibody structural genes.";
RL EMBO J. 3:517-523(1984).
DR PIR; A02037; MEMS15.
DR HSP; P01810; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 98 V SEGMENT.
FT DOMAIN 99 105 D SEGMENT.
FT DOMAIN 106 120 J SEGMENT.
FT DISULFID 122 96 BY SIMILARITY.
FT NON_TER 120 120
SQ SEQUENCE 120 AA; 13311 MW; 914453F426F09834 CRC64;

Query Match 68.9%; Score 309.5; DB 1; Length 120;
Best Local Similarity 54.3%; Pred. No. 8.5e-29;
Matches 65; Conservative 12; Mismatches 10; Indels 33; Gaps 3;

QY 1 QIQLVQSGEVKPKGASVRVSCASGYSTFT-----WVRQSPGKLEWIG-----44
DB 1 QVQLQGTGLVLPKASVNLSCASGYTFTSYGNWVKRQPGQGLEWIGVINGVTKYN 60
QY 45 -----KATLVTKSTAYMELSLRSEDVAVFCAR-----WGO 79
DB 61 NEKFKKATLVTKSSATYMQSLSTPESDAVYCARWDYEGDRYFDVNGTGTIVTSS 120

RESULT 9
HV02_MOUSE
ID HV02_MOUSE STANDARD; PRT; 140 AA.
AC P01746;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region 93G7 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=A/J;
RX MEDLINE=82152818; PubMed=6801765;
RA Sims J., Rabbitts T.H., Estes P., Slaughter C., Tucker P.W.,
RA Capra J.D.;
RA "Somatic mutation in genes for the variable portion of the
RT immunoglobulin heavy chain.";
RL Science 216:309-311(1982).
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL; J00493; AAA38128.1; --
CC PIR; A94264; HVM5G7.
CC HSP; P01810; 2FBJ.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003006; Ig_MHC.
CC InterPro; IPR003596; Ig_V.
CC Pfam; PF00047; Ig; 1.

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DR SMART; SMO0406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Hybridoma; Signal.
FT SIGNAL 1 19 IG HEAVY CHAIN V REGION 93G7.
FT CHAIN 20 140 IG-LIKE.
FT DOMAIN 20 139
FT NON_TER 140 140
SQ SEQUENCE 140 AA; 15514 MW; 25A4CBBE31D5AC88 CRC64;

Query Match 68.2%; Score 306; DB 1; Length 140;
Best Local Similarity 52.9%; Pred. No. 2.6e-28;
Matches 64; Conservative 14; Mismatches 9; Indels 34; Gaps 3;

QY 1 QIQLVQSGGEVKKPGASVRSCKASGYSTFT-----WVRSQPKGLEW----- 43
DB 20 EVQLQQGAEIVRAGSSVYMSCKASGYSTFTSYGNWYKQRPQGLEWIGVYINPENGVIY 79
QY 44 -----GKATLTVDKSTSTAYMELSLRSRSEDVAVFCAR----- 86
DB 80 NEKFKGKTLTVDKSSSTAYMELSLRSRSEDVAVFCARSHYGGSYDFDYGQGTPLTVS 139
QY 87 S 87
DB 140 S 140

RESULT 10
HVB_HUMAN
ID HVB_HUMAN STANDARD; PRT; 117 AA.
AC P01743;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-I region HG3 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8114028; PubMed=6298778;
RA Rechavi G., Ram D., Glazer L., Zakut R., Glivol D.;
RT "Evolutionary aspects of immunoglobulin heavy chain variable region (VH) gene subgroups."
RL Proc. Natl. Acad. Sci. U.S.A. 80:855-859(1983).
CC 1- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to licenses@isb-sib.ch).
CC
CC EMBL; J00240; AAA52988.1; -.
CC PIR; A02024; HVHUG.
CC HSSP; P01772; 2FE4.
CC GO; GO:0005576; C:extracellular; NAS.
CC GO; GO:0003823; F:antigen binding activity; NAS.
CC GO; GO:0006955; P:immune response; NAS.
CC InterPro; IPR007110; IG-like.
CC InterPro; IPR003006; IG_MHC.
CC InterPro; IPR003596; IG_V.
CC Pfam; PF00047; Ig; 1.
CC SMART; SM00406; IGV; 1.
CC PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT CHAIN 1 19 IG HEAVY CHAIN V REGION HG3.
FT DOMAIN 20 117 IG-LIKE.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12946 MW; 2D3F92FC60CD1FE7 CRC64;

Query Match 67.3%; Score 302; DB 1; Length 117;
Best Local Similarity 62.2%; Pred. No. 6.1e-28;
Matches 61; Conservative 9; Mismatches 6; Indels 22; Gaps 2;

QY 1 QIQLVQSGGEVKKPGASVRSCKASGYSTFT-----WVRSQPKGLEW----- 43
DB 20 QVQLVQSGAEIVKPGASVRSCKASGYSTFTSYNMFVWVRAQPGQGLEWGIINPFGSGTSY 79
QY 44 -----GKATLTVDKSTSTAYMELSLRSRSEDVAVFCAR 76
DB 80 AQKFGGRVTMTDSTSTVYMWELSLRSRSEDVAVYCAR 117

RESULT 11
H48_MOUSE
ID H48_MOUSE STANDARD; PRT; 138 AA.
AC P03960;
DT 23-OCT-1986 (Rel. 02, Created)
DT 23-OCT-1986 (Rel. 02, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region TEPC 1017 precursor.
OS Mus musculus (Mouse).
OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84248078; PubMed=6429663;
RA Gilliam A.C., Shen A., Richards J.E., Blattner F.R., Mushinski J.F.,
RA Tucker P.W.;
RT "Illegitimate recombination generates a class switch from C mu to C
RT delta in an IgD-secreting plasmacytoma."
RL Proc. Natl. Acad. Sci. U.S.A. 81:4164-4168(1984).
DR FIR; A02033; HVMS77.
DR HSSP; P01810; 2FEJ.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT CHAIN 1 20 IG HEAVY CHAIN V REGION TEPC 1017.
FT DOMAIN 21 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DOMAIN 118 127 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 128 138 FRAMEWORK-4.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 138 138
SQ SEQUENCE 138 AA; 15576 MW; 748157E4C6907B8E CRC64;

Query Match 67.3%; Score 302; DB 1; Length 138;
Best Local Similarity 53.8%; Pred. No. 7.3e-28;
Matches 64; Conservative 13; Mismatches 10; Indels 32; Gaps 3;

QY 1 QIQLVQSGGEVKKPGASVRSCKASGYSTFT-----WVRSQPKGLEWIG----- 44
DB 20 QVQLQQGAEIVKPGASVRSCKASGYSTFTSYNMFVWVRAQPGQGLEWIGVYINPFGSGTSY 79
QY 45 -----KATLTVDKSTSTAYMELSLRSRSEDVAVFCAR-----WGQGTITVTVSS 87
DB 80 NEKFKKATLTVDKSSSTAYMELSLRSRSEDVAVYCARSDGYDFVFWVGQGLTVTFA 138

RESULT 12
HVO1_MOUSE
ID HVO1_MOUSE STANDARD; PRT; 121 AA.
AC P01745;

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DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Ig heavy chain V region MPC 11.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=81053741; PubMed=6253904;  
 RA Zakut R., Cohen J., Givol D.;  
 RT "Cloning and sequence of the cDNA corresponding to the variable  
 region of immunoglobulin heavy chain MPC11.";  
 RL Nucleic Acids Res. 8:3591-3601(1980).  
 RN [2]  
 RP REVISIONS.  
 RA Zakut R., Cohen J., Givol D.;  
 RL Nucleic Acids Res. 8:4839-4840(1980).  
 CC -1- MISCELLANEOUS: THIS SEQUENCE WAS TRANSLATED FROM AN MRNA ISOLATED  
 FROM A MYELOMA THAT SECRETES IGG2B.  
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
 DR PIR; A93708; GWS11.  
 DR HSP; P01810; 2FBJ.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IG; 1.  
 DR PROSITE; PS00835; IG LIKE; 1.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IG; 1.  
 DR PROSITE; PS00835; IG LIKE; 1.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IG; 1.  
 FT DOMAIN 1 112 IG-LIKE.  
 FT NON\_TER 121 121  
 SQ SEQUENCE 121 AA; 13135 MW; 227AEF3EC56ED0BF CRC64;  
 Query Match 65.9%; Score 296; DB 1; Length 121;  
 Best Local Similarity 50.4%; Pred. No. 3.1e-27;  
 Matches 61; Conservative 15; Mismatches 11; Indels 34; Gaps 3;  
 QY 1 QIQLVSGGEVKKPGASVRVSCASGYST-----WVROSPGKGLW----- 43  
 DB 1 EAQLQSGAELVPGTGVSKISCAAGYTFYTWIGWVKRPGHLEWIGDIYPGGGFTNY 60  
 QY 44 -----GKATLTVDKSTAYMELSSLRSDTAVYFCAR-----WQGGTTVTVS 86  
 DB 61 NDNLKGKATLTATSTSTAYIQLSSLTSDSAIYHCARGIYNSPYFDSWQGGTTLTVS 120  
 QY 87 S 87  
 DB 121 S 121  
 RESULT 13  
 ID HVIA\_HUMAN STANDARD; PRT; 117 AA.  
 AC P01742;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Ig heavy chain V-I region EU.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=71064024; PubMed=5489771;  
 RA Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,  
 RA Waxdal M.J., Edelman G.M.;  
 RT "The covalent structure of a human gamma G-immunoglobulin. VII. Amino  
 acid sequence of heavy-chain cyanogen bromide fragments H1-H4.";  
 RL Biochemistry 9:3161-3170(1970).  
 RN [2]

RP DISULFIDE BOND.  
 RX MEDLINE=71064027; PubMed=4923144;  
 RA Gall W.E., Edelman G.M.;  
 RT "The covalent structure of a human gamma G-immunoglobulin. X.  
 RT Intrachain disulfide bonds.";  
 RL Biochemistry 9:3188-3196(1970).  
 CC -1- MISCELLANEOUS: THE SEQUENCE OF THE GAMMA-1 C REGION OF THIS  
 MYELOMA PROTEIN HAS ALSO BEEN DETERMINED.  
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
 DR PIR; A90563; GIHUEU.  
 DR HSP; P01772; 2FB4.  
 DR GO; GO:0005576; C:extracellular; NAS.  
 DR GO; GO:0003823; F:antigen binding activity; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IG; 1.  
 DR PROSITE; PS00835; IG LIKE; 1.  
 DR Immunoglobulin V region; Pyrrolidone carboxylic acid.  
 FT DOMAIN 1 112 IG-LIKE.  
 FT MOD\_RES 1 96 PYRROLIDONE CARBOXYLIC ACID.  
 FT DISULFID 22 117  
 FT NON\_TER 117 117  
 SQ SEQUENCE 117 AA; 12472 MW; 99D60ADAE8B52818 CRC64;  
 Query Match 65.7%; Score 295; DB 1; Length 117;  
 Best Local Similarity 55.6%; Pred. No. 3.9e-27;  
 Matches 65; Conservative 13; Mismatches 9; Indels 30; Gaps 4;  
 QY 1 QIQLVSGGEVKKPGASVRVSCASGYST-----WVROSPGKGLW----- 43  
 DB 1 QVQLVQSGAEVKKPGSSVKVSCASGTFPSRAIIWVRQAPGQGLEWMGIVPMFPNNY 60  
 QY 44 -----GKATLTVDKSTAYMELSSLRSDTAVYFCAR-----QQTIVTVSS 87  
 DB 61 AQKFGQGVTTTADSTWYMWELSSLRSDTAVYFCAGGYIYSPPEYNGGLTVSS 117  
 RESULT 14  
 ID HVID\_HUMAN STANDARD; PRT; 124 AA.  
 AC P01760;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Ig heavy chain V-I region WOL.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=82046599; PubMed=7028111;  
 RA Andrews D.W., Capra J.D.;  
 RT "Amino acid sequence of the variable regions of heavy chains from two  
 RT idiotypically cross-reactive human IgM anti-gamma-globulins of the Wa  
 group.";  
 RL Biochemistry 20:5822-5830(1981).  
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA  
 GLOBULIN ACTIVITY.  
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
 DR PIR; A02043; M1HWL.  
 DR HSP; P01772; 2FB4.  
 DR GO; GO:0005576; C:extracellular; NAS.  
 DR GO; GO:0003823; F:antigen binding activity; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IG; 1.

DR PROSITE; PS50835; IG-LIKE; 1.  
 KW Immunoglobulin V region; Pyrrolidone carboxylic acid.  
 FT DOMAIN 1 112 IG-LIKE.  
 FT MOD RES 1 124 PYRROLIDONE CARBOXYLIC ACID.  
 FT NON-TER 124 124  
 SQ SEQUENCE 124 AA; 13684 MW; CB98F365D004EC8B CRC64;

Query Match 64.7%; Score 290.5; DB 1; Length 124;  
 Best Local Similarity 50.8%; Pred.No.1.4e-26;  
 Matches 62; Conservative 14; Mismatches 11; Indels 35; Gaps 3;

QY 1 QIQLVQSGGEVKKPGASVRVSKASGYST-----WVRSQPGKLEWIG-----44  
 DB 1 QVQLMQSGAEVKKPGSSVRVSKTSGTFTVDYKGLWVRQAPGKLEWVGQIPRFNVEVK 60  
 QY 45 -----KATLTVDKSTAYMELSSLRSEDTAVYFCAR-----WCQGTITVTV 85  
 DB 61 NPGSVRVSVSLKPSFQAHMELSSLSFSEDTAVYCYAREYGFDTSDYIIYYWGQGLTVTV 120  
 QY 86 SS 87  
 DB 121 SS 122

## RESULT 15

HV1G\_HUMAN STANDARD; PRT; 117 AA.  
 AC P23083;  
 DT 01-NOV-1991 (Rel. 20, Created)  
 DT 01-NOV-1991 (Rel. 20, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Ig heavy chain V-I region V35 precursor.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=88296408; PubMed=2841108;  
 RA Matsuda F., Lee K.H., Nakai S., Sato T., Kodaira M., Zong S.Q.,  
 RA Ohno H., Fukuhara S., Honjo T.;  
 RT "Dispersed localization of D segments in the human immunoglobulin  
 heavy-chain locus."  
 RL EMBO J. 7:1047-1051(1988).  
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 the European Bioinformatics Institute. There are no restrictions on its  
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 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL; X07448; -; NOT\_ANNOTATED\_CDS.  
 DR PIR; S00476; HVHU35.  
 DR HSSP; P01772; 2PB4.  
 DR GO; GO:0005576; C:extracellular; NAS.  
 DR GO; GO:0003823; F:antigen binding activity; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; IG-LIKE.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_V.  
 DR Pfam; PF00047; IG; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG-LIKE; 1.  
 KW Immunoglobulin V region; Signal.  
 SIGNAL 1 19  
 FT CHAIN 20 117 IG HEAVY CHAIN V-I REGION V35.  
 FT DOMAIN 20 >117 IG-LIKE.  
 FT NON-TER 117 117  
 SQ SEQUENCE 117 AA; 13009 MW; BB61CE63F8CE97BD CRC64;

Query Match 64.4%; Score 289; DB 1; Length 117;  
 Best Local Similarity 60.2%; Pred.No.1.9e-26;  
 Matches 59; Conservative 9; Mismatches 8; Indels 22; Gaps 2;  
 QY 1 QIQLVQSGGEVKKPGASVRVSKASGYST-----WVRSQPGKLEWIG-----43  
 DB 20 QVQLVQSGAEVKKPGASVKVSKASGYTFTGYVMHWVRQAPGQGLEWMGRINPNSGGTNY 79  
 QY 44 -----GKATLTVDKSTAYMELSSLRSEDTAVYFCAR 76  
 DB 80 AQKFGQRTVSTRDTSISTAYMELSLRLSRSDDTVYVCAR 117

Search completed: January 13, 2004, 12:39:26  
 Job time : 3.79913 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 13, 2004, 12:20:44 ; Search time 15.5764 Seconds  
(without alignments)  
1441.318 Million cell updates/sec

Title: US-09-990-586-91  
Perfect score: 449  
Sequence: 1 Q1QLVSGGEVKKPGASVRV.....DRAVFCARWGQTTVTWSS 87

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258032604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

- SPTREMBL\_23:\*
- 1: sp\_archaea:\*
  - 2: sp\_bacteria:\*
  - 3: sp\_fungi:\*
  - 4: sp\_human:\*
  - 5: sp\_invertebrate:\*
  - 6: sp\_mammal:\*
  - 7: sp\_mhc:\*
  - 8: sp\_organelle:\*
  - 9: sp\_phage:\*
  - 10: sp\_plant:\*
  - 11: sp\_rodent:\*
  - 12: sp\_virus:\*
  - 13: sp\_vertebrate:\*
  - 14: sp\_unclassified:\*
  - 15: sp\_rvirus:\*
  - 16: sp\_bacteriap:\*
  - 17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	337	75.1	119	5 Q9GYZ2	Q9GYZ2 schistosoma
2	333	74.2	119	4 Q9UL94	Q9UL94 homo sapien
3	332.5	74.1	124	4 Q9UL92	Q9UL92 homo sapien
4	331	73.7	473	11 Q9DSL4	Q9DSL4 mus musculus
5	330.5	73.6	137	11 Q92XR6	Q92XR6 mus musculus
6	330.5	73.6	159	4 Q9EQS0	Q9EQS0 homo sapien
7	329	73.3	142	11 Q924Q1	Q924Q1 mus musculus
8	328.5	73.2	141	11 Q924Q4	Q924Q4 mus musculus
9	328	73.1	140	11 Q924R2	Q924R2 mus musculus
10	326.5	72.7	143	11 Q924R0	Q924R0 mus musculus
11	326.5	72.7	145	11 Q924Q7	Q924Q7 mus musculus
12	326	72.6	146	11 Q924R8	Q924R8 mus musculus
13	326	72.6	146	11 Q924Q8	Q924Q8 mus musculus
14	325.5	72.5	145	11 Q924Q6	Q924Q6 mus musculus
15	325.5	72.5	145	11 Q924Q9	Q924Q9 mus musculus
16	325.5	72.5	145	11 Q924R1	Q924R1 mus musculus

17	325.5	72.5	145	11 Q924R4	Q924R4 mus musculus
18	325	72.4	146	11 Q924Q3	Q924Q3 mus musculus
19	324.5	72.3	143	11 Q924Q5	Q924Q5 mus musculus
20	323.5	72.0	145	11 Q924R3	Q924R3 mus musculus
21	323	71.9	117	11 Q9QXF0	Q9QXF0 mus musculus
22	323	71.9	125	4 Q9UL95	Q9UL95 homo sapien
23	322.5	71.8	482	11 Q8K172	Q8K172 mus musculus
24	322	71.7	117	11 Q9QX89	Q9QX89 mus musculus
25	321.5	71.6	143	11 Q924R7	Q924R7 mus musculus
26	320	71.3	147	11 Q925S3	Q925S3 mus musculus
27	320	71.3	614	4 Q96GA6	Q96GA6 homo sapien
28	319.5	71.2	143	11 Q924Q0	Q924Q0 mus musculus
29	319.5	71.2	145	11 Q924P7	Q924P7 mus musculus
30	319	71.0	150	4 Q9Y298	Q9Y298 homo sapien
31	319	71.0	481	11 Q91WR1	Q91WR1 mus musculus
32	318.5	70.9	143	11 Q924P9	Q924P9 mus musculus
33	318.5	70.9	463	11 Q991C4	Q991C4 mus musculus
34	318	70.8	142	11 Q924Q2	Q924Q2 mus musculus
35	318	70.8	144	11 Q924P5	Q924P5 mus musculus
36	317.5	70.7	116	4 Q9UL89	Q9UL89 homo sapien
37	316.5	70.5	143	11 Q91VA2	Q91VA2 mus musculus
38	316.5	70.5	500	4 Q9BRV0	Q9BRV0 homo sapien
39	316	70.4	140	11 Q924P8	Q924P8 mus musculus
40	315.5	70.3	143	11 Q924P6	Q924P6 mus musculus
41	314.5	70.0	118	11 Q921C4	Q921C4 mus musculus
42	314	69.9	120	11 Q920E8	Q920E8 mus musculus
43	314	69.9	123	11 Q8VLJ1	Q8VLJ1 mus musculus
44	313.5	69.8	139	11 Q924R5	Q924R5 mus musculus
45	310.5	69.2	613	11 Q8VCX7	Q8VCX7 mus musculus

ALIGNMENTS

RESULT 1

Q9GYZ2 PRELIMINARY; PRT; 119 AA.  
AC Q9GYZ2;  
DT 01-MAR-2001 (TremBLrel. 16, Created)  
DT 01-MAR-2001 (TremBLrel. 16, Last sequence update)  
DT 01-MAR-2003 (TremBLrel. 23, Last annotation update)  
DE Monoclonal anti-idiotypic antibody NP30 heavy chain variable region (fragment).  
OS Schistosoma japonicum (Blood fluke).  
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;  
OC Schistosomatidae; Schistosomatidae; Schistosoma.  
OX NCBI\_TaxID=6182;  
[1]  
RN  
RP SEQUENCE FROM N.A.  
RA Song X.T., Feng Z.Q., Guan X.H.;  
RT "Amplification, cloning and sequence analysis of the heavy chain variable region gene of monoclonal anti-idiotypic antibody NP30 of Schistosoma japonicum";  
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF282622; AAG01452.1; --  
DR HSSP; F01772; 2FB4.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR Pfam; PF00047; Ig\_1.  
DR SMART; SM00406; Igv; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
FT NON\_TER 1  
FT NON\_TER 119  
SQ SEQUENCE 119 AA; 13567 MW; BA993873FD5FA6AB CRC64;

Query Match 75.1%; Score 337; DB 5; Length 119;  
Best Local Similarity 58.8%; Pred. No. 1.3e-30;  
Matches 70; Conservative 10; Mismatches 7; Indels 32; Gaps 3;  
QY 1 Q1QLVSGGEVKKPGASVRVSCKASGYFT-----WYQSPKGLGWIG----- 44  
DB 1 QVQLVESGAERVKPGASVRVSCKASGYFTTGTGYMNVVRQAPGHGLEWIGYNPSRGYTN 60

```
QY 45 -----KATLTVDKSTAYMELSLRSEDATVFCAR-----WGQTTVTSS 87
Db 61 NQFKDQVMTTKSPSTAYMDLRSADSASVYCYARYDDHYCLDYGQTTVTSS 119

RESULT 2
Q9UL94
ID Q9UL94 PRELIMINARY; PRT; 119 AA.
AC Q9UL94
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98271139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.,
RA "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus."
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035020; AAD56256.1; -.
DR HSP; P01810; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG_LIKE; 1.
FT NON TER 1
FT NON TER 119
FT NON TER 119
SQ SEQUENCE 119 AA; 13205 MW; 13E64F5345P4A16E CRC64;

Query Match 74.2%; Score 333; DB 4; Length 119;
Best Local Similarity 58.0%; Pred. No. 3.8e-30;
Matches 69; Conservative 11; Mismatches 7; Indels 32; Gaps 3;

QY 1 QIQLVQSGGKPKGASVRYSCASGYST-----WVQSPGKGLWMI-----43
Db 1 EVQLVESGAEVKPKGASVKVKSCASGYTFGYMHWVRQAPGQGLEWMGINSWTNY 60

QY 44 -----GKATLTVDKSTAYMELSLRSEDATVFCAR-----WGQTTVTSS 87
Db 61 AQKFGKVTMTKDTSTAYMELSLRSDATVYFCAR-----WGQTTVTSS 119

RESULT 3
Q9UL92
ID Q9UL92 PRELIMINARY; PRT; 124 AA.
AC Q9UL92
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98271139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.,
RA "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus."
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035020; AAD56256.1; -.
DR HSP; P01810; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG_LIKE; 1.
FT NON TER 1
FT NON TER 119
FT NON TER 119
SQ SEQUENCE 119 AA; 13205 MW; 13E64F5345P4A16E CRC64;

Query Match 74.2%; Score 333; DB 4; Length 119;
Best Local Similarity 58.0%; Pred. No. 3.8e-30;
Matches 69; Conservative 11; Mismatches 7; Indels 32; Gaps 3;

QY 1 QIQLVQSGGKPKGASVRYSCASGYST-----WVQSPGKGLWMI-----43
Db 1 EVQLVESGAEVKPKGASVKVKSCASGYTFGYMHWVRQAPGQGLEWMGINSWTNY 60

QY 44 -----GKATLTVDKSTAYMELSLRSEDATVFCAR-----WGQTTVTSS 87
Db 61 AQKFGKVTMTKDTSTAYMELSLRSDATVYFCAR-----WGQTTVTSS 119

RESULT 3
Q9UL92
ID Q9UL92 PRELIMINARY; PRT; 124 AA.
AC Q9UL92
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98271139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.,
RA "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus."
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035020; AAD56256.1; -.
DR HSP; P01810; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG_LIKE; 1.
FT NON TER 1
FT NON TER 119
FT NON TER 119
SQ SEQUENCE 119 AA; 13205 MW; 13E64F5345P4A16E CRC64;

Query Match 74.2%; Score 333; DB 4; Length 124;
Best Local Similarity 55.6%; Pred. No. 4.6e-30;
Matches 69; Conservative 12; Mismatches 6; Indels 37; Gaps 3;

QY 1 QIQLVQSGGKPKGASVRYSCASGYST-----WVQSPGKGLWMI-----43
Db 1 EVQLVESGAEVKPKGASVKVKSCASGYTFGYMHWVRQAPGQGLEWMGINSWTNY 60

QY 44 -----GKATLTVDKSTAYMELSLRSEDATVFCAR-----WGQTTV 83
Db 61 AQKFGKVTMTKDTSTAYMELSLRSDATVYFCAR-----WGQTTV 120

RESULT 4
Q9DL84
ID Q9DL84 PRELIMINARY; PRT; 473 AA.
AC Q9DL84
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE 181006009Rik protein.
DE IGH-1 OR 181006009RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=Pancreas;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Saito T., Okazaki Y., Gojohori T., Sono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tonita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boilelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Saeki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Hayashizaki Y.,
RA Watanabe-Borja A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
DR EMBL; AK007918; BAB25349.1; -.
DR HSP; P01842; 7FAB.
DR MGD; MGI:96443; Igh-1.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 4.
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DR SMART, SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG MHC; 1.
SQ SEQUENCE 473 AA; 5:699 MW; 9DED57A514475PBB CRC64;

Query Match
Best Local Similarity 73.7%; Score 331; DB 11; Length 473;
Matches 69; Conservative 11; Mismatches 7; Indels 32; Gaps 3;

Qy 1 QIQLVSGGGEVKKPGASVVRVSKASGYSTFT-----WVRSQPGKGLWIG----- 43
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 20 QVQLVSGAEVKKPGASVKISCKASGYTFDYINWVKRPGQGLEWIKIGPGSGSTVY 79
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 44 -----GKATLTVDKSTSTAYMELSSLRSEDTAVYFCAR-----WGQGTITVTVSS 87
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 80 NEXFKGKATLTADKSSSTAYMQLSSLTSDSAVYFCARSDYDWFAYWGQGTITVTVSA 138
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 5
Q924R6 PRELIMINARY; PRT; 137 AA.
ID Q924R6 PRELIMINARY; PRT; 137 AA.
AC Q924R6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Vhl86 2-D-J-C mu protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RL Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RE Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB067783; BAB63268.1; -
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
FT NON_TER 1
FT NON_TER 137
SQ SEQUENCE 137 AA; 15171 MW; 5C38D966DC6A4124 CRC64;

Query Match
Best Local Similarity 60.7%; Score 330.5; DB 11; Length 137;
Matches 66; Conservative 12; Mismatches 7; Indels 25; Gaps 3;

Qy 1 QIQLVSGGGEVKKPGASVVRVSKASGYSTFT-----WVRSQPGKGLWIG----- 44
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 QVQLVSGAEVKKPGASVKLSCKASGYTFSTYVWVWVKRPGQGLEWIKRIPDPSGGTKY 60
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 45 -----KATLTVDKSTSTAYMELSSLRSEDTAVYFCAR-----WGQGTITVTVSS 87
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 NEXFKGKATLTVDKPSSTAYMQLSSLTSDSAVYFCARWDYWGQGTITVTVSS 112
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 6
Q96QSO PRELIMINARY; PRT; 159 AA.
ID Q96QSO PRELIMINARY; PRT; 159 AA.
AC Q96QSO;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Putative matrix cell adhesion molecule-3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```

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OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Tilson M.D.;
RT "Homo sapiens putative microfibrillar protein with Ig-like domain 3
RT mRNA (Matrix Cell Adhesion Molecule-3, Mat-CAM 3).";
RE Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY039025; AAK82649.1; -
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
DR PROSITE; PS50835; IG LIKE; 1.
SQ SEQUENCE 159 AA; 17497 MW; 5D29537E881FAF02 CRC64;

Query Match
Best Local Similarity 73.6%; Score 330.5; DB 4; Length 159;
Matches 70; Conservative 11; Mismatches 6; Indels 43; Gaps 3;

Qy 1 QIQLVSGGGEVKKPGASVVRVSKASGYSTFT-----WVRSQPGKGLWIG----- 43
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 20 QVQLVSGAEVKKPGASVKYKSKASGYTFSTYVWVWVKRPGQGLEWIKRIPDPSGGARY 79
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 44 -----GKATLTVDKSTSTAYMELSSLRSEDTAVYFCAR-----WGQGTITVTVSS 77
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 80 SQKFGRLTWTRDTSTSTVYMDLSSLRSDTAVYFCAREMEITFGGAVSKGFFYYGMDVW 139
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 78 GQGTITVTVSS 87
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 140 GQGTITVTVSS 149
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 7
Q924Q1 PRELIMINARY; PRT; 142 AA.
ID Q924Q1 PRELIMINARY; PRT; 142 AA.
AC Q924Q1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE V23-D-J-C mu protein (Fragment).
DE V23-D-J-C MU.
GN Mus musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RL Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RE Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB069913; BAB63929.1; -
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
DR PROSITE; PS50835; IG LIKE; 1.
FT NON_TER 1
FT NON_TER 142
SQ SEQUENCE 142 AA; 15622 MW; 24A265CE4EA4318B CRC64;

Query Match
Best Local Similarity 73.3%; Score 329; DB 11; Length 142;
Matches 69; Conservative 12; Mismatches 6; Indels 30; Gaps 3;

Qy 1 QIQLVSGGGEVKKPGASVVRVSKASGYSTFT-----WVRSQPGKGLWIG----- 44
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 QVQLVSGAEVKKPGASVKLSCKASGYTFSTYVWVWVKRPGQGLEWIKRIPDPSGGTNY 60
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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QY 45 -----KATLTVDKSTSTAYMELSSRLSSEDTAVYFCAR-----WGQTTVTIVSS 87
DB 61 NEKFKSKATLTVDKSSSTAYMQLSSLTSDSAVYICARWEADYWGQTSVTIVSS 117

RESULT 8
Q924Q4 PRELIMINARY; PRT; 141 AA.
AC Q924Q4;
DT 01-DEC-2001 (T-REMBLrel. 19, Created)
DT 01-DEC-2001 (T-REMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (T-REMBLrel. 23, Last annotation update)
DE VH186.2-D-J-C mu protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB067796; BAB63281.1;
DR InterPro; IPR007110; Ig_Like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 141
SQ SEQUENCE 141 AA; 15561 MW; DDD80482D66B76A0 CRC64;

Query Match 73.2%; Score 328.5; DB 11; Length 141;
Best Local Similarity 58.6%; Pred. No. 1.5e-29;
Matches 68; Conservative 12; Mismatches 7; Indels 29; Gaps 3;

QY 1 QIQLVSGGEVKKPGASRVSCASGYST-----WVROSPGKLEWIG----- 44
DB 1 QVQLQQPQAGELVPGASVKLSCKASGYTFTSYMHWVKQRPGRGLEWIGRIDPNSGGTKY 60

QY 45 -----KATLTVDKSTSTAYMELSSRLSSEDTAVYFCAR-----WGQTTVTIVSS 87
DB 61 NEKFKSKATLTVDKPSSTAYMQLSSLTSDSAVYICARDYGRTFWGQTTIVTSS 116

RESULT 9
Q924R2 PRELIMINARY; PRT; 140 AA.
AC Q924R2;
DT 01-DEC-2001 (T-REMBLrel. 19, Created)
DT 01-DEC-2001 (T-REMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (T-REMBLrel. 23, Last annotation update)
DE VH186.2-D-J-C mu protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB067798; BAB63273.1;
DR InterPro; IPR007110; Ig_Like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.

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DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 140
SQ SEQUENCE 140 AA; 15361 MW; 60739B790FC6AF24 CRC64;

Query Match 73.1%; Score 328; DB 11; Length 140;
Best Local Similarity 59.1%; Pred. No. 1.7e-29;
Matches 68; Conservative 12; Mismatches 7; Indels 28; Gaps 3;

QY 1 QIQLVSGGEVKKPGASRVSCASGYST-----WVROSPGKLEWIG----- 44
DB 1 QVQLQQPQAGELVPGASVKLSCKASGYTFTSYMHWVKQRPGRGLEWIGRIDPNSGGTKY 60

QY 45 -----KATLTVDKSTSTAYMELSSRLSSEDTAVYFCAR-----WGQTTVTIVSS 87
DB 61 NEKFKSKATLTVDKPSSTAYMQLSSLTSDSAVYICARYAGDYWGQTSVTIVSS 115

RESULT 10
Q924R0 PRELIMINARY; PRT; 143 AA.
AC Q924R0;
DT 01-DEC-2001 (T-REMBLrel. 19, Created)
DT 01-DEC-2001 (T-REMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (T-REMBLrel. 23, Last annotation update)
DE VH186.2-D-J-C mu protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB067790; BAB63275.1;
DR InterPro; IPR007110; Ig_Like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 143
SQ SEQUENCE 143 AA; 15868 MW; 139B2E966B81E07F CRC64;

Query Match 72.7%; Score 326.5; DB 11; Length 143;
Best Local Similarity 57.6%; Pred. No. 2.6e-29;
Matches 68; Conservative 12; Mismatches 7; Indels 31; Gaps 3;

QY 1 QIQLVSGGEVKKPGASRVSCASGYST-----WVROSPGKLEWIG----- 44
DB 1 QVQLQQPQAGELVPGASVKLSCKASGYTFTSYMHWVKQRPGRGLEWIGRIDPNSGGTKY 60

QY 45 -----KATLTVDKSTSTAYMELSSRLSSEDTAVYFCAR-----WGQTTVTIVSS 87
DB 61 NEKFKSKATLTVDKPSSTAYMQLSSLTSDSAVYICARWDEYAMDYWGQTSVTIVSS 118

RESULT 11
Q924Q7 PRELIMINARY; PRT; 145 AA.
AC Q924Q7;
DT 01-DEC-2001 (T-REMBLrel. 19, Created)
DT 01-DEC-2001 (T-REMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (T-REMBLrel. 23, Last annotation update)
DE VH186.2-D-J-C mu protein (Fragment).
OS Mus musculus (Mouse).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RC SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6;  
 RA Kozono Y., Kozono H., Azuma T.;  
 RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals  
 RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-  
 RT Hydroxy-3-Nitrophenyl)Acetyl (NP).";  
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB067793; BAB63278.1; -  
 DR InterPro; IPR007110; IG-LIKE; 1.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR Pfam; PF00047; IG; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 FT NON\_TER 145 145  
 FT NON\_TER 145 145  
 SQ SEQUENCE 145 AA; 16141 MW; 55A59A7908B2CD6A CRC64;

Query Match 72.7%; Score 326.5; DB 11; Length 145;  
 Best Local Similarity 56.7%; Pred. No. 2.7e-29;  
 Matches 68; Conservative 12; Mismatches 7; Indels 33; Gaps 3;  
 QY 1 QIQLVQSGGEVKKPGASVRVSKASGYSTFT-----WVRQSPGKGLWIG----- 44  
 DB 1 QVQLQPGAEIVKPGASVKLSCKASGYFTSYNMHWYKQRPGRGLEWIGRIDPNSGGTKY 60  
 QY 45 -----KATLTVDKSTSTAYMELSLRSEDYAVYFCAR-----WGQGTITVVS 86  
 DB 61 NEKPKSKATLTVDKPSSTAYMQLSLTSEDSAVYVCARTFTTIVVAPFDYWGQGTITLVS 120

RESULT 12  
 Q924R8 PRELIMINARY; PRT; 146 AA.  
 AC Q924R8;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DE 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE VH186.2-D-J-C mu protein (Fragment).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RC SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6;  
 RA Kozono Y., Kozono H., Azuma T.;  
 RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals  
 RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-  
 RT Hydroxy-3-Nitrophenyl)Acetyl (NP).";  
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB067781; BAB63266.1; -  
 DR InterPro; IPR007110; IG-LIKE.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_V.  
 DR Pfam; PF00047; IGV; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 FT NON\_TER 146 146  
 FT NON\_TER 146 146  
 SQ SEQUENCE 146 AA; 16216 MW; 92460F1FDF1B7538 CRC64;

Query Match 72.6%; Score 326; DB 11; Length 145;  
 Best Local Similarity 56.2%; Pred. No. 3.1e-29;  
 Matches 68; Conservative 12; Mismatches 7; Indels 34; Gaps 3;  
 QY 1 QIQLVQSGGEVKKPGASVRVSKASGYSTFT-----WVRQSPGKGLWIG----- 44  
 DB 1 QVQLQPGAEIVKPGASVKLSCKASGYFTSYNMHWYKQRPGRGLEWIGRIDPNSGGTKY 60

QY 45 -----KATLTVDKSTSTAYMELSLRSEDYAVYFCAR-----WGQGTITVVS 86  
 DB 61 NEKPKSKATLTVDKPSSTAYMQLSLTSEDSAVYVCARTFTTIVVAPFDYWGQGTITLVS 120  
 QY 87 S 87  
 DB 121 S 121  
 RESULT 13  
 Q924Q8 PRELIMINARY; PRT; 146 AA.  
 AC Q924Q8;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DE 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE VH186.2-D-J-C mu protein (Fragment).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RC SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6;  
 RA Kozono Y., Kozono H., Azuma T.;  
 RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals  
 RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-  
 RT Hydroxy-3-Nitrophenyl)Acetyl (NP).";  
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB067792; BAB63277.1; -  
 DR InterPro; IPR007110; IG-LIKE.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_V.  
 DR Pfam; PF00047; IGV; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 FT NON\_TER 146 146  
 FT NON\_TER 146 146  
 SQ SEQUENCE 146 AA; 16023 MW; 4B04959991D49159 CRC64;

Query Match 72.6%; Score 326; DB 11; Length 146;  
 Best Local Similarity 56.2%; Pred. No. 3.1e-29;  
 Matches 68; Conservative 12; Mismatches 7; Indels 34; Gaps 3;  
 QY 1 QIQLVQSGGEVKKPGASVRVSKASGYSTFT-----WVRQSPGKGLWIG----- 44  
 DB 1 QVQLQPGAEIVKPGASVKLSCKASGYFTSYNMHWYKQRPGRGLEWIGRIDPNSGGTKY 60  
 QY 45 -----KATLTVDKSTSTAYMELSLRSEDYAVYFCAR-----WGQGTITVVS 86  
 DB 61 NEKPKSKATLTVDKPSSTAYMQLSLTSEDSAVYVCARTFTTIVVAPFDYWGQGTITLVS 120  
 QY 87 S 87  
 DB 121 S 121  
 RESULT 14  
 Q924Q6 PRELIMINARY; PRT; 145 AA.  
 AC Q924Q6;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DE 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE VH186.2-D-J-C mu protein (Fragment).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RC SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6;

Search completed: January 13, 2004, 12:43:07  
Job time : 16.5764 secs

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RA Kozono Y., Kozono H., Azuma T.;  
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals  
RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-  
RT Hydroxy-3-Nitrophenyl)Acetyl (NP).";  
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB067794; BAB63279.1; -  
DR InterPro; IPR007110; IG-Like.  
DR InterPro; IPR003006; IG_MHC.  
DR InterPro; IPR003596; IG_V.  
DR Pfam; PF00047; IG_1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PSS0835; IG_LIKE; 1.  
FT NON_TER 1  
FT NON_TER 145 145  
SQ SEQUENCE 145 AA; 16011 MW; 9BC0846D40DF97EA CRC64;  
  
Query Match 72.5%; Score 325.5; DB 11; Length 145;  
Best Local Similarity 56.7%; Pred. No. 3.5e-29;  
Matches 68; Conservative 12; Mismatches 7; Indels 33; Gaps 3;  
  
QY 1 QIQLVQSGGEVKKPGASVRVSCASGYFT-----WVRQSPGKGLWIG----- 44  
Db 1 QVQLQPGAEVLKPGASVKLSCKASGYFTSYMHVWVKQRPGRGLEWIGRIDPNSGGTKY 60  
QY 45 -----KATLTVDKSTSTAYMELSLRSDDTAVYFCAR-----WGQGTITVTVSS 87  
Db 61 NEKFVKATLTVDKPSSTAYMQLSLTSDSAVYCARSTLSHYIYANDYWGQGTITVTVSS 120  
  
RESULT 15  
Q924Q9 PRELIMINARY; PRT; 145 AA.  
AC Q924Q9;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE VH186.2-D-J-C mu protein (Fragment).  
OS Mus musculus (Mouse)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6;  
RA Kozono Y., Kozono H., Azuma T.;  
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals  
RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-  
RT Hydroxy-3-Nitrophenyl)Acetyl (NP).";  
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB067791; BAB63276.1; -  
DR InterPro; IPR007110; IG-Like.  
DR InterPro; IPR003006; IG_MHC.  
DR InterPro; IPR003596; IG_V.  
DR Pfam; PF00047; IG_1.  
DR SMART; SMC0406; IGV; 1.  
DR PROSITE; PSS0835; IG_LIKE; 1.  
FT NON_TER 1  
FT NON_TER 145 145  
SQ SEQUENCE 145 AA; 16001 MW; 0F409EB09FA333D2 CRC64;  
  
Query Match 72.5%; Score 325.5; DB 11; Length 145;  
Best Local Similarity 56.7%; Pred. No. 3.5e-29;  
Matches 68; Conservative 12; Mismatches 7; Indels 33; Gaps 3;  
  
QY 1 QIQLVQSGGEVKKPGASVRVSCASGYFT-----WVRQSPGKGLWIG----- 44  
Db 1 QVQLQPGAEVLKPGASVKLSCKASGYFTSYMHVWVKQRPGRGLEWIGRIDPNSGGTKY 60  
QY 45 -----KATLTVDKSTSTAYMELSLRSDDTAVYFCAR-----WGQGTITVTVSS 87  
Db 61 NEKFVKATLTVDKPSSTAYMQLSLTSDSAVYCARSLITTYIYANDYWGQGTITVTVSS 120
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

PR 30-JUN-1994; 94CU-0000080.  
XX (IMMU-) CENT IMMUNOLOGIA MOLECULAR.  
PA Rodriguez RP, Valladares JL, Mateo De Acosta Del Rio CM;  
XX WPI; 1996-130770/14.  
XX  
XX Identifying interspecies differences in amino acid sequence of Ig  
XX T-cell epitopes - by sequence comparison, also humanised antibodies  
XX contg. altered T-cell epitopes, retaining antigen specificity but  
XX not immunogenicity, esp. for tumour treatment  
XX  
XX Claim 14; Fig 2; 33pp; English.  
XX  
XX The sequence represents residues from a human immunoglobulin with  
XX homology to the heavy chain variable region from monoclonal antibody  
XX IOR-R3 (AAR2990), specific for epidermal growth factor receptor,  
XX produced by a mouse hybridoma. The sequence is partial, and  
XX complementarity determining regions are omitted. The sequence is  
XX isolated by comparison of human and mouse immunoglobulins and  
XX analysis for T-lymphocyte antigenic sequences using a computer  
XX algorithm. Residues not within a complementarity determining region,  
XX canonical structure or Vennier zone may be modified to reduce  
XX immunogenicity in humans (e.g. in sequence AAR2992). This method,  
XX which involves the introduction of only a few point mutations into  
XX T-cell epitope coding regions, is generally applicable in humanisation  
XX of mouse antibodies. The resulting humanised antibodies may be used  
XX e.g. as antitumour agents. They retain the antigen recognition of the  
XX original antibody, but are not immunogenic in humans.  
XX (Updated on 25-MAR-2003 to correct PI field.)  
XX  
XX Sequence 87 AA;  
SQ  
Query Match 86.0%; Score 386; DB 17; Length 87;  
Best Local Similarity 81.6%; Pred. No. 3.9e-29;  
Matches 71; Conservative 9; Mismatches 7; Indels 0; Gaps 0;  
QY 1 QIQLVQSGGVEVKPGASVRSCKASGYFTNWVRSQPGKLEWIGKATLTVDKSTSTAYME 60  
Db 1 QVQLVQSGAEVKPGASVRSCKASGYFTNWVRSQPGKLEWIGKATLTVDKSTSTAYME 60  
QY 61 LSSLRSEDYAVYFCARWGQGTITVSS 87  
Db 61 LSSLRSEDYAVYFCARWGQGTITVSS 87  
RESULT 2  
ABG74721  
ID ABG74721 standard; Protein; 87 AA.  
XX  
XX ABG74721;  
AC  
XX  
XX 10-MAY-2003 (first entry)  
DT  
XX  
XX Murine humanised Mu007-associated protein DP-5.  
DE  
XX  
XX Murine, light chain; variable region; antibody; Crohn's disease;  
XX human interleukin (IL)-1beta; antirheumatic; antiarthritic; humanised;  
XX antiinflammatory; osteopathic; antiallergic; cerebroprotective;  
XX antiasthmatic; immunosuppressive; antibacterial; vaccine; Mu007;  
XX rheumatoid arthritis; osteoarthritis; cartilage destruction; asthma;  
XX allergy; septic shock; endotoxemia; stroke; asthma;  
XX graft versus host disease; inflammatory bowel disease; DP-5.  
XX  
XX Unidentified.  
OS  
XX  
XX Key Location/Qualifiers  
XX Region 26..30  
XX FT /note= "Amino acid involved in tertiary structure"  
XX PN WO2003010282-A2.  
XX  
XX 06-FEB-2003.  
PD  
XX  
XX 18-JUL-2002; 2002WO-US21281.  
XX  
XX

PR 26-JUL-2001; 2001US-307973P.  
XX 14-AUG-2001; 2001US-312278P.  
PA (ELIL ) LILLY & CO ELI.  
XX  
XX Bright SW, Jia AY, Kuhstoss SA, Manetta JV, Tsurushita N;  
XX Vasquez MJ;  
XX WPI; 2003-248068/24.  
XX  
XX New IL-1beta antibodies, useful for treating allergy, septic or  
XX endotoxic shock, septicemia, stroke, asthma, graft versus host disease,  
XX Crohn's disease, or inflammatory bowel disease -  
XX  
XX Disclosure; Fig 2; 98pp; English.  
XX  
XX This invention describes a novel antibody that specifically binds mature  
XX human interleukin (IL)-1beta, and binds the same epitope on mature human  
XX IL-1beta as mouse monoclonal antibody Mu007 or humanized antibody Hu007.  
XX The antibody of the invention have antirheumatic, antiarthritic,  
XX antiinflammatory, osteopathic, antiallergic, cerebroprotective,  
XX antiasthmatic, immunosuppressive and antibacterial activity and can be  
XX used in a vaccine. The antibody is useful for manufacturing a medicament  
XX for treating rheumatoid arthritis or osteoarthritis, or for inhibiting  
XX cartilage destruction in a subject. The antibody is also useful for  
XX treating allergy, septic or endotoxic shock, septicemia, stroke, asthma,  
XX graft versus host disease, Crohn's disease, or inflammatory bowel  
XX disease. This sequence represents a protein associated with the  
XX humanised murine Mu007 antibody described in the disclosure of the  
XX invention.  
XX  
XX Sequence 87 AA;  
SQ  
Query Match 84.6%; Score 380; DB 24; Length 87;  
Best Local Similarity 80.5%; Pred. No. 1.4e-28;  
Matches 70; Conservative 8; Mismatches 9; Indels 0; Gaps 0;  
QY 1 QIQLVQSGGVEVKPGASVRSCKASGYFTNWVRSQPGKLEWIGKATLTVDKSTSTAYME 60  
Db 1 QVQLVQSGAEVKPGASVRSCKVSGYFTLTWVRQAPGKLEWIGKATLTVDKSTSTAYME 60  
QY 61 LSSLRSEDYAVYFCARWGQGTITVSS 87  
Db 61 LSSLRSEDYAVYFCARWGQGTITVSS 87  
RESULT 3  
AAR93003  
ID AAR93003 standard; Protein; 87 AA.  
XX  
XX AAR93003;  
AC  
XX  
XX 25-MAR-2003 (updated)  
DT 18-MAY-1996 (first entry)  
XX  
XX Homologous sequences to antibody IOR-CEA-1 variable region heavy chain.  
DE  
XX  
XX IOR-CEA-1; monoclonal antibody; human; mouse; heavy chain; homology;  
XX variable region; framework; cloning; computer; algorithm;  
XX immunogenicity; site-directed mutagenesis; T-lymphocyte epitope;  
XX tertiary structure; point mutation; antibody engineering;  
XX protein engineering; humanised antibody; antitumour; cancer; therapy.  
XX  
XX Homo sapiens.  
OS  
XX  
XX Key Location/Qualifiers  
XX Region 26..30  
XX FT /note= "Amino acid involved in tertiary structure"  
XX PN 50  
XX FT /note= "Amino acid involved in tertiary structure"  
XX PD 76  
XX FT /note= "Amino acid involved in tertiary structure"  
XX

FN EP699755-A2.  
 XX 06-MAR-1996.  
 XX 27-JUN-1995; 95EP-0201752.  
 XX 30-JUN-1994; 94CU-0000080.  
 XX (IMMU-) CENT IMMUNOLOGIA MOLECULAR.  
 XX Rodriguez RP, Valladares JL, Mateo De Acosta Del Rio CM;  
 XX WPI; 1996-130770/14.  
 XX  
 XX Identifying interspecies differences in amino acid sequence of Ig  
 XX T-cell epitopes - by sequence comparison, also humanised antibodies  
 XX contg. altered T-cell epitopes, retaining antigen specificity but  
 XX not immunogenicity, esp. for tumour treatment  
 XX  
 XX Claim 22; Fig 9; 33pp; English.  
 XX  
 XX The sequence represents residues from a human immunoglobulin with  
 XX homology to the heavy chain variable region from mouse monoclonal  
 XX antibody IOR-CEA-1 (AA93002). The sequence is partial, and  
 XX complementarity determining regions are omitted. The sequence is  
 XX isolated by comparison of human and mouse immunoglobulins and  
 XX analysis for T-lymphocyte antigenic sequences using a computer  
 XX algorithm. Residues not within a complementarity determining region,  
 XX canonical structure or Verner zone may be modified to reduce  
 XX immunogenicity in humans (e.g. in sequence AA93004). This method,  
 XX which involves the introduction of only a few point mutations into  
 XX T-cell epitope coding regions, is generally applicable in humanisation  
 XX of mouse antibodies. The resulting humanised antibodies may be used  
 XX e.g. as antitumour agents. They retain the antigen recognition of the  
 XX original antibody, but are not immunogenic in humans.  
 XX (Updated on 25-MAR-2003 to correct PI field.)  
 XX  
 XX Sequence 87 AA;  
 XX  
 XX Query Match 83.7%; Score 376; DB 17; Length 87;  
 XX Best Local Similarity 79.3%; Pred. No. 3.4e-28;  
 XX Matches 69; Conservative 11; Mismatches 7; Indels 0; Gaps 0;  
 QY 1 QIQLVQSGGEVKKPGASVRSCKASGYSTFTWVRSQSGKLGWIGKATLTVDKSTSTAYME 60  
 Db 1 QVQLVQSGAEVKKPGASLVKSCASGFTFTWRQAPQGRLEWGRVTITRDTSASTAYME 60  
 QY 61 LSSLRSEDYAVFCARMGGQTTVTSS 87  
 Db 61 LSSLRSEDYAVYFCARMGGQTTVTSS 87  
 RESULT 4  
 AA984097  
 ID AA984097 standard; Protein; 117 AA.  
 XX  
 XX AA984097;  
 XX  
 XX 15-MAR-1999 (first entry)  
 XX  
 XX Humanised anti-alpha-v beta-3 MAb D12H2HC 1-0 VH.  
 XX  
 XX Humanised antibody; monoclonal antibody; MAb; antibody engineering;  
 XX mouse; human; vitronectin; alpha-v beta-3; receptor; restenosis;  
 XX cancer; metastasis; rheumatoid arthritis; atherosclerosis;  
 XX angiogenesis; diabetic retinopathy; inflammation;  
 XX macular degeneration; osteoporosis; Paget's disease;  
 XX hyperparathyroidism; hypercalcaemia; therapy; immunotherapy;  
 XX D12H2HC-10.  
 XX  
 XX Homo sapiens.  
 XX Synthetic.  
 XX

FH Key Location/Qualifiers  
 FT Region 31..35  
 FT /label= CDR1  
 FT Region 50..66  
 FT /label= CDR2  
 FT Region 99..106  
 FT /label= CDR3  
 XX  
 XX WO9840488-A1.  
 XX  
 XX 17-SEP-1998.  
 XX  
 XX 12-MAR-1998; 98WO-US04987.  
 XX  
 XX 12-MAR-1997; 97US-0039609.  
 XX (SMIK ) SMITHKLINE BEECHAM CORP.  
 XX  
 XX Johanson KO, Jonak ZL, Taylor AH;  
 XX  
 XX WPI; 1999-034590/03.  
 XX N-PSDB; AAV71799.  
 XX  
 XX New anti alpha v beta 3 vitronectin receptor antibodies - used for  
 XX immunotherapeutic treatment of e.g. diabetic retinopathy,  
 XX inflammatory disorders, atherosclerosis, restenosis, cancers or  
 XX osteoporosis  
 XX  
 XX Claim 1; Page 58; 97pp; English.  
 XX  
 XX This is the amino acid sequence of the heavy chain variable region  
 XX (VH) of humanised anti-alpha-v beta-3 vitronectin receptor  
 XX monoclonal antibody D12H2HC 1-0. It is based on the VH sequence  
 XX (see AA984095) of human Kabat subgroup I VH, with complementarity  
 XX determining regions (CDRs) from the murine anti-human alpha-v  
 XX beta-3 vitronectin receptor monoclonal antibody D12 (see AA984093).  
 XX 7 Murine framework residues (24, 48, 67, 68, 70, 72 and 74)  
 XX are retained. The humanised heavy chain can be expressed in host  
 XX cells using nucleic acid molecules (see AAV71799) of the invention.  
 XX Humanised D12 VL is also provided (see AA984098). The humanised  
 XX antibodies can be used for passive immunotherapy of disorders  
 XX mediated by the alpha-v beta-3 receptor, e.g. cardiovascular or  
 XX angiogenic-related disorders, such as angiogenesis associated  
 XX with diabetic retinopathy, atherosclerosis and restenosis, chronic  
 XX inflammatory disorders, macular degeneration, rheumatoid arthritis  
 XX and cancer, e.g. solid tumour metastasis, and diseases where bone  
 XX resorption is associated with pathology such as osteoporosis,  
 XX hyperparathyroidism, Paget's disease, hypercalcaemia of malignancy,  
 XX osteolytic lesions produced by bone metastasis, bone loss due to  
 XX immobilisation or sex hormone deficiency. They can also be used for  
 XX targeted drug therapy, and for detection and diagnosis.  
 XX  
 XX Sequence 117 AA;  
 XX  
 XX Query Match 83.5%; Score 375; DB 20; Length 117;  
 XX Best Local Similarity 67.5%; Pred. No. 5.6e-28;  
 XX Matches 79; Conservative 6; Mismatches 2; Indels 30; Gaps 3;  
 QY 1 QIQLVQSGGEVKKPGASVRSCKASGYSTFTWVRSQSGKLGLEWIGIDPYNGDTFF 60  
 Db 1 QVQLVQSGAEVKKPGASVRSCKASGYSTFTWVRSQSGKLGLEWIGIDPYNGDTFF 60  
 QY 44 -----GKATLTVDKSTSTAYMELSLRSEDYAVFCAR-----WGQITVTSS 87  
 Db 61 NQKFKGKATLTVDKSTSTAYMELSLRSEDYAVYFCARQNYGSPAYWGQITLTVTSS 117  
 RESULT 5  
 AA907965  
 ID AA907965 standard; Protein; 135 AA.  
 XX  
 XX AA907965;  
 XX

DT 14-NOV-2000 (first entry)  
 DE A heavy chain variable region of humanised 351 antibody.  
 XX  
 XX Antibody 3D1; B7 molecule; B7; humanised immunoglobulin;  
 XX autoimmune disease; infectious disease; inflammatory disorder;  
 XX systemic lupus erythematosus; diabetes mellitus; asthma;  
 XX arthritis; inflammatory bowel disease; cancer; inflammatory dermatitis;  
 XX multiple sclerosis; transplant rejection; proliferative disease;  
 XX leukemia; lymphoma; anaemia; sickle-cell anaemia; thalassemia;  
 XX aplastic anaemia; myeloid dysplasia syndrome.  
 XX  
 OS Synthetic.  
 OS Mus sp.  
 OS Homo sapiens.  
 XX  
 XX  
 PH Key Location/Qualifiers  
 FT Peptide 1..19  
 FT /note= "signal peptide"  
 FT Protein 20..135  
 FT /note= "mature protein"  
 FT Region 50..54  
 FT /note= "complementarity determining region 1"  
 FT Region 69..85  
 FT /note= "complementarity determining region 2"  
 FT Region 118..124  
 FT /note= "complementarity determining region 3"  
 XX  
 XX WO200047625-A2.  
 XX  
 XX 17-AUG-2000.  
 XX  
 XX 09-FEB-2000; 2000WO-US03303.  
 XX  
 XX 12-FEB-1999; 99US-0249011.  
 XX 24-JUN-1999; 99US-0339596.  
 XX  
 XX (GEMY ) GENETICS INST INC.  
 XX  
 XX Co MS. Vasquez M, Carreno B, Celniker AC, Collins M, Goldman S;  
 XX Gray GS, Knight A, O'hara D, Rup B, Veldman GM;  
 XX  
 XX WPI; 2000-524532/47.  
 XX N-PSDB; AAA59694.  
 XX  
 XX Humanized immunoglobulin having a binding specificity to B7-1 (derived  
 XX from ATCC PTA-263), or B7-2 (derived from ATCC CRL-12524) molecules,  
 XX PT modulates immune responses and can therefore treat e.g. autoimmune  
 XX PT diseases, infectious diseases -  
 XX  
 XX Example 3; Fig 2A; 162pp; English.  
 XX  
 XX The present sequence represents the heavy chain variable region  
 XX of the humanised murine antibody 3D1. The antibody has a binding  
 XX specificity to B7 molecules. The antibody is used to construct humanized  
 XX immunoglobulins, which comprise an antigen binding region of non-human  
 XX origin and a portion of a human immunoglobulin. The humanized  
 XX immunoglobulins are useful for treating autoimmune diseases, infectious  
 XX diseases, inflammatory disorders, systemic lupus erythematosus, diabetes  
 XX mellitus, insulinitis, asthma, arthritis, inflammatory bowel disease,  
 XX inflammatory dermatitis, and multiple sclerosis. The immunoglobulins are  
 XX also useful for treating a transplant recipient or preventing transplant  
 XX rejection in a transplant recipient, and treating proliferative disease  
 XX (leukemia, lymphoma and cancer), anaemia (sickle-cell anaemia,  
 XX thalassemia and aplastic anaemia), inborn errors of metabolism,  
 XX congenital immunodeficiency diseases, and myeloid dysplasia syndrome.  
 XX  
 XX Sequence 135 AA;  
 SQ Query Match 82.5%; Score 370.5; DB 21; Length 135;  
 Best Local Similarity 66.4%; Pred. No. 1.7e-27;  
 Matches 77; Conservative 8; Mismatches 2; Indels 29; Gaps 3;

QY 1 QIQLVQSGGEVKKPGASVRVSCKASGYSTFT-----WVROSPGKGLWV----- 43  
 DB 20 QVQLVQSGAEVKKPGSSVKVSKASGYTFDTYAIQWVROAPGQGLEWIVGINTYDNTNY 79  
 QY 44 -----GKATLTVDKSTSTAYWELSSLRSEDTAVYFCAR-----WGQGTLVTVSS 87  
 DB 80 NQKPKGKATVTDKSTSTAYWELSSLRSEDTAVYCARAWYNDYWGQGLTVTVSS 135  
 RESULT 6  
 ID AAW06442 standard; Protein; 136 AA.  
 XX AAW06442;  
 AC AAW06442;  
 XX  
 XX 04-FEB-1997 (first entry)  
 XX HuMc3 VH region.  
 XX Humanised antibody; variable heavy region; buried residue modification;  
 KW VH; HuMc3 VH; BA46 antigen; human; milk fat globule; HMF; lactation;  
 KW fat globule membrane; murine; mammary; epithelial cell; breast cancer;  
 KW breast membrane glycoprotein; therapy; immunotherapy.  
 XX  
 OS Synthetic.  
 XX WO9608565-A2.  
 XX  
 XX 21-MAR-1996.  
 XX  
 XX 14-SEP-1995; 95WO-US11683.  
 XX  
 XX 07-JUN-1995; 95US-0487598.  
 XX 16-SEP-1994; 94US-0307868.  
 XX  
 XX (CANC-) CANCER RES FUND CONTRA COSTA.  
 XX  
 XX Ceriani RI, Do Couto FJR, Peterson JA;  
 XX WPI; 1996-179941/18.  
 XX N-PSDB; AAT42717.  
 XX  
 XX Recombinant Mc3 antibody which binds BA46 antigen of HMF -  
 XX comprises a modified heavy or light chain variable region, useful in  
 XX the diagnosis and therapy of breast cancer  
 XX  
 XX Claim 13; Fig 18; 91pp; English.  
 XX  
 XX This sequence represents the variable heavy (VH) chain of the humanised  
 XX murine antibody HuMc3 VH. The Mc3 VH sequence was humanised using the  
 XX buried residue modification technique, where important non-human  
 XX framework residues are unaffected. The Mc3 antibody binds to the BA46  
 XX antigen of the human milk fat globule (HMF). The milk fat globule  
 XX membrane is derived from the apical surface of the mammalian epithelial  
 XX cell during lactation, and therefore is a source for breast membrane  
 XX glycoproteins. The antibody can be used in an in vitro method to detect  
 XX a HMF antigen (or antigen fragment), and to diagnose the presence of the  
 XX antigen in a subject. The antibody can also be used to deliver an agent  
 XX to a target (within a subjects body), containing a HMF antigen. The  
 XX antibodies can also be used for diagnosis, prognosis, and therapeutic  
 XX applications of breast cancer. As the humanised antibodies retain their  
 XX high affinity binding to the antigen, they are useful for  
 XX immunodiagnostic and immunotherapeutic applications in humans.  
 XX  
 XX Sequence 136 AA;  
 SQ Query Match 82.4%; Score 370; DB 17; Length 136;  
 Best Local Similarity 67.5%; Pred. No. 1.9e-27;  
 Matches 79; Conservative 4; Mismatches 4; Indels 30; Gaps 3;  
 QY 1 QIQLVQSGGEVKKPGASVRVSCKASGYSTFT-----WVROSPGKGLWV----- 44  
 DB 20 EVQLVQSGAEVKKPGASVKVSKASGYSTFTGYTHWVKQSPGMNLEWIGLINFYNGTIV 79

QY 45 -----KATLVKSTSTAYMELSSLRSEDTAVYFCAR-----WGQTTVTYSS 87  
 DB 80 NQKFDKATLVKSTSTAYMELSSLRSEDTAVYFCARRWRYTMDYWGQTTVTYSS 136

RESULT 7  
 AAB12168  
 ID AAB12168 standard; Protein; 115 AA.  
 XX  
 AC AAB12168;  
 XX  
 DT 17-JAN-2001 (first entry)  
 XX  
 DE Humanised HBV pre-S1 antibody HKR127HC(I) heavy chain variable region.  
 XX  
 KW Humanised antibody; HBV surface antigen pre-S1; mouse;  
 KW human; hepatitis B; liver cirrhosis; liver cancer.  
 XX  
 OS Chimeric - Homo sapiens.  
 OS Chimeric - Mus sp.  
 XX  
 PN WO200031141-A1.  
 XX  
 PD 02-JUN-2000.  
 XX  
 PF 19-NOV-1999; 99WO-KR00699.  
 XX  
 PR 19-NOV-1998; 98KR-0049663.  
 XX  
 PA (KOAD ) KOREA ADV INST SCI & TECHNOLOGY.  
 PA (GREC ) KOREA GREEN CROSS CORP.  
 XX  
 PI Hong HJ, Ryu CJ, Hur H;  
 XX  
 DR WPI; 2000-400049/34.  
 DR N-PSDB; AAA62118.  
 XX  
 XX Humanized antibody specific for hepatitis B virus surface antigen  
 PT pre-S1, containing humanized heavy and light chain regions, useful for  
 PT preventing hepatitis B virus (HBV) infection and for treating chronic  
 PT hepatitis B -  
 XX  
 PS Claim 2; Fig 1; 61pp; English.  
 CC  
 CC Hepatitis B virus (HBV) is responsible for hepatitis infection in  
 CC humans, which may progress to liver cirrhosis or cancer. One of HBV's  
 CC surface antigens is pre-S1. Monoclonal antibodies specific for pre-S1  
 CC antigen may efficiently neutralise HBV. The present invention relates to  
 CC humanised antibodies specific for HBV surface antigen pre-S1. The  
 CC humanised antibodies are useful for preventing HBV infection and for  
 CC treating chronic hepatitis B. The Complementarity Determining Regions of  
 CC mouse pre-S1 antibody KR127 were grafted onto human antibody to produce  
 CC the humanised antibodies of the present invention. The present sequence  
 CC is the humanised pre-S1 antibody HKR127HC(I) heavy chain variable region  
 CC (VH). The coding sequence for the present sequence was produced from the  
 CC coding sequence of the mouse pre-S1 antibody VH sequence (AAA62115).  
 XX  
 XX Sequence 115 AA;  
 SQ

Query Match 81.1%; Score 364; DB 21; Length 115;  
 Best Local Similarity 67.0%; Pred. No. 6e-27;  
 Matches 77; Conservative 6; Mismatches 3;  
 Indels 28; Gaps 3;

QY 1 QIQLVOSGEVKKPGASVRSCKAGYSFT-----WVRSQPKGLEWT-----43  
 DB 1 QIQLVOSGAEVKKPGASVRSCKAGYAFSSWNWVRQAPQGLEWIGRIYFGDGTNY 60

QY 44 -----GRATLVKSTSTAYMELSSLRSEDTAVYFCAR-----WGQTTVTYSS 87  
 DB 61 AQKFGKATLADKSTSTAYMELSSLRSEDTAVYFCAREYDEAYWGQTTVTYSS 115

RESULT 8  
 AAW90935  
 ID AAW90935 standard; Protein; 470 AA.  
 XX  
 AC AAW90935;  
 XX  
 DT 08-AUG-2000 (first entry)  
 XX  
 DE Humanised anti-Fas designed heavy chain Heu 3 protein.  
 XX  
 KW Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;  
 KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiac;  
 KW dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;  
 KW nephrotropic; antifertility; neuroprotective; antiarteriosclerotic;  
 KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus;  
 KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;  
 KW Sjogren's syndrome; anemia; Addison's disease; scleroderma; sterility;  
 KW Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;  
 KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;  
 KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;  
 KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.  
 XX  
 OS Synthetic.  
 XX  
 PN EP990663-A2.  
 XX  
 PD 05-APR-2000.  
 XX  
 PF 29-SEP-1999; 99EP-0307711.  
 XX  
 PR 30-SEP-1998; 98JP-0276881.  
 PR 30-SEP-1998; 98JP-0276882.  
 XX  
 PA (SANY ) SANKYO CO LTD.  
 XX  
 PI Serizawa N, Haryuyama H, Nakahara K, Tamaki I, Takahashi T;  
 XX  
 DR WPI; 2000-258930/23.  
 DR N-PSDB; AAA11646.  
 XX  
 XX New humanized anti-Fas antibody, useful for treating or preventing e.g.  
 PT inflammatory or autoimmune disease, induces apoptosis selectively in  
 PT cells with abnormal Fas-Fas ligand systems -  
 XX  
 PS Claim 2; Page 180-182; 263pp; English.  
 CC  
 CC This invention describes a novel humanized anti-Fas antibody-like  
 CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas  
 CC ligand system, by binding to Fas on the cell surface, and prevents  
 CC apoptosis in cells with a normal system, by inhibiting binding between  
 CC Fas and its ligand. The products of the invention have anti-inflammatory,  
 CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,  
 CC immunomodulatory, dermatological immunosuppressive, thyromimetic,  
 CC antirheumatic, nephrotropic, antifertility, neuroprotective,  
 CC antiarteriosclerotic, cardiac and hepatotropic activity. (I) induce  
 CC apoptosis by binding to cell surface Fas or inhibit it by competitive  
 CC inhibition of ligand binding. (I) are used to treat and/or prevent  
 CC diseases associated with the Fas/Fas ligand system, especially systemic  
 CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft  
 CC versus host disease, Sjogren's syndrome, Goodpasture syndrome, Crohn's  
 CC anemia, Addison's disease, scleroderma, Cooopasture syndrome, Crohn's  
 CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,  
 CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin  
 CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,  
 CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral  
 CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively  
 CC inhibit apoptosis in normal cells but selectively induce it in abnormal  
 CC cells. They bind to both human and murine Fas, so can be evaluated in  
 CC murine disease models. (I) act on the active site of Fas, i.e. they mimic  
 CC the native ligand, do not induce liver disease, and have reduced risk of  
 CC inducing a human anti-murine antibody response. This sequence represents  
 CC a humanised anti-Fas antibody heavy chain construct designated Heu 3  
 CC which is described in the method of the invention.

XX SQ Sequence 470 AA;  
Query Match 81.1%; Score 364; DB 21; Length 470;  
Best Local Similarity 63.6%; Pred. No. 2.3e-26;  
Matches 77; Conservative 7; Mismatches 3; Indels 34; Gaps 3;  
QY 1 QIQLVQSGGEVKPGASVRYSCKASGYFTFTSYMWQVRQAPGGLEWMEIDPDSYTNV 79  
DB 20 QVQLVQSGAEVKKFGASVKYSCKASGYFTFTSYMWQVRQAPGGLEWMEIDPDSYTNV 79  
QY 44 -----GKATLTVDKSTSTAYMELSSLRSEDTAVYFCAR-----WGQGITVTVS 86  
DB 80 NQKFKGKATLTVDSTSTAYMELSSLRSEDTAVYICARNRDYSNNWYFDWVGQGLTVTS 139  
QY 87 S 87  
DB 140 S 140  
RESULT 9  
AB074904  
ID ABB74904 standard; Protein; 470 AA.  
XX AC ABB74904;  
XX DT 26-APR-2002 (first entry)  
XX DE Mouse humanised anti-Fas antibody related protein SEQ ID NO 9.  
XX KW Human; mouse; humanised anti-Fas antibody; Fas/Fas ligand;  
XX KW light chain subunit; apoptosis; immunosuppressive; antiallergic;  
XX KW autoimmune disease; allergy; atopic.  
XX OS Mus musculus.  
XX PN J2P2001342148-A.  
XX PD 11-DEC-2001.  
XX PF 28-MAR-2001; 2001JP-0093106.  
XX PR 29-MAR-2000; 2000JP-0090918.  
XX PA (SANY ) SANKYO CO LTD.  
XX DR WPI; 2002-145113/19.  
XX DR N-PSDB; ABL45926.  
XX PT Drug containing humanised anti-Fas antibody, used for preventing and  
XX PT treating autoimmune diseases, allergy, and atopy -  
XX PS Example 4 (Preparatory); Page 79-80; 194pp; Japanese.  
XX CC The invention relates to a preventive or treating agent for diseases  
XX CC caused by abnormality in Fas/Fas ligand system containing as the active  
XX CC component an antibody having as the light chain subunit a polypeptide  
XX CC containing residues 1-218 of one of 3, 239 residue amino acid sequences,  
XX CC or residues 1-451 of one of 3, 470 residue amino acid sequences, all  
XX CC fully defined in the specification and having an activity of inducing  
XX CC specifically with mammalian Fas and an activity of inducing apoptosis  
XX CC in a cell expressing Fas. The agent has immunosuppressive and  
XX CC antiallergic activity and is used for preventing and treating autoimmune  
XX CC diseases, allergy, atopy and others.  
XX SQ Sequence 470 AA;  
Query Match 81.1%; Score 364; DB 23; Length 470;  
Best Local Similarity 63.6%; Pred. No. 2.3e-26;  
Matches 77; Conservative 7; Mismatches 3; Indels 34; Gaps 3;  
QY 1 QIQLVQSGGEVKPGASVRYSCKASGYFTFTSYMWQVRQAPGGLEWMEIDPDSYTNV 79

DB 20 QVQLVQSGAEVKKFGASVKYSCKASGYFTFTSYMWQVRQAPGGLEWMEIDPDSYTNV 79  
QY 44 -----GKATLTVDKSTSTAYMELSSLRSEDTAVYFCAR-----WGQGITVTVS 86  
DB 80 NQKFKGKATLTVDSTSTAYMELSSLRSEDTAVYICARNRDYSNNWYFDWVGQGLTVTS 139  
QY 87 S 87  
DB 140 S 140  
RESULT 10  
AAR92218  
ID AAR92218 standard; Protein; 116 AA.  
XX AC AAR92218;  
XX DT 28-MAY-1996 (first entry)  
XX DE Humanised LL2 MAb VH region.  
XX KW Humanised antibody; monoclonal antibody; MAb; LL2; B-cell lymphoma;  
XX KW leukaemia; therapy; diagnosis; complementarity determining region;  
XX KW CDR; antibody engineering.  
XX OS Synthetic.  
XX FH Key Location/Qualifiers  
XX FT Region 31..35  
XX FT /label= CDR1  
XX FT Region 50..66  
XX FT /label= CDR2  
XX FT Region 99..105  
XX FT /label= CDR3  
XX PN WO9604925-A1.  
XX PD 22-FEB-1996.  
XX PF 11-AUG-1995; 95WO-US09641.  
XX PR 12-AUG-1994; 94US-0289576.  
XX PA (IMMU-) IMMUNOMEDICS INC.  
XX PI Hansen H, Leung S;  
XX DR WPI; 1996-139454/14.  
XX DR N-PSDB; AAT15804.  
XX PT Chimeric and humanised LL2 antibodies - used to produce conjugates  
XX PT for the therapy and diagnosis of B-cell lymphoma(s) and  
XX PT leukaemia(s).  
XX PS Claim 5; Page 39; 70pp; English.  
XX CC The complementarity determining regions (CDRs) of mouse monoclonal  
XX CC antibody (MAb) LL2 VK (AAR92215) and VH (AAR92216) regions were  
XX CC recombinantly linked to the framework sequences of human VK and VH  
XX CC regions, respectively, to give humanised LL2 VK (AAR92217) and VH  
XX CC (AAR92218). These were subsequently linked, respectively, to human  
XX CC kappa and IgG1 constant regions. A humanised MAb was obt'd. that  
XX CC retained the B-lymphoma and leukaemia cell targeting and  
XX CC internalisation characteristics of the parental LL2 MAb, and which  
XX CC exhibited a lowered HAMA reaction. It can be linked to e.g. a  
XX CC cytostatic agent for therapeutic appln.  
XX SQ Sequence 116 AA;  
Query Match 81.0%; Score 363.5; DB 17; Length 116;  
Best Local Similarity 64.7%; Pred. No. 6.7e-27;  
Matches 75; Conservative 9; Mismatches 3; Indels 29; Gaps 3;



QY 1 QIQLVQSGEVKPKGASVVRVSKAGSYFT-----WVRQSPKGLWIG----- 44  
 Db 1 QVOLVQSGAEVKPKGSSVKVSKAGSYFTTSYWLHWRQAPQGLWIGYINPRNDYTEY 60  
 QY 45 -----KATLTVDKSTSTAYMELSLRSDTAVFCAR-----WGQGTTVTVSS 87  
 Db 61 NONFXDKATITADESTNTAYMELSLRSDTAVFCARRDITTFYWGQGTTVTVSS 116

RESULT 11  
 AAW27698  
 ID AAW27698 standard; Protein; 116 AA.  
 XX  
 AC AAW27698;  
 XX  
 DT 14-APR-1998 (first entry)  
 XX  
 DE Variable heavy chain of MAb hLL2.  
 XX  
 KW Variable heavy chain; B cell; monoclonal antibody; MAb; hLL2;  
 KW B cell lymphoma; lymphocytic leukaemia cell; murine; humanised;  
 KW diagnosis; treatment; B cell malignancy; non-Hodgkins lymphoma;  
 KW chronic lymphocytic leukaemia.  
 XX  
 OS Chimeric - Mus sp.  
 XX Chimeric - Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Region 31..35  
 FT /note= "complementarity determining region 1"  
 FT Region 50..66  
 FT /note= "complementarity determining region 2"  
 FT Region 99..105  
 FT /note= "complementarity determining region 3"  
 XX  
 PN WO9734632-A1.  
 XX  
 PD 25-SEP-1997.  
 XX  
 PF 19-MAR-1997; 97WO-US04196.  
 XX  
 PR 20-MAR-1996; 96US-0013709.  
 XX  
 PA (IMMU-) IMMUNOMEDICS INC.  
 XX  
 PI Hansen H, Leung S, Qu Z;  
 XX  
 DR WPI; 1997-479995/44.  
 DR N-PSDB; AAT88131.  
 XX  
 PT Monoclonal antibody engineered to contain glycosylation site - in  
 PT non-Fc constant heavy or light chain region, useful to diagnose or  
 PT treat B cell malignancies, e.g. non-Hodgkins lymphoma  
 XX  
 PS Example 3; Fig 5B; 88pp; English.  
 XX  
 CC The present sequence is the variable heavy chain of the  
 CC B cell specific monoclonal antibody (MAb) hLL2. hLL2 is a highly  
 CC specific anti-B cell lymphoma and anti-lymphocytic leukaemia cell  
 CC humanised murine MAb. The MAb can be used to diagnose or treat B  
 CC cell malignancies, e.g. non-Hodgkins lymphoma or chronic  
 CC lymphocytic leukaemia.  
 XX  
 SQ Sequence 116 AA;  
 Query Match 81.0%; Score 363.5; DB 18; Length 116;  
 Best Local Similarity 64.7%; Pred. No. 6.7e-27;  
 Matches 75; Conservative 9; Mismatches 3; Indels 29; Gaps 3;

QY 1 QIQLVQSGEVKPKGASVVRVSKAGSYFT-----WVRQSPKGLWIG----- 44  
 Db 1 QVOLVQSGAEVKPKGSSVKVSKAGSYFTTSYWLHWRQAPQGLWIGYINPRNDYTEY 60

QY 45 -----KATLTVDKSTSTAYMELSLRSDTAVFCAR-----WGQGTTVTVSS 87  
 Db 61 NONFXDKATITADESTNTAYMELSLRSDTAVFCARRDITTFYWGQGTTVTVSS 116

RESULT 12  
 AAR29017  
 ID AAR29017 standard; Protein; 135 AA.  
 XX  
 AC AAR29017;  
 XX  
 DT 25-MAR-2003 (updated)  
 DT 30-MAR-1993 (first entry)  
 XX  
 DE pUC-RVh-1220d.  
 XX  
 KW Human; antibody; interleukin-6; receptor; IL-6R; CDR; PCR; mouse;  
 KW complementarity determining region; monoclonal; hybridoma; PCR;  
 KW plasmid; polymerase chain reaction; amplify.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..19  
 FT /note= "Leader peptide"  
 FT Region 20..49  
 FT /label= PR1  
 FT Region 50..54  
 FT /label= CDR1  
 FT Region 55..68  
 FT /label= PR2  
 FT Region 69..85  
 FT /label= CDR2  
 FT Region 86..117  
 FT /label= PR3  
 FT Region 118..124  
 FT /label= CDR3  
 FT Region 125..135  
 FT /label= PR4  
 XX  
 PN WO9219759-A1.  
 XX  
 PD 12-NOV-1992.  
 XX  
 PF 24-APR-1992; 92WO-JP00544.  
 XX  
 PR 25-APR-1991; 91JP-0095476.  
 PR 19-FEB-1992; 92JP-0032084.  
 XX  
 PA (CHUS) CHUGAI SEIYAKU KK.  
 XX  
 PI Bendig MM, Jones ST, Saldanha JW, Sato K, Tsuchiya M;  
 XX  
 DR WPI; 1992-398882/48.  
 DR N-PSDB; AAQ31391.  
 XX  
 PT Reconstituted human antibody to human interleukin-6 receptor -  
 PT has low antigenicity and contains mouse V-region complementarity  
 PT determining regions  
 XX  
 PS Disclosure; Page 159-60; 207pp; Japanese.  
 XX  
 CC The sequences given in AAR29016-17 are portions of monoclonal antibodies  
 CC which were encoded by plasmids contained within the mouse hybridoma,  
 CC AUK12-20. The DNA encoding the complementarity determining regions  
 CC (CDR's) was isolated by polymerase chain reaction. These antibodies  
 CC recognise human interleukin-6 receptor (IL-6R). The hybridoma cells  
 CC were transformed with plasmids containing fragments of the antibody  
 CC gene which caused the production of the antibody from the hybridoma  
 CC cell line.  
 CC (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 SQ Sequence 135 AA;

Query Match 81.0%; Score 363.5; DB 13; Length 135;  
Best Local Similarity 65.5%; Pred. No. 7.8e-27; Indels 29; Gaps 3;  
Matches 76; Conservative 7; Mismatches 4;

QY 1 QIQLVQSGGEVKKPGASVRVSCKASGYSTFT-----WVRSFGKGLWMI----- 43  
DB 20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTHWVRQAPGQGLEWMGSIFFPGDTRY 79

QY 44 -----GKATLTVDKSTSTAYMELSSLRSEDTAVYFCAR-----WGQGTITVSS 87  
DB 80 SQKPKGRVTMTADKSTSTAYMELSSLRSEDTAVYFCARGLRGGYFDYWGQGTITVSS 139

RESULT 13  
AAW65773  
ID AAW65773 standard; Protein; 139 AA.  
XX AC AAW65773;  
XX DT 16-NOV-1998 (first entry)  
XX DE Anti-human HM1.24 antibody heavy chain variable region r.  
XX KW Cytotoxic antibody; anti-human HM1.24; lymphocytic tumours;  
XX OS pre-B lymphoma; Burkitt's lymphoma; T-cell tumour; B-cell tumour.  
XX Synthetic.  
XX FH Key Location/Qualifiers  
XX FT Peptide 1..19  
XX FT Peptide /note= "Signal peptide"  
XX FT Peptide 20..139  
XX FN WO3835698-A1.  
XX PD 20-AUG-1998.  
XX PF 12-FEB-1998; 98WO-JP00568.  
XX PR 12-FEB-1997; 97JP-0041410.  
XX PA (CHUS ) CHUGAI SEIYAKU KK.  
XX PI Koishihara Y, Yoshimura Y;  
XX WPI; 1998-456869/39.  
XX DR N-PSDB; AAV07581.  
XX Treatment of lymphocytic tumours using cytotoxic antibody - binding  
XX to specific antigen such as HM1.24 and effective against T-cell  
XX tumours and B-cell tumours other than myeloma  
XX Disclosure; Page 47-48; 82pp; Japanese.  
XX The anti-human HM1.24 antibody is the preferred cytotoxic antibody to be  
XX used in the treatment of lymphocytic tumours, including T-cell tumours  
XX and B-cell tumours other than myeloma. The antibody is preferably  
XX monoclonal and has ADCC or CDC type cytotoxicity. It may be chimeric or  
XX humanised, and preferably contains a human antibody constant region C  
XX gamma (such as C gamma 1 or C gamma 3). A preferred antibody is an  
XX anti-human HM1.24 antibody or an antibody which binds to an epitope  
XX recognising anti-human HM1.24 antibody. The cytotoxic antibody is useful  
XX in the treatment of lymphocytic tumours such as acute or chronic B  
XX lymphocytic leukaemia, pre-B lymphoma, Burkitt's lymphoma, or acute or  
XX chronic T lymphocytic leukaemia.  
XX Sequence 139 AA;  
Query Match 81.0%; Score 363.5; DB 19; Length 139;  
Best Local Similarity 62.5%; Pred. No. 8e-27; Indels 33; Gaps 3;  
Matches 75; Conservative 9; Mismatches 3;

QY 1 QIQLVQSGGEVKKPGASVRVSCKASGYSTFT-----WVRSFGKGLWMI----- 43  
DB 20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTHWVRQAPGQGLEWMGSIFFPGDTRY 79

QY 1 QIQLVQSGGEVKKPGASVRVSCKASGYSTFT-----WVRSFGKGLWMI----- 43  
DB 20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTHWVRQAPGQGLEWMGSIFFPGDTRY 79

QY 44 -----GKATLTVDKSTSTAYMELSSLRSEDTAVYFCAR-----WGQGTITVSS 87  
DB 80 SQKPKGRVTMTADKSTSTAYMELSSLRSEDTAVYFCARGLRGGYFDYWGQGTITVSS 139

RESULT 14  
AAW65774  
ID AAW65774 standard; Protein; 139 AA.  
XX AC AAW65774;  
XX DT 16-NOV-1998 (first entry)  
XX DE Anti-human HM1.24 antibody heavy chain variable region s.  
XX KW Cytotoxic antibody; anti-human HM1.24; lymphocytic tumours;  
XX OS pre-B lymphoma; Burkitt's lymphoma; T-cell tumour; B-cell tumour.  
XX Synthetic.  
XX FH Key Location/Qualifiers  
XX FT Peptide 1..19  
XX FT Peptide /note= "Signal peptide"  
XX FT Peptide 20..139  
XX FN WO9835698-A1.  
XX PD 20-AUG-1998.  
XX PF 12-FEB-1998; 98WO-JP00568.  
XX PR 12-FEB-1997; 97JP-0041410.  
XX PA (CHUS ) CHUGAI SEIYAKU KK.  
XX PI Koishihara Y, Yoshimura Y;  
XX WPI; 1998-456869/39.  
XX DR N-PSDB; AAV07582.  
XX Treatment of lymphocytic tumours using cytotoxic antibody - binding  
XX to specific antigen such as HM1.24 and effective against T-cell  
XX tumours and B-cell tumours other than myeloma  
XX Disclosure; Page 48-49; 82pp; Japanese.  
XX The anti-human HM1.24 antibody is the preferred cytotoxic antibody to be  
XX used in the treatment of lymphocytic tumours, including T-cell tumours  
XX and B-cell tumours other than myeloma. The antibody is preferably  
XX monoclonal and has ADCC or CDC type cytotoxicity. It may be chimeric or  
XX humanised, and preferably contains a human antibody constant region C  
XX gamma (such as C gamma 1 or C gamma 3). A preferred antibody is an  
XX anti-human HM1.24 antibody or an antibody which binds to an epitope  
XX recognising anti-human HM1.24 antibody. The cytotoxic antibody is useful  
XX in the treatment of lymphocytic tumours such as acute or chronic B  
XX lymphocytic leukaemia, pre-B lymphoma, Burkitt's lymphoma, or acute or  
XX chronic T lymphocytic leukaemia.  
XX Sequence 139 AA;  
Query Match 81.0%; Score 363.5; DB 19; Length 139;  
Best Local Similarity 62.5%; Pred. No. 8e-27; Indels 33; Gaps 3;  
Matches 75; Conservative 9; Mismatches 3;

QY 1 QIQLVQSGGEVKKPGASVRVSCKASGYSTFT-----WVRSFGKGLWMI----- 43  
DB 20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTHWVRQAPGQGLEWMGSIFFPGDTRY 79



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OM protein - protein search, using sw model

Run on: January 13, 2004, 12:43:20 ; Search time 13.9048 Seconds  
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1260.912 Million cell updates/sec

Title: US-09-990-586-91

Perfect score: 449  
Sequence: 1 QIQLVQSGGVKKPGASVRV.....DTAVYFCARWGQGTIVTVSS 87

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 747907 seqs, 201509753 residues

Total number of hits satisfying chosen parameters: 747907

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	449	100.0	87	11	US-09-990-586-91
2	449	100.0	87	11	US-09-990-586-92
3	449	100.0	87	12	US-10-230-880-91
4	449	100.0	87	12	US-10-230-880-92
5	441	98.2	87	11	US-09-990-586-93
6	441	98.2	87	12	US-10-230-880-93
7	439	97.8	87	11	US-09-990-586-90
8	439	97.8	87	12	US-10-230-880-90
9	438	97.6	87	11	US-09-990-586-94
10	438	97.6	87	12	US-10-230-880-94
11	434	96.7	87	11	US-09-990-586-96
12	434	96.7	87	12	US-10-230-880-96
13	431	96.0	87	11	US-09-990-586-95
14	431	96.0	87	12	US-10-230-880-95
15	430	95.8	87	11	US-09-990-586-89

16	430	95.8	87	12	US-10-230-880-89	Sequence 89, Appl
17	417	92.9	87	11	US-09-990-586-88	Sequence 88, Appl
18	417	92.9	87	12	US-10-230-880-88	Sequence 88, Appl
19	415	92.4	87	12	US-10-230-880-156	Sequence 156, Appl
20	415	92.4	87	12	US-10-230-880-172	Sequence 172, Appl
21	406	90.4	87	11	US-09-990-586-87	Sequence 87, Appl
22	406	90.4	87	12	US-10-230-880-87	Sequence 87, Appl
23	400	89.1	87	12	US-10-230-880-168	Sequence 168, Appl
24	398	88.6	87	11	US-09-990-586-86	Sequence 86, Appl
25	398	88.6	87	12	US-10-230-880-86	Sequence 86, Appl
26	392	87.3	87	11	US-09-509-098-200	Sequence 200, Appl
27	387	86.2	87	12	US-10-412-703A-7	Sequence 7, Appl
28	385	85.7	87	11	US-09-990-586-85	Sequence 85, Appl
29	385	85.7	87	12	US-10-230-880-85	Sequence 85, Appl
30	382	85.1	87	12	US-10-230-880-159	Sequence 159, Appl
31	379	84.4	87	12	US-10-230-880-160	Sequence 160, Appl
32	378	84.2	87	12	US-10-230-880-167	Sequence 167, Appl
33	375	83.5	117	12	US-10-223-880-5	Sequence 5, Appl
34	373	83.1	87	12	US-10-230-880-157	Sequence 157, Appl
35	371	82.6	87	12	US-10-230-880-171	Sequence 171, Appl
36	370.5	82.5	135	10	US-09-249-011A-6	Sequence 6, Appl
37	370.5	82.5	461	10	US-09-249-011A-24	Sequence 24, Appl
38	370	82.4	87	11	US-09-990-586-84	Sequence 84, Appl
39	370	82.4	87	12	US-10-230-880-84	Sequence 84, Appl
40	370	82.4	117	10	US-09-956-206A-78	Sequence 78, Appl
41	370	82.4	136	10	US-09-956-206A-63	Sequence 63, Appl
42	366	81.5	87	11	US-09-509-098-139	Sequence 139, Appl
43	364	81.1	87	11	US-09-990-586-83	Sequence 83, Appl
44	364	81.1	87	12	US-10-230-880-83	Sequence 83, Appl
45	364	81.1	470	12	US-10-384-933-147	Sequence 147, Appl

ALIGNMENTS

RESULT 1  
US-09-990-586-91  
; Sequence 91, Application US/09990586  
; Publication No. US20030109680A1  
; GENERAL INFORMATION:  
; APPLICANT: JIAO, JIN-AN  
; TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD COAGULATION AND METHODS  
; TITLE OF INVENTION: OF USE THEREOF  
; FILE REFERENCE: 71758/46943-CIP2  
; CURRENT APPLICATION NUMBER: US/09/990,586  
; CURRENT FILING DATE: 2001-11-21  
; PRIOR APPLICATION NUMBER: 09/293,854  
; PRIOR FILING DATE: 1999-04-16  
; NUMBER OF SEQ ID NOS: 102  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 91  
; LENGTH: 87  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-990-586-91

Query Match	100.0%;	Score 449;	DB 11;	Length 87;
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Matches	87;	Conservative 0;	Mismatches 0;	Indels 0; Gaps 0;
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Db	1	QIQLVQSGGVKKPGASVRVSCASGYSTFTWQSPKGLWIGKATLTVDKSTSTAYME	60	
Qy	61	LSSLRSEDTAVYFCARWGQGTIVTVSS	87	
Db	61	LSSLRSEDTAVYFCARWGQGTIVTVSS	87	
RESULT 2				
US-09-990-586-92				
; Sequence 92, Application US/09990586				

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; Publication No. US20030109680A1
; GENERAL INFORMATION:
; APPLICANT: JIAO, JIN-AN
; APPLICANT: WONG, HING C.
; TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD COAGULATION AND METHODS
; FILE REFERENCE: 71758/46943-CIP2
; CURRENT APPLICATION NUMBER: US/09/990,586
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 09/293,854
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 92
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-990-586-92

Query Match      100.0%; Score 449; DB 11; Length 87;
Best Local Similarity 100.0%; Pred. No. 9.1e-38;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 QIQLVQSGGEVKKPGASVRVSCKASGYFTWVRQSPGKGLWIGKATLTVDKSTSTAYME 60
Qy 61 LSSLRSEDTAVYFCARWGQGTIVTVSS 87
Db 61 LSSLRSEDTAVYFCARWGQGTIVTVSS 87

RESULT 3
US-10-230-880-91
; Sequence 91, Application US/10230880
; Publication No. US20030109705A1
; GENERAL INFORMATION:
; APPLICANT: WONG, HING C.
; APPLICANT: STINSON, JEFFREY L.
; APPLICANT: MOSQUERA, LUIS A.
; TITLE OF INVENTION: METHOD OF HUMANIZING IMMUNE SYSTEM MOLECULES
; FILE REFERENCE: 71758/58066
; CURRENT APPLICATION NUMBER: US/10/230,880
; PRIOR FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: 09/990,586
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/343,306
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/293,854
; PRIOR FILING DATE: 1999-04-16
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 91
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-230-880-91

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Best Local Similarity 100.0%; Pred. No. 9.1e-38;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 QIQLVQSGGEVKKPGASVRVSCKASGYFTWVRQSPGKGLWIGKATLTVDKSTSTAYME 60
Qy 61 LSSLRSEDTAVYFCARWGQGTIVTVSS 87
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RESULT 4
US-10-230-880-92
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; Sequence 92, Application US/10230880
; Publication No. US20030109705A1
; GENERAL INFORMATION:
; APPLICANT: WONG, HING C.
; APPLICANT: STINSON, JEFFREY L.
; APPLICANT: MOSQUERA, LUIS A.
; TITLE OF INVENTION: METHOD OF HUMANIZING IMMUNE SYSTEM MOLECULES
; FILE REFERENCE: 71758/58066
; CURRENT APPLICATION NUMBER: US/10/230,880
; PRIOR FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: 09/990,586
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/343,306
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/293,854
; PRIOR FILING DATE: 1999-04-16
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; ORGANISM: Homo sapiens
US-10-230-880-92

Query Match      100.0%; Score 449; DB 12; Length 87;
Best Local Similarity 100.0%; Pred. No. 9.1e-38;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QIQLVQSGGEVKKPGASVRVSCKASGYFTWVRQSPGKGLWIGKATLTVDKSTSTAYME 60
Db 1 QIQLVQSGGEVKKPGASVRVSCKASGYFTWVRQSPGKGLWIGKATLTVDKSTSTAYME 60
Qy 61 LSSLRSEDTAVYFCARWGQGTIVTVSS 87
Db 61 LSSLRSEDTAVYFCARWGQGTIVTVSS 87

RESULT 5
US-09-990-586-93
; Sequence 93, Application US/09990586
; Publication No. US20030109680A1
; GENERAL INFORMATION:
; APPLICANT: JIAO, JIN-AN
; APPLICANT: WONG, HING C.
; TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD COAGULATION AND METHODS
; FILE REFERENCE: 71758/46943-CIP2
; CURRENT APPLICATION NUMBER: US/09/990,586
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 09/293,854
; PRIOR FILING DATE: 1999-04-16
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 93
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-990-586-93

Query Match      98.2%; Score 441; DB 11; Length 87;
Best Local Similarity 98.9%; Pred. No. 5.7e-37;
Matches 86; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QIQLVQSGGEVKKPGASVRVSCKASGYFTWVRQSPGKGLWIGKATLTVDKSTSTAYME 60
Db 1 QIQLVQSGGEVKKPGASVRVSCKASGYFTWVRQSPGKGLWIGKATLTVDKSTSTAYME 60
Qy 61 LSSLRSEDTAVYFCARWGQGTIVTVSS 87
Db 61 LSSLRSEDTAVYFCARWGQGTIVTVSS 87

RESULT 6
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US-10-230-880-93  
; Sequence 93, Application US/10230880  
; Publication No. US20030190705A1  
; GENERAL INFORMATION:  
; APPLICANT: WONG, HING C.  
; APPLICANT: STINSON, JEFFREY L.  
; APPLICANT: MOSQUERA, LUIS A.  
; TITLE OF INVENTION: METHOD OF HUMANIZING IMMUNE SYSTEM MOLECULES  
; FILE REFERENCE: 71758/58066  
; CURRENT APPLICATION NUMBER: US/10/230,880  
; CURRENT FILING DATE: 2002-12-23  
; PRIOR APPLICATION NUMBER: 09/990,586  
; PRIOR FILING DATE: 2001-11-21  
; PRIOR APPLICATION NUMBER: 60/343,306  
; PRIOR FILING DATE: 2001-10-29  
; PRIOR APPLICATION NUMBER: 09/293,854  
; PRIOR FILING DATE: 1999-04-16  
; NUMBER OF SEQ ID NOS: 174  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 93  
; LENGTH: 87  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-230-880-93

Query Match 98.2%; Score 441; DB 12; Length 87;  
Best Local Similarity 98.9%; Pred. No. 5.7e-37;  
Matches 86; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 QIQLVQSGGEVKKPGASVRVSKASGYSTWVRQSPGKLEWIGKATLTVDKSTSTAYME 60  
DB 1 QIQLVQSGPEVKKPGASVRVSKASGYSTWVRQSPGKLEWIGKATLTVDKSTSTAYME 60  
QY 61 LSSLRSDETAIVFCARWGQGTIVTVSS 87  
DB 61 LSSLRSDETAIVFCARWGQGTIVTVSS 87

RESULT 7  
US-09-990-586-90  
; Sequence 90, Application US/09990586  
; Publication No. US20030109680A1  
; GENERAL INFORMATION:  
; APPLICANT: WONG, HING C.  
; APPLICANT: JIAO, JIN-AN  
; TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD COAGULATION AND METHODS  
; TITLE OF INVENTION: OF USE THEREOF  
; FILE REFERENCE: 71758/46943-CIP2  
; CURRENT APPLICATION NUMBER: US/09/990,586  
; CURRENT FILING DATE: 2001-11-21  
; PRIOR APPLICATION NUMBER: 09/293,854  
; PRIOR FILING DATE: 1999-04-16  
; NUMBER OF SEQ ID NOS: 102  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 90  
; LENGTH: 87  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-990-586-90

Query Match 97.8%; Score 439; DB 11; Length 87;  
Best Local Similarity 97.7%; Pred. No. 9.1e-37;  
Matches 85; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 1 QIQLVQSGGEVKKPGASVRVSKASGYSTWVRQSPGKLEWIGKATLTVDKSTSTAYME 60  
DB 1 QIQLVQSGGELVKPGASVRVSKASGYSTWVRQSPGKLEWIGKATLTVDKSTSTAYME 60  
QY 61 LSSLRSDETAIVFCARWGQGTIVTVSS 87  
DB 61 LSSLRSDETAIVFCARWGQGTIVTVSS 87

RESULT 8  
US-10-230-880-90  
; Sequence 90, Application US/10230880  
; Publication No. US20030190705A1  
; GENERAL INFORMATION:  
; APPLICANT: WONG, HING C.  
; APPLICANT: STINSON, JEFFREY L.  
; APPLICANT: MOSQUERA, LUIS A.  
; TITLE OF INVENTION: METHOD OF HUMANIZING IMMUNE SYSTEM MOLECULES  
; FILE REFERENCE: 71758/58066  
; CURRENT APPLICATION NUMBER: US/10/230,880  
; CURRENT FILING DATE: 2002-12-23  
; PRIOR APPLICATION NUMBER: 09/990,586  
; PRIOR FILING DATE: 2001-11-21  
; PRIOR APPLICATION NUMBER: 60/343,306  
; PRIOR FILING DATE: 2001-10-29  
; PRIOR APPLICATION NUMBER: 09/293,854  
; PRIOR FILING DATE: 1999-04-16  
; NUMBER OF SEQ ID NOS: 174  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 90  
; LENGTH: 87  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-230-880-90

Query Match 97.8%; Score 439; DB 12; Length 87;  
Best Local Similarity 97.7%; Pred. No. 9.1e-37;  
Matches 85; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 1 QIQLVQSGGEVKKPGASVRVSKASGYSTWVRQSPGKLEWIGKATLTVDKSTSTAYME 60  
DB 1 QIQLVQSGGELVKPGASVRVSKASGYSTWVRQSPGKLEWIGKATLTVDKSTSTAYME 60  
QY 61 LSSLRSDETAIVFCARWGQGTIVTVSS 87  
DB 61 LSSLRSDETAIVFCARWGQGTIVTVSS 87

RESULT 9  
US-09-990-586-94  
; Sequence 94, Application US/09990586  
; Publication No. US20030109680A1  
; GENERAL INFORMATION:  
; APPLICANT: WONG, HING C.  
; APPLICANT: JIAO, JIN-AN  
; TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD COAGULATION AND METHODS  
; TITLE OF INVENTION: OF USE THEREOF  
; FILE REFERENCE: 71758/46943-CIP2  
; CURRENT APPLICATION NUMBER: US/09/990,586  
; CURRENT FILING DATE: 2001-11-21  
; PRIOR APPLICATION NUMBER: 09/293,854  
; PRIOR FILING DATE: 1999-04-16  
; NUMBER OF SEQ ID NOS: 102  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 94  
; LENGTH: 87  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-990-586-94

Query Match 97.6%; Score 438; DB 11; Length 87;  
Best Local Similarity 97.7%; Pred. No. 1.1e-36;  
Matches 85; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 1 QIQLVQSGGEVKKPGASVRVSKASGYSTWVRQSPGKLEWIGKATLTVDKSTSTAYME 60  
DB 1 QIQLVQSGELVKPGASVRVSKASGYSTWVRQSPGKLEWIGKATLTVDKSTSTAYME 60  
QY 61 LSSLRSDETAIVFCARWGQGTIVTVSS 87  
DB 61 LSSLRSDETAIVFCARWGQGTIVTVSS 87

## RESULT 10

US-10-230-880-94  
; Sequence 94, Application US/10230880  
; Publication No. US20030190705A1  
; GENERAL INFORMATION:  
; APPLICANT: WONG, HING C.  
; APPLICANT: STINSON, JEFFREY L.  
; APPLICANT: MOSQUERA, LUIS A.  
; TITLE OF INVENTION: METHOD OF HUMANIZING IMMUNE SYSTEM MOLECULES  
; FILE REFERENCE: 71758/58066  
; CURRENT APPLICATION NUMBER: US/10/230,880  
; CURRENT FILING DATE: 2002-12-23  
; PRIOR APPLICATION NUMBER: 09/990,586  
; PRIOR FILING DATE: 2001-11-21  
; PRIOR APPLICATION NUMBER: 60/343,306  
; PRIOR FILING DATE: 2001-10-29  
; PRIOR APPLICATION NUMBER: 09/293,854  
; PRIOR FILING DATE: 1999-04-16  
; NUMBER OF SEQ ID NOS: 174  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 94  
; LENGTH: 87  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-230-880-94

Query Match 97.6%; Score 438; DB 12; Length 87;  
Best Local Similarity 97.7%; Pred. No. 1.1e-36;  
Matches 85; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 QIQLVQSGGEVKKPGASVRVSCKASGYSTFWRSQPKGLEWIGKATLTVDKSTSTAYME 60  
DB 1 QIQLVQSGPELVKPGASVRVSCKASGYSTFWRSQPKGLEWIGKATLTVDKSTSTAYME 60  
  
QY 61 LSSLRSEDTAVYFCARWGQGTITVSS 87  
DB 61 LSSLRSEDTAVYFCARWGQGTITVSS 87

## RESULT 11

US-09-990-586-96  
; Sequence 96, Application US/09990586  
; Publication No. US20030109680A1  
; GENERAL INFORMATION:  
; APPLICANT: JIAO, JIN-AN  
; APPLICANT: WONG, HING C.  
; TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD COAGULATION AND METHODS  
; FILE REFERENCE: 71758/46943-CIP2  
; CURRENT APPLICATION NUMBER: US/09/990,586  
; CURRENT FILING DATE: 2001-11-21  
; PRIOR APPLICATION NUMBER: 09/293,854  
; PRIOR FILING DATE: 1999-04-16  
; NUMBER OF SEQ ID NOS: 102  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 96  
; LENGTH: 87  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-990-586-96

Query Match 96.7%; Score 434; DB 11; Length 87;  
Best Local Similarity 97.7%; Pred. No. 2.9e-36;  
Matches 85; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 1 QIQLVQSGGEVKKPGASVRVSCKASGYSTFWRSQPKGLEWIGKATLTVDKSTSTAYME 60  
DB 1 QIQLVQSGPELVKPGASVRVSCKASGYSTFWRSQPKGLEWIGKATLTVDKSTSTAYME 60  
  
QY 61 LSSLRSEDTAVYFCARWGQGTITVSS 87  
DB 61 LSSLRSEDTAVYFCARWGQGTITVSS 87

## RESULT 12

US-10-230-880-96  
; Sequence 96, Application US/10230880  
; Publication No. US20030190705A1  
; GENERAL INFORMATION:  
; APPLICANT: WONG, HING C.  
; APPLICANT: STINSON, JEFFREY L.  
; APPLICANT: MOSQUERA, LUIS A.  
; TITLE OF INVENTION: METHOD OF HUMANIZING IMMUNE SYSTEM MOLECULES  
; FILE REFERENCE: 71758/58066  
; CURRENT APPLICATION NUMBER: US/10/230,880  
; CURRENT FILING DATE: 2002-12-23  
; PRIOR APPLICATION NUMBER: 09/990,586  
; PRIOR FILING DATE: 2001-11-21  
; PRIOR APPLICATION NUMBER: 60/343,306  
; PRIOR FILING DATE: 2001-10-29  
; PRIOR APPLICATION NUMBER: 09/293,854  
; PRIOR FILING DATE: 1999-04-16  
; NUMBER OF SEQ ID NOS: 174  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 96  
; LENGTH: 87  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-230-880-96

Query Match 96.7%; Score 434; DB 12; Length 87;  
Best Local Similarity 97.7%; Pred. No. 2.9e-36;  
Matches 85; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 1 QIQLVQSGGEVKKPGASVRVSCKASGYSTFWRSQPKGLEWIGKATLTVDKSTSTAYME 60  
DB 1 QIQLVQSGPELVKPGASVRVSCKASGYSTFWRSQPKGLEWIGKATLTVDKSTSTAYME 60  
  
QY 61 LSSLRSEDTAVYFCARWGQGTITVSS 87  
DB 61 LSSLRSEDTAVYFCARWGQGTITVSS 87

## RESULT 13

US-09-990-586-95  
; Sequence 95, Application US/09990586  
; Publication No. US20030109680A1  
; GENERAL INFORMATION:  
; APPLICANT: JIAO, JIN-AN  
; APPLICANT: WONG, HING C.  
; TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD COAGULATION AND METHODS  
; FILE REFERENCE: 71758/46943-CIP2  
; CURRENT APPLICATION NUMBER: US/09/990,586  
; CURRENT FILING DATE: 2001-11-21  
; PRIOR APPLICATION NUMBER: 09/293,854  
; PRIOR FILING DATE: 1999-04-16  
; NUMBER OF SEQ ID NOS: 102  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 95  
; LENGTH: 87  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-990-586-95

Query Match 96.0%; Score 431; DB 11; Length 87;  
Best Local Similarity 96.6%; Pred. No. 5.7e-36;  
Matches 84; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
  
QY 1 QIQLVQSGGEVKKPGASVRVSCKASGYSTFWRSQPKGLEWIGKATLTVDKSTSTAYME 60  
DB 1 QIQLVQSGPELVKPGASVRVSCKASGYSTFWRSQPKGLEWIGKATLTVDKSTSTAYME 60  
  
QY 61 LSSLRSEDTAVYFCARWGQGTITVSS 87  
DB 61 LSSLRSEDTAVYFCARWGQGTITVSS 87

Db 61 LSSLRSEDTAVYFCARWGQTTVTSS 87

Search completed: January 13, 2004, 13:13:43  
Job time : 13.9048 secs

Db 61 LSSLRSEDTAVYFCARWGQTTVTSS 87

## RESULT 14

US-10-230-880-95  
; Sequence 95, Application US/10230880  
; Publication No. US20030190705A1  
; GENERAL INFORMATION:  
; APPLICANT: WONG, HING C.  
; APPLICANT: STINSON, JEFFREY L.  
; APPLICANT: MOSQUERA, LUIS A.  
; TITLE OF INVENTION: METHOD OF HUMANIZING IMMUNE SYSTEM MOLECULES  
; FILE REFERENCE: 71758/58066  
; CURRENT APPLICATION NUMBER: US/10/230,880  
; CURRENT FILING DATE: 2002-12-23  
; PRIOR APPLICATION NUMBER: 09/990,586  
; PRIOR FILING DATE: 2001-11-21  
; PRIOR APPLICATION NUMBER: 60/343,306  
; PRIOR FILING DATE: 2001-10-29  
; PRIOR APPLICATION NUMBER: 09/293,854  
; PRIOR FILING DATE: 1999-04-16  
; NUMBER OF SEQ ID NOS: 174  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 95  
; LENGTH: 87  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-230-880-95

Query Match 96.0%; Score 431; DB 12; Length 87;  
Best Local Similarity 96.6%; Pred. No. 5.7e-36;  
Matches 84; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QIQLVSGGVKPGASVRVSKASGYSTWVRSQPGKLEWIGKATLTVDKSTSTAYME 60  
DB 1 QIQLVSGPELVKPGASVRVSKASGYSTWVRSQPGKLEWIGKATLTVDKSTSTAYME 60

QY 61 LSSLRSEDTAVYFCARWGQTTVTSS 87  
DB 61 LSSLRSEDTAVYFCARWGQTTVTSS 87

## RESULT 15

US-09-990-586-89  
; Sequence 89, Application US/09990586  
; Publication No. US20030109680A1  
; GENERAL INFORMATION:  
; APPLICANT: JIAO, JIN-AN  
; APPLICANT: WONG, HING C.  
; TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD COAGULATION AND METHODS  
; TITLE OF INVENTION: OF USE THEREOF  
; FILE REFERENCE: 71758/46943-CIP2  
; CURRENT APPLICATION NUMBER: US/09/990,586  
; CURRENT FILING DATE: 2001-11-21  
; PRIOR APPLICATION NUMBER: 09/293,854  
; PRIOR FILING DATE: 1999-04-16  
; NUMBER OF SEQ ID NOS: 102  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 89  
; LENGTH: 87  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-990-586-89

Query Match 95.8%; Score 430; DB 11; Length 87;  
Best Local Similarity 95.4%; Pred. No. 7.2e-36;  
Matches 83; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 QIQLVSGGVKPGASVRVSKASGYSTWVRSQPGKLEWIGKATLTVDKSTSTAYME 60  
DB 1 QMQLQSGGELVKPGASVRVSKASGYSTWVRSQPGKLEWIGKATLTVDKSTSTAYME 60

QY 61 LSSLRSEDTAVYFCARWGQTTVTSS 87



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OM protein - protein search, using sw model

Run on: January 13, 2004, 12:33:50 ; Search time 7.52227 Seconds  
(without alignments)  
489.353 Million cell updates/sec

Title: US-09-990-586-91

Perfect score: 449

Sequence: 1 QIQLVSGGVBKPKGASVRV.....DTAVYFCARWGQTTVTSS 87

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 4231058 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.\*

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- 2: /cgm2\_6/ptodata/1/iaa/5B\_COMB.pep.\*
- 3: /cgm2\_6/ptodata/1/iaa/6A\_COMB.pep.\*
- 4: /cgm2\_6/ptodata/1/iaa/6B\_COMB.pep.\*
- 5: /cgm2\_6/ptodata/1/iaa/PTCUS\_COMB.pep.\*
- 6: /cgm2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	386	86.0	87	1	US-08-497-312-16
2	370	82.4	117	4	US-08-525-539A-78
3	370	82.4	136	4	US-08-525-539A-63
4	364.5	81.2	86	1	US-08-497-312-27
5	363.5	81.0	116	1	US-08-690-102A-8
6	363.5	81.0	116	3	US-09-137-902-8
7	363.5	81.0	116	3	US-09-155-107-8
8	363.5	81.0	116	5	PT-US95-09641-8
9	363.5	81.0	135	1	US-08-137-117D-102
10	363.5	81.0	135	2	US-08-436-717-102
11	363.5	81.0	139	4	US-09-355-925-7
12	363.5	81.0	139	4	US-09-355-925-8
13	362.5	80.7	116	2	US-08-561-521-41
14	362.5	80.7	116	5	PT-US95-01219-41
15	360	80.2	119	1	US-08-498-516-10
16	360	80.2	136	4	US-09-450-520A-8
17	360	80.2	222	1	US-08-458-516-22
18	360	80.2	235	1	US-08-458-516-23
19	360	80.2	449	1	US-08-458-516-13
20	359.5	80.1	116	1	US-07-634-278-5
21	359.5	80.1	116	1	US-07-634-278-57
22	359.5	80.1	116	1	US-07-634-278-73
23	359.5	80.1	116	1	US-08-477-728-5
24	359.5	80.1	116	1	US-08-477-728-57
25	359.5	80.1	116	1	US-08-477-728-73
26	359.5	80.1	116	1	US-08-474-040-5
27	359.5	80.1	116	1	US-08-474-040-57

28	359.5	80.1	116	1	US-08-474-040-73	Sequence 73, Appl
29	359.5	80.1	116	1	US-08-487-200-5	Sequence 5, Appl
30	359.5	80.1	116	1	US-08-487-200-57	Sequence 57, Appl
31	359.5	80.1	116	1	US-08-487-200-73	Sequence 73, Appl
32	359.5	80.1	116	1	US-08-488-113B-169	Sequence 169, App
33	359.5	80.1	116	1	US-08-477-484B-169	Sequence 169, App
34	359.5	80.1	116	1	US-08-107-669D-55	Sequence 55, Appl
35	359.5	80.1	116	1	US-08-472-788A-86	Sequence 86, Appl
36	359.5	80.1	116	2	US-08-477-531B-55	Sequence 55, Appl
37	359.5	80.1	116	2	US-08-646-360-169	Sequence 169, App
38	359.5	80.1	116	2	US-08-082-842A-86	Sequence 86, Appl
39	359.5	80.1	116	3	US-08-934-841-1	Sequence 1, Appl
40	359.5	80.1	116	3	US-09-393-409-1	Sequence 1, Appl
41	359.5	80.1	116	3	US-08-839-785-169	Sequence 169, App
42	359.5	80.1	116	3	US-09-136-389-169	Sequence 169, App
43	359.5	80.1	116	3	US-08-484-537-5	Sequence 5, Appl
44	359.5	80.1	116	3	US-08-484-537-57	Sequence 57, Appl
45	359.5	80.1	116	3	US-08-484-537-73	Sequence 73, Appl

ALIGNMENTS

RESULT 1

US-08-497-312-16  
; Sequence 16, Application US/08497312  
; Patent No. 5712120  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: Method for obtaining modified  
; TITLE OF INVENTION: immunoglobulins with reduced immunogenicity of murine  
; TITLE OF INVENTION: antibody variable domains, compositions containing them.  
; NUMBER OF SEQUENCES: 31  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: CENTRO DE INMUNOLOGIA MOLECULAR  
; STREET: 215 Y 15, ATABEY PLAYA  
; CITY: HAVANA  
; STATE:  
; COUNTRY: CUBA  
; ZIP: 11600  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/497,312  
; FILING DATE: 30-JUN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: CU 80/94  
; FILING DATE: 30-JUN-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BOND, LAURENCE B.  
; REGISTRATION NUMBER: 30,549  
; REFERENCE/DOCKET NUMBER: 2629US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 801/532-1922  
; TELEFAX: 801/531-9168  
; TELEX: 388961 1PM04UT  
; INFORMATION FOR SEQ ID NO: 16:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 87 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: NO  
; US-08-497-312-16

Query Match 86.0%; Score 386; DB 1; Length 87;  
Best Local Similarity 81.6%; Pred. No. 2.6e-33;  
Matches 71; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

QY 1 QIQLVQSGGEVKPGASVRSCKASGYSTFWRSQPGKLEWIKATLVDKSTSTAYME 60  
 Db 1 QVQLVQSGAEVKPGASVRSCKASGYTFNWRQAPGQGLEWVRGRTVTRTSTSTAYME 60  
 QY 61 LSSLRSSEDTAVYFCARWGQGTITVSS 87  
 Db 61 LSSLRSSEDTAVYFCARWGQGTITVSS 87

## RESULT 2

US-08-525-539A-78  
 ; Sequence 78, Application US/08525539A  
 ; Patent No. 6309636  
 ; GENERAL INFORMATION:  
 ; APPLICANT: DO COUTO, FERNANDO J.R.  
 ; APPLICANT: CERIANI, ROBERTO L.  
 ; APPLICANT: PETERSON, JERRY A.  
 ; TITLE OF INVENTION: RECOMBINANT PEPTIDES DERIVED FROM THE  
 ; TITLE OF INVENTION: MC3 ANTI-BA46 ANTIBODY, METHODS OF USE THEREOF, AND  
 ; TITLE OF INVENTION: METHODS OF HUMANIZING ANTIBODY PEPTIDES  
 ; NUMBER OF SEQUENCES: 81  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: MORRISON & FOERSTER  
 ; STREET: 755 Page Mill Road  
 ; CITY: Palo Alto  
 ; STATE: CA  
 ; COUNTRY: USA  
 ; ZIP: 94304-1018  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent in Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; FILING DATE: 14-SEP-1995  
 ; APPLICATION NUMBER: US/08/525,539A  
 ; CLASSIFICATION: 424  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: DYLAN, TYLER  
 ; REGISTRATION NUMBER: 37,612  
 ; REFERENCE/DOCKET NUMBER: 27633-20001.21  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (415) 813-5600  
 ; TELEFAX: (415) 494-0792  
 ; TELEX: 706141  
 ; INFORMATION FOR SEQ ID NO: 78:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 117 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; US-08-525-539A-78

Query Match 82.4%; Score 370; DB 4; Length 117;  
 Best Local Similarity 67.5%; Pred. No. 1.7e-3;  
 Matches 79; Conservative 4; Mismatches 4; Indels 30; Gaps 3;  
 QY 1 QIQLVQSGGEVKPGASVRSCKASGYSTFWRSQPGKLEWIKATLVDKSTSTAYME 44  
 Db 1 EVQLVQSGAEVKPGASVRSCKASGYSTFGYTHHWKQSPGMNLEWIGLINPYNGTIVY 60  
 QY 45 -----KATLVDKSTSTAYMELSSLRSEDTAVYFCAR-----WGQGTITVSS 87  
 Db 61 NQKFDKATLVDKSTSTAYMELSSLRSEDTAVYFCARRWRYTMDYWGQGTITVSS 117

## RESULT 3

US-08-525-539A-63  
 ; Sequence 63, Application US/08525539A  
 ; Patent No. 6309636  
 ; GENERAL INFORMATION:  
 ; APPLICANT: DO COUTO, FERNANDO J.R.  
 ; APPLICANT: CERIANI, ROBERTO L.

APPLICANT: PETERSON, JERRY A.  
 ; TITLE OF INVENTION: RECOMBINANT PEPTIDES DERIVED FROM THE  
 ; TITLE OF INVENTION: MC3 ANTI-BA46 ANTIBODY, METHODS OF USE THEREOF, AND  
 ; TITLE OF INVENTION: METHODS OF HUMANIZING ANTIBODY PEPTIDES  
 ; NUMBER OF SEQUENCES: 81  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: MORRISON & FOERSTER  
 ; STREET: 755 Page Mill Road  
 ; CITY: Palo Alto  
 ; STATE: CA  
 ; COUNTRY: USA  
 ; ZIP: 94304-1018  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent in Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; FILING DATE: 14-SEP-1995  
 ; APPLICATION NUMBER: US/08/525,539A  
 ; CLASSIFICATION: 424  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: DYLAN, TYLER  
 ; REGISTRATION NUMBER: 37,612  
 ; REFERENCE/DOCKET NUMBER: 27633-20001.21  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (415) 813-5600  
 ; TELEFAX: (415) 494-0792  
 ; TELEX: 706141  
 ; INFORMATION FOR SEQ ID NO: 63:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 136 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; US-08-525-539A-63

Query Match 82.4%; Score 370; DB 4; Length 136;  
 Best Local Similarity 67.5%; Pred. No. 2e-31;  
 Matches 79; Conservative 4; Mismatches 4; Indels 30; Gaps 3;  
 QY 1 QIQLVQSGGEVKPGASVRSCKASGYSTFWRSQPGKLEWIKATLVDKSTSTAYME 44  
 Db 20 EVQLVQSGAEVKPGASVRSCKASGYSTFGYTHHWKQSPGMNLEWIGLINPYNGTIVY 79  
 QY 45 -----KATLVDKSTSTAYMELSSLRSEDTAVYFCAR-----WGQGTITVSS 87  
 Db 80 NQKFDKATLVDKSTSTAYMELSSLRSEDTAVYFCARRWRYTMDYWGQGTITVSS 136

RESULT 4  
 US-08-497-312-27  
 ; Sequence 27, Application US/08497312  
 ; Patent No. 5712120  
 ; GENERAL INFORMATION:  
 ; APPLICANT:  
 ; TITLE OF INVENTION: Method for obtaining modified  
 ; TITLE OF INVENTION: immunoglobulins with reduced immunogenicity of murine  
 ; TITLE OF INVENTION: antibody variable domains, compositions containing them.  
 ; NUMBER OF SEQUENCES: 31  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: CENTRO DE INMUNOLOGIA MOLECULAR  
 ; STREET: 215 y 15, ATABEY PLAYA  
 ; CITY: HAVANA  
 ; STATE:  
 ; COUNTRY: CUBA  
 ; ZIP: 11600  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)  
 ; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/497,312  
FILING DATE: 30-JUN-1995  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: CU 80/94  
FILING DATE: 30-JUN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: BOND, LAURENCE B.  
REGISTRATION NUMBER: 30,549  
REFERENCE/DOCKET NUMBER: 2629US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 801/532-1922  
TELEFAX: 801/531-9168  
TELEX: 388961 LPMO4UT  
INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 86 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
US-08-497-312-27

Query Match 81.2%; Score 364.5; DB 1; Length 86;  
Best Local Similarity 79.3%; Pred. No. 4,4e-31;  
Matches 69; Conservative 10; Mismatches 7; Indels 1; Gaps 1;  
QY 1 QIQLVQSGGEVKKPGASVRVSKASGYFTWVRQSPGKGLWIGKATLTVDKSTSTAYME 60  
DB 1 QVOLVQSGAEVKKPGASLKVSKASGY-FTWVRQAPGQRLEWVGRTITRDTASTAYME 59  
QY 61 LSSLRSDETAVYFCARWGCGTTVTSS 87  
DB 60 LSSLRSDETAVYFCARWGEGTLTVTSS 86

## RESULT 5

US-08-690-102A-8  
Sequence 8, Application US/08690102A  
Patent No. 5789554  
GENERAL INFORMATION:  
APPLICANT: LEUNG, Shui-on  
TITLE OF INVENTION: IMMUNOCONJUGATES AND HUMANIZED  
NUMBER OF SEQUENCES: 21  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington, D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/690,102A  
FILING DATE: 01-JUL-1996  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/289,576  
FILING DATE: 12-AUG-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: SAXE, Bernhard D.  
REGISTRATION NUMBER: 28,665  
REFERENCE/DOCKET NUMBER: 18733/463/IMIN  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 9041136  
INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:  
LENGTH: 116 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-690-102A-8

Query Match 81.0%; Score 363.5; DB 1; Length 116;  
Best Local Similarity 64.7%; Pred. No. 7.8e-31;  
Matches 75; Conservative 9; Mismatches 3; Indels 29; Gaps 3;  
QY 1 QIQLVQSGGEVKKPGASVZVSKASGYFT-----WVROSPGKGLWIG----- 44  
DB 1 QVOLVQSGAEVKKPGSSVKVSKASGYFTSTWLHWVRQAPGQGLWIGYINPRNDYTY 60  
QY 45 -----KATLTVDKSTSTAYMELSLRSDETAVYFCAR-----WGQFTTVTVSS 87  
DB 61 NQNFKDKAITADESINTAYMELSLRSDETAFYFCARRDITTFYWGQGTIVTVSS 116

## RESULT 6

US-09-127-902-8  
Sequence 8, Application US/09127902  
Patent No. 6187287  
GENERAL INFORMATION:  
APPLICANT: LEUNG, Shui-on  
TITLE OF INVENTION: IMMUNOCONJUGATES AND HUMANIZED  
NUMBER OF SEQUENCES: 21  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington, D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/127,902  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/690,102  
FILING DATE: 01-JUL-1996  
APPLICATION NUMBER: US 08/289,576  
FILING DATE: 12-AUG-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: SAXE, Bernhard D.  
REGISTRATION NUMBER: 28,665  
REFERENCE/DOCKET NUMBER: 18733/463/IMIN  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 9041136  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 116 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-127-902-8  
Query Match 81.0%; Score 363.5; DB 3; Length 116;  
Best Local Similarity 64.7%; Pred. No. 7.8e-31;  
Matches 75; Conservative 9; Mismatches 3; Indels 29; Gaps 3;  
QY 1 QIQLVQSGGEVKKPGASVRVSKASGYFT-----WVROSPGKGLWIG----- 44  
DB 1 QVOLVQSGAEVKKPGSSVKVSKASGYFTSTWLHWVRQAPGQGLWIGYINPRNDYTY 60

QY 45 -----KATLVKSTSTAYMELSSLRSDTAVYFCAR-----WGQGTIVTVSS 87  
 DB 61 NQNFKATITADESTNTAYMELSSLRSDTAVYFCARRDITTFYWGQGTIVTVSS 116

RESULT 7  
 US-09-155-107-8  
 ; Sequence 8, Application US/09155107  
 ; Patent No. 6254868  
 ; GENERAL INFORMATION:  
 ; APPLICANT: LEUNG, Shui-on  
 ; APPLICANT: HANSEN, Hans  
 ; APPLICANT: QU, Zhengxing  
 ; TITLE OF INVENTION: GLYCOSYLATED HUMANIZED B-CELL SPECIFIC ANTIBODIES  
 ; FILE REFERENCE: 018733/0879  
 ; CURRENT APPLICATION NUMBER: US/09/155,107  
 ; CURRENT FILING DATE: 1998-11-17  
 ; EARLIER APPLICATION NUMBER: WO PCT/US97/04196  
 ; EARLIER FILING DATE: 1997-03-19  
 ; EARLIER APPLICATION NUMBER: US 60/013,709  
 ; EARLIER FILING DATE: 1996-03-20  
 ; NUMBER OF SEQ ID NOS: 47  
 ; SOFTWARE: Patent in Ver. 2.0  
 ; SEQ ID NO 8  
 ; LENGTH: 116  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-155-107-8

Query Match 81.0%; Score 363.5; DB 3; Length 116;  
 Best Local Similarity 64.7%; Pred. No. 7.8e-31;  
 Matches 75; Conservative 9; Mismatches 3; Indels 29; Gaps 3;

QY 1 QIQLVQSGGEVKKPGASVRSCKASGYSTFTSYHLHWVRQAPGGQLEWIGVINPRNDYTEY 44  
 DB 1 QVQLVQSGAEVKKPGSSVKVSKASGYSTFTSYHLHWVRQAPGGQLEWIGVINPRNDYTEY 60

QY 45 -----KATLVKSTSTAYMELSSLRSDTAVYFCAR-----WGQGTIVTVSS 87  
 DB 61 NQNFKATITADESTNTAYMELSSLRSDTAVYFCARRDITTFYWGQGTIVTVSS 116

RESULT 8  
 PCT-US95-09641-8  
 ; Sequence 8, Application PC/TUS9509641  
 ; GENERAL INFORMATION:  
 ; APPLICANT:  
 ; TITLE OF INVENTION: IMMUNOCONJUGATES AND HUMANIZED  
 ; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR B-CELL LYMPHOMA AND LEUKEMIA CELLS  
 ; NUMBER OF SEQUENCES: 21  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent in Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: PCT/US95/09641  
 ; FILING DATE: 11-AUG-1995  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/289,576  
 ; FILING DATE: 12-AUG-1994  
 ; INFORMATION FOR SEQ ID NO: 8:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 116 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 PCT-US95-09641-8

Query Match 81.0%; Score 363.5; DB 5; Length 116;  
 Best Local Similarity 64.7%; Pred. No. 7.8e-31;  
 Matches 75; Conservative 9; Mismatches 3; Indels 29; Gaps 3;

QY 1 QIQLVQSGGEVKKPGASVRSCKASGYSTFTSYHLHWVRQAPGGQLEWIGVINPRNDYTEY 44  
 DB 1 QVQLVQSGAEVKKPGSSVKVSKASGYSTFTSYHLHWVRQAPGGQLEWIGVINPRNDYTEY 60

QY 45 -----KATLVKSTSTAYMELSSLRSDTAVYFCAR-----WGQGTIVTVSS 87  
 DB 61 NQNFKATITADESTNTAYMELSSLRSDTAVYFCARRDITTFYWGQGTIVTVSS 116

RESULT 9  
 US-08-137-117D-102  
 ; Sequence 102, Application US/08137117D  
 ; Patent No. 5795965  
 ; GENERAL INFORMATION:  
 ; APPLICANT: TSUCHIYA, Masayuki  
 ; APPLICANT: SATO, Koh  
 ; APPLICANT: BENDIG, Mary  
 ; APPLICANT: JONES, Steven  
 ; APPLICANT: SALDANHA, Jose  
 ; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN  
 ; TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR  
 ; NUMBER OF SEQUENCES: 158  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Foley & Lardner  
 ; STREET: 3000 K Street, N.W., Suite 500  
 ; CITY: Washington  
 ; STATE: D.C.  
 ; COUNTRY: USA  
 ; ZIP: 20007-5109  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent in Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/137,117D  
 ; FILING DATE: 20-DEC-1993  
 ; CLASSIFICATION: 530  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: WO PCT/JPS92/00544  
 ; FILING DATE: 24-APR-1992  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: JP 4-32084  
 ; FILING DATE: 19-FEB-1992  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: JP 3-95476  
 ; FILING DATE: 25-APR-1991  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: WEGNER, Harold C.  
 ; REGISTRATION NUMBER: 25,258  
 ; REFERENCE/DOCKET NUMBER: 53466/126/AAOK  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (202)672-5300  
 ; TELEFAX: (202)672-5399  
 ; TELEX: 904136  
 ; INFORMATION FOR SEQ ID NO: 102:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 135 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-08-137-117D-102

Query Match 81.0%; Score 363.5; DB 1; Length 135;  
 Best Local Similarity 65.5%; Pred. No. 9.2e-31;  
 Matches 76; Conservative 7; Mismatches 4; Indels 29; Gaps 3;

QY 1 QIQLVQSGGEVKKPGASVRSCKASGYSTFTSYHLHWVRQAPGGQLEWIGVINPRNDYTEY 43  
 DB 20 QVQLVQSGAEVKKPGSSVKVSKASGYSTFTSYHLHWVRQAPGGQLEWIGVINPRNDYTEY 79

QY 44 -----GKATLVKSTSTAYMELSSLRSDTAVYFCAR-----WGQGTIVTVSS 87

Db 80 NQKFKGKVTMTVDTSTNTAYMELSLRSEDVAVYCARGNRFAYWGQGLTVTVSS 135

## RESULT 10

US-08-436-717-102  
; Sequence 102, Application US/08436717  
; Patent No. 5817790  
; GENERAL INFORMATION:  
; APPLICANT: TSUCHIYA, Masayuki  
; APPLICANT: SATO, Koh  
; APPLICANT: BENDIG, Mary  
; APPLICANT: JONES, Steven  
; APPLICANT: SALDANA, Jose  
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN  
; TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR  
; NUMBER OF SEQUENCES: 158  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20007-5109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/436,717  
; FILING DATE:  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/137,117  
; FILING DATE: 20-DEC-1993  
; APPLICATION NUMBER: WO PCT/JP92/00544  
; FILING DATE: 24-APR-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 4-32084  
; FILING DATE: 19-FEB-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 3-95476  
; FILING DATE: 25-APR-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: WEGNER, Harold C.  
; REGISTRATION NUMBER: 25,258  
; REFERENCE/DOCKET NUMBER: 53466/126/AAOK  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)672-5300  
; TELEFAX: (202)672-5399  
; TELEX: 904136  
; INFORMATION FOR SEQ ID NO: 102:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 135 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-436-717-102

Query Match 81.0%; Score 363.5; DB 2; Length 135;  
Best Local Similarity 65.5%; Pred. No. 9.2e-31;  
Matches 76; Conservative 7; Mismatches 4; Indels 29; Gaps 3;

QY 1 QIQLVQSGGEVKKPGASVRVSKASGYST-----WVRQSPGKGLEW----- 43

Db 20 QVQLVQSGAEVKKPGASVKVSKASGYSTFYIHVVRQAPGQGLEWIGYIDPENGQTSY 79

QY 44 -----GKATLVDKSTSTAYMELSLRSEDVAVFCAR-----WGQGTIVTVSS 87

Db 80 NQKFKGKVTMTVDTSTNTAYMELSLRSEDVAVYCARGNRFAYWGQGLTVTVSS 135

## RESULT 11

US-09-355-925-7  
; Sequence 7, Application US/09355925  
; Patent No. 6503510  
; GENERAL INFORMATION:  
; APPLICANT: KOISHIHARA, YASUO  
; APPLICANT: YOSHIMURA, YASUSHI  
; TITLE OF INVENTION: THERAPEUTIC AGENT FOR LYMPHATIC TUMORS  
; FILE REFERENCE: 053466/0255  
; CURRENT APPLICATION NUMBER: US/09/355,925  
; CURRENT FILING DATE: 1999-08-11  
; PRIOR APPLICATION NUMBER: PCT/JP98/00568  
; PRIOR FILING DATE: 1998-02-12  
; PRIOR APPLICATION NUMBER: JP 9-41410  
; PRIOR FILING DATE: 1997-02-12  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 7  
; LENGTH: 139  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Amino acid  
; OTHER INFORMATION: sequence of H chain V region version r of  
; OTHER INFORMATION: humanized anti-HM1.24 antibody  
US-09-355-925-7

Query Match 81.0%; Score 363.5; DB 4; Length 139;  
Best Local Similarity 62.5%; Pred. No. 9.5e-31;  
Matches 75; Conservative 9; Mismatches 3; Indels 33; Gaps 3;

QY 1 QIQLVQSGGEVKKPGASVRVSKASGYST-----WVRQSPGKGLEW----- 43

Db 20 QVQLVQSGAEVKKPGASVKVSKASGYTFPYMQWVRQAPGQGLEWMSIFPGDGDTY 79

QY 44 -----GKATLVDKSTSTAYMELSLRSEDVAVFCAR-----WGQGTIVTVSS 87

Db 80 SQKFKGRVTMTADKSTSTAYMELSLRSEDVAVYCARGLRGGYFDYWGQGTIVTVSS 139

## RESULT 12

US-09-355-925-8  
; Sequence 8, Application US/09355925  
; Patent No. 6503510  
; GENERAL INFORMATION:  
; APPLICANT: KOISHIHARA, YASUO  
; APPLICANT: YOSHIMURA, YASUSHI  
; TITLE OF INVENTION: THERAPEUTIC AGENT FOR LYMPHATIC TUMORS  
; FILE REFERENCE: 053466/0255  
; CURRENT APPLICATION NUMBER: US/09/355,925  
; CURRENT FILING DATE: 1999-08-11  
; PRIOR APPLICATION NUMBER: PCT/JP98/00568  
; PRIOR FILING DATE: 1998-02-12  
; PRIOR APPLICATION NUMBER: JP 9-41410  
; PRIOR FILING DATE: 1997-02-12  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 8  
; LENGTH: 139  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Amino acid  
; OTHER INFORMATION: sequence H chain V region version s of  
; OTHER INFORMATION: anti-HM1.24 antibody  
US-09-355-925-8

Query Match 81.0%; Score 363.5; DB 4; Length 139;  
Best Local Similarity 62.5%; Pred. No. 9.5e-31;  
Matches 75; Conservative 9; Mismatches 3; Indels 33; Gaps 3;

QY 1 QIQLVQSGGEVKKPGASVRVSKASGYST-----WVRQSPGKGLEW----- 43

```
Db 20 QVQLVQSGAEVKKPGASVKSCASGYTFPTYNMQWVRQAPQGQLEWNGSIFFGQGDTRY 79
Qy 44 -----GKATLTVDKSTSTAYMELSLRSEDATVYFCAR-----WGQGTIVTVSS 87
Db 80 SQKFKGRVTITADKSTSTAYMELSLRSEDATVYFCARGLRGGYFDYWGQGTIVTVSS 139

RESULT 13
US-08-561-521-41
; Sequence 41, Application US/08561521
; Patent No. 5840299
; GENERAL INFORMATION:
; APPLICANT: Bendig, Mary M.
; APPLICANT: Leger, Olivier J.
; APPLICANT: Saldanha, Jose
; APPLICANT: Jones, S. Tarran
; TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
; TITLE OF INVENTION: Adhesion Molecule VLA-4
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/561,521
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/186,269A
; FILING DATE: 25-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William L.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15270-14
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-543-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 116 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US95-521-41

Query Match 80.7%; Score 362.5; DB 2; Length 116;
Best Local Similarity 64.7%; Pred. No. 9.9e-31;
Matches 75; Conservative 8; Mismatches 4; Indels 29; Gaps 3;

Qy 1 QIQLVQSGGEVKKPGASVRVSCKASGYST-----WYRQSPGKGLW-----43
Db 1 QVQLVQSGAEVKKPGASVKSCASGYSTSYTHWVRQAPQGQLEWGVDPNGGTSY 60
Qy 44 -----GKATLTVDKSTSTAYMELSLRSEDATVYFCAR-----WGQGTIVTVSS 87
Db 61 NQKFKGVTMTVDSTNTAYMELSLRSEDATVYFCARGNRFAYWGQGLTVTVSS 116

RESULT 14
PCT-US95-01219-41
; Sequence 41, Application PC/TUS9501219
; GENERAL INFORMATION:
; APPLICANT: Bendig, Mary M.
; APPLICANT: Leger, Olivier J.
```

```
APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/01219
FILING DATE: 25-JAN-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/186,269
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15270-14
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-01219-41

Query Match 80.7%; Score 362.5; DB 5; Length 116;
Best Local Similarity 64.7%; Pred. No. 9.9e-31;
Matches 75; Conservative 8; Mismatches 4; Indels 29; Gaps 3;

Qy 1 QIQLVQSGGEVKKPGASVRVSCKASGYST-----WYRQSPGKGLW-----43
Db 1 QVQLVQSGAEVKKPGASVKSCASGYSTSYTHWVRQAPQGQLEWGVDPNGGTSY 60
Qy 44 -----GKATLTVDKSTSTAYMELSLRSEDATVYFCAR-----WGQGTIVTVSS 87
Db 61 NQKFKGVTMTVDSTNTAYMELSLRSEDATVYFCARGNRFAYWGQGLTVTVSS 116

RESULT 15
US-08-458-516-10
; Sequence 10, Application US/08458516
; Patent No. 577085
; GENERAL INFORMATION:
; APPLICANT: Co, Man Sung
; APPLICANT: Tso, J. Yun
; TITLE OF INVENTION: Humanized Antibodies Reactive with
; TITLE OF INVENTION: GPIIb/IIIa
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: William M. Smith
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.125  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/458,516  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/059,159  
FILING DATE: 03-MAY-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 11823-37-3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-326-2400  
TELEFAX: 415-326-2422  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: N-terminal fragment  
US-08-458-516-10

Query Match 80.2%; Score 360; DB 1; Length 119;  
Best Local Similarity 63.0%; Pred. No. 1.9e-30;  
Matches 75; Conservative 9; Mismatches 3; Indels 32; Gaps 3;  
QY 1 QIQLVQSGGEVVKPGASVRSCKASGYST-----WYRQSPKGLW----- 43  
Db 1 QVQLVQSGAEVVKPGSSVKVSKASGYFTNYLIEWVRQAPGQGLEWIGVYPGSGGTNY 60  
QY 44 -----GKATLTVDKSTSTAYMELSLRSEDYAVYFCAR-----WQGGTIVTVSS 87  
Db 61 NEKFKGRVTLTVDESTNTAYMELSLRSEDYAVYFCARRDGNYGWFAYWGQGLTVTVSS 119

Search completed: January 13, 2004, 12:46:33  
Job time : 8.52227 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 13, 2004, 12:22:35 ; Search time 7.75633 Seconds  
(without alignments)  
1326.664 Million cell updates/sec

Title: US-09-990-586-97  
Perfect score: 553  
Sequence: 1 RTVAAPSVFIFPPSDEQLKLS.....EVTHQGLSSPVTKSFNRGEC 107

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues  
Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_76:.\*  
1: PIR1:.\*  
2: PIR2:.\*  
3: PIR3:.\*  
4: PIR4:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	553	100.0	215	2 JE0244	Ig kappa chain NIG
2	553	100.0	215	2 JE0242	Ig kappa chain NIG
3	553	100.0	215	2 JE0243	Ig kappa chain NIG
4	550	99.5	135	2 S52059	JC-kappa protein -
5	548	99.1	106	1 K3HU	Ig kappa chain C r
6	537	97.1	216	2 JE0241	Ig kappa chain Am3
7	520	94.0	215	2 A23746	Ig kappa chain V-I
8	513	92.8	99	2 A37927	Ig kappa chain C r
9	507	91.7	99	2 S26653	Ig kappa chain C r
10	372	67.3	240	2 S04084	Ig kappa chain pre
11	367	66.4	106	1 K1RTB	Ig kappa chain C r
12	366	66.2	178	2 PT0219	Ig kappa chain V-C
13	359	64.9	106	1 K1RTA	Ig kappa chain C r
14	358	64.7	217	2 S42772	Ig kappa chain - m
15	358	64.7	218	2 S68241	Ig kappa chain V r
16	358	64.7	219	2 S38865	Ig kappa chain - m
17	352	63.7	218	2 JC5810	monoclonal antibody
18	352	63.7	219	2 FC4203	Ig kappa chain (mo
19	352	63.7	219	2 S16112	Ig kappa chain V r
20	352	63.7	219	2 S52028	Ig kappa chain - m
21	352	63.7	220	2 A31790	Ig kappa chain V r
22	352	63.7	225	2 S37484	Ig kappa chain - m
23	352	63.7	234	2 S14237	Ig kappa chain pre
24	352	63.7	234	2 S01320	Ig kappa chain pre
25	352	63.7	235	2 S25058	Ig kappa chain - m
26	350	63.3	106	1 K1MS	Ig kappa chain C r
27	350	63.3	126	2 I54782	gene Pvt-1a/Ig-Ck
28	348	62.9	225	2 JLO029	Ig kappa chain pre
29	345	62.4	230	2 S33161	Ig kappa chain - s

Ig kappa chain (Ma  
Ig kappa chain V r  
Ig kappa-B4 chain  
Ig kappa-2 chain C  
Ig kappa chain pre  
Ig kappa-B4 chain  
Ig kappa-1 chain C  
Ig kappa-B9 chain  
Ig lambda-like cha  
Ig kappa chain C r  
Ig l1 chain J-C re  
Ig lambda chain C  
Ig light chain pre  
Ig light chain C r  
Ig kappa-B5 chain  
Ig kappa chain (WM

ALIGNMENTS

RESULT 1  
JE0244  
Ig kappa chain NIG2 precursor - human  
C:Species: Homo sapiens (man)  
C:Date: 05-Dec-1998 #sequence\_revision 05-Dec-1998 #text\_change 21-Jan-2000  
C:Accession: JE0244  
R:Alim, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Kazi, H.;  
submitted to JIPID, November 1998  
A:Description: A new subgroup of k type light chains (VKV) identified in cases of AL am  
A:Reference number: JE0243  
A:Accession: JE0244  
A:Molecule type: protein  
A:Residues: 1-215 <ALI>  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 553; DB 2; Length 215;  
Best Local Similarity 100.0%; Pred. No. 2.6e-47;  
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFFPREAKYQWKVDNALQSGNSQESVTEQD 60  
Db 109 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFFPREAKYQWKVDNALQSGNSQESVTEQD 168  
Qy 61 SKDSTYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 107  
Db 169 SKDSTYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 215

RESULT 2  
JE0242  
Ig kappa chain NIG26 precursor - human  
C:Species: Homo sapiens (man)  
C:Date: 05-Dec-1998 #sequence\_revision 05-Dec-1998 #text\_change 21-Jan-2000  
C:Accession: JE0242  
R:Alim, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda, J  
submitted to JIPID, November 1998  
A:Description: Structure relationship of kappa type light chains with AL amyloidosis: Mul  
A:Reference number: JE0241  
A:Accession: JE0242  
A:Molecule type: protein  
A:Residues: 1-215 <ALI>  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
F:16-91/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 553; DB 2; Length 215;  
Best Local Similarity 100.0%; Pred. No. 2.6e-47;  
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFFPREAKYQWKVDNALQSGNSQESVTEQD 60  
Db 109 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFFPREAKYQWKVDNALQSGNSQESVTEQD 168



A;Contents: annotation  
A;Gene: GDB:IGKC  
A;Cross-references: GDB:120086; OMIM:147200  
A;Map position: 2p12-2p12  
C;Complex: an immunoglobulin heterotrimer subunit consists of two identical light (kappa) chain disulfide bonds, in some cases, such as IgA and IgM, the subunits associate into larger disulfide bonds; immunoglobulin C region; immunoglobulin homology  
C;Superfamily: heterotrimer; immunoglobulin  
C;Keywords: heterotrimer; immunoglobulin homology <IMM>  
F;19-88/Domain: immunoglobulin homology <IMM>  
F;25-86/Disulfide bonds: #status experimental  
F;106/Disulfide bonds: interchain (to heavy chain) #status experimental

Query Match 99.1%; Score 548; DB 1; Length 106;  
Best Local Similarity 100.0%; Pred. No. 3.4e-47;  
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TVAAPSVFIPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS 61  
DB 1 TVAAPSVFIPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS 60

QY 62 KSTYSLSTLTLSKADYKHKYKHYACEVTHQGLSSPVTKSFNRGEC 107  
DB 61 KSTYSLSTLTLSKADYKHKYKHYACEVTHQGLSSPVTKSFNRGEC 106

RESULT 6  
JE0241  
Ig kappa chain Am37 precursor - human  
C;Species: Homo sapiens (man)  
C;Date: 05-Dec-1998 #sequence\_revision 05-Dec-1998 #text\_change 21-Jan-2000  
C;Accession: JE0241  
R;Alim, M.A.; Yanaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda, T.  
submitted to JIPID, November 1998  
A;Description: Structure relationship of kappa type light chains with AL amyloidosis: Mul  
A;Reference number: JE0241  
A;Accession: JE0241  
A;Molecule type: protein  
A;Residues: 1-216 <ALI>  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
F;16-92/Domain: immunoglobulin homology <IMM>

Query Match 97.1%; Score 537; DB 2; Length 216;  
Best Local Similarity 97.2%; Pred. No. 9.9e-46;  
Matches 104; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60  
DB 110 RTVAAPSVFIPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 169

QY 61 SKDSTYSLSTLTLSKADYKHKYKHYACEVTHQGLSSPVTKSFNRGEC 107  
DB 170 SKDSTYSLSTLTLSKADYKHKYKHYACEVTHQGLSSPVTKSFNRGEC 216

RESULT 7  
A23746  
Ig kappa chain V-III (KAU cold agglutinin) - human  
C;Species: Homo sapiens (man)  
C;Date: 30-Dec-1991 #sequence\_revision 30-Dec-1991 #text\_change 21-Jan-2000  
C;Accession: A23746  
R;Leon, J.; Ghiso, J.; Goni, F.; Frangione, B.  
J. Biol. Chem. 266, 2836-2842, 1991  
A;Title: The primary structure of the Fab fragment of protein KAU, a monoclonal immunoglobulin  
A;Reference number: A23746; MUID:9131575; PMID:1993660  
A;Accession: A23746  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-215 <LEO>  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotrimer; immunoglobulin  
F;16-91/Domain: immunoglobulin homology <IMM>

Query Match 94.0%; Score 520; DB 2; Length 215;  
Best Local Similarity 98.1%; Pred. No. 4.7e-44;  
Matches 104; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60  
DB 109 RTVAAPSVFIPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 168

QY 61 SKDSTYSLSTLTLSKADYKHKYKHYACEVTHQGLSSPVTKSFNRGE 106  
DB 169 SKDSTYSLSTLTLSKADYKHKYKHYACEVTHQGLSSPVTKSFNRGE 214

RESULT 8  
A37927  
Ig kappa chain C region (allotype Inv(1,2)) - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 28-Feb-1992 #sequence\_revision 28-Feb-1992 #text\_change 21-Jan-2000  
C;Accession: A37927  
R;Kurtz, J.H.; Bowcock, A.M.; Erlich, H.A.; Nevo, S.; Cavalli-Sforza, L.L.  
Am. J. Hum. Genet. 48, 613-620, 1991  
A;Title: Km typing with PCR: application to population screening.  
A;Reference number: A37927; MUID:91150772; PMID:1900145  
A;Accession: A37927  
A;Status: preliminary; not compared with conceptual translation  
A;Molecule type: DNA  
A;Residues: 1-99 <KUR>  
C;Superfamily: immunoglobulin C region; immunoglobulin homology  
C;Keywords: heterotrimer; immunoglobulin  
F;12-81/Domain: immunoglobulin homology <IMM>

Query Match 92.8%; Score 513; DB 2; Length 99;  
Best Local Similarity 99.0%; Pred. No. 9e-44;  
Matches 98; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 9 FIPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 68  
DB 1 FIPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 60

QY 69 SSTLTLSKADYKHKYKHYACEVTHQGLSSPVTKSFNRGEC 107  
DB 61 SSTLTLSKADYKHKYKHYACEVTHQGLSSPVTKSFNRGEC 99

RESULT 9  
S26653  
Ig kappa chain C region - chimpanzee (fragment)  
C;Species: Pan troglodytes (chimpanzee)  
C;Date: 19-Mar-1997 #sequence\_revision 18-Jul-1997 #text\_change 21-Jan-2000  
C;Accession: S26653  
R;Ehrlich, P.H.; Moustafa, Z.A.; Harfeldt, K.E.; Isaacson, C.; Oestberg, L.  
Hum. Antibodies Hybrids 1, 23-26, 1990  
A;Title: Potential of primate monoclonal antibodies to substitute for human antibodies:  
A;Reference number: S26652; MUID:91355693; PMID:2129418  
A;Accession: S26653  
A;Status: translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-99 <EHR>  
A;Cross-references: EMBL:X65287  
C;Superfamily: immunoglobulin C region; immunoglobulin homology  
C;Keywords: immunoglobulin  
F;19-88/Domain: immunoglobulin homology <IMM>

Query Match 91.7%; Score 507; DB 2; Length 99;  
Best Local Similarity 100.0%; Pred. No. 3.5e-43;  
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TVAAPSVFIPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS 61  
DB 1 TVAAPSVFIPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS 60

QY 62 KSTYSLSTLTLSKADYKHKYKHYACEVTHQGLSSPVTK 100

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112 RADAAPTYSIIPPSSSEOLTSGASWCFLLNFPKOINVXWKIDGSRQNGVLNSWTDQ 171
QY 61 SKDSFYSLSSLTITUSKADYKHKYACVETHQGLSSPVTKSFNRGEC 107
DB 172 SKDSFYNSMSLTITKDEYBRHNSYTCETHKTSTGPIVKSFNRGEC 218

```

RESULT 14

S42772

Query Match	64.7%	Score 358;	DB 2;	Length 217;
Best Local Similarity	61.7%	Pred. No. 4.8e-28;		
Matches 66;	Conservative 15;	Mismatches 26;	Indels 0;	Gaps 0

**QY**

```
1 RTVAAPSVEIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNALQGNSEQSVTEQD 60
| | | : | | | | | | | | | | | : | | | : | |
| | | | | | | | | | | | | | | | | | | | |
Dd 111 RADAAPTIVSIFPSPSEQLTGGGSAWCFLLNFFPKIDINVKWKIDGSEQRGVLSWTDD 170
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QY 61 SKDSTYSLSSTLTLSKADYEKKHVACVETHQGLSSPVTKSFNRGEC 107  
 |||||  
 171 SKDSTYSMSSTLTLDKEYEYRHNSVYCEATHKTSTPIVKSFNRGEC 217  
 |||||

## RESULT 15

S68241  
Ig kappa chain V region (Mab13-1) - mouse (fragment)  
N/Alternate names: immunoglobulin light chain  
C/Species: Mus musculus (house mouse)  
C/Date: 24-Aug-1996 #sequence\_revision 13-Mar-1997 #text\_change 20-Jun-2000  
C/Accession: S68241; S68214  
R/Takagi, M.; Kohda, K.; Hamuro, T.; Hazada, A.; Yamaguchi, H.; Kamachi, M.; Imanaka, T.  
submitted to the EMBL Data Library, March 1994  
A/Description: Specific peroxidase activity by formation of an antibody L-chain-porphyrin  
A/Reference number: S68241  
A/Accession: S68241  
A/Molecule type: mRNA  
A/Residues: 1-218 <EMBL>  
A/Cross-references: EMBL:D29670; NID:g473962; PID:g473963  
R/Takagi, M.; Kohda, K.; Hamuro, T.; Hazada, A.; Yamaguchi, H.; Kamachi, M.; Imanaka, T.  
FEBS Lett. 375, 273-276, 1995  
A/Title: Thermostable peroxidase activity with a recombinant antibody L chain-porphyrin  
A/Reference number: S68211; MUID:96085223; PMID:7498516  
A/Accession: S68214  
A/Status: nucleic acid sequence not shown  
A/Molecule type: mRNA  
A/Residues: 'N1',3-212 <TAW>  
A/Cross-references: EMBL:D29670  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: immunoglobulin

Query Match	64.7%;	Score 358;	DB 2;	Length 218;
Best Local Similarity	61.7%;	Pred. No. 4.9e-28;		
Matches 66;	Conservative 15;	Mismatches 26;	Indels 0;	Gaps 0

1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQD 60

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OM protein - protein search, using sw model

Run on: January 13, 2004, 12:19:34 ; Search time 4.67249 Seconds  
(without alignments)  
1076.912 Million cell updates/sec

Title: US-09-990-586-97

Perfect score: 553

Sequence: 1 RTVAAPSVFIPPPDQLKS.....EVTHQGLSSPVTKSFNRGEC 107

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	548	99.1	106	1 KAC HUMAN	P01834 homo sapien
2	367	66.4	106	1 KACB RAT	P01835 rattus norv
3	359	64.9	106	1 KACA RAT	P01836 rattus norv
4	350	63.3	106	1 KAC MOUSE	P01837 mus musculu
5	306.5	55.4	106	1 KACH RABIT	P01839 oryctolagus
6	257.5	46.6	103	1 KAC4 RABIT	P01840 oryctolagus
7	246.5	44.6	104	1 KAC9 RABIT	P01838 oryctolagus
8	241	43.6	104	1 KAC6 RABIT	P03984 oryctolagus
9	231	41.8	103	1 LAC CHICK	P20763 gallus gall
10	225	40.7	108	1 KAC RANCA	P11272 rana catesb
11	223.5	40.4	103	1 KAC5 RABIT	P01841 oryctolagus
12	210.5	38.1	105	1 LAC1 MOUSE	P01843 mus musculu
13	208.5	37.7	105	1 LAC HUMAN	P01842 homo sapien
14	203.5	36.8	105	1 LAC RABIT	P01847 oryctolagus
15	190	34.4	104	1 LAC1 RAT	P20766 rattus norv
16	187.5	33.9	213	1 IL11 HUMAN	P15814 homo sapien
17	183	33.1	104	1 LAC2 RAT	P20767 rattus norv
18	180.5	32.6	105	1 LAC PIG	P01846 sus scrofa
19	178	32.2	104	1 LAC3 MOUSE	P01845 mus musculu
20	174	31.5	104	1 LAC2 MOUSE	P01844 mus musculu
21	164.5	29.7	329	1 GC2 CAVPO	P01862 cavia porce
22	161.5	29.2	105	1 LAC5 MUSSP	P20765 mus spretus
23	157.5	28.5	421	1 EPC MOUSE	P03336 mus musculu
24	153.5	27.8	330	1 GCA4 MOUSE	P01863 mus musculu
25	153.5	27.8	339	1 GCMA MOUSE	P01865 mus musculu
26	151	27.3	326	1 GC2 HUMAN	P01859 homo sapien
27	151	27.3	327	1 GC4 HUMAN	P01861 homo sapien
28	150.5	27.2	335	1 GC4E MOUSE	P01864 mus musculu
29	149	26.9	290	1 GC3 HUMAN	P01860 homo sapien
30	148	26.8	330	1 GC1 HUMAN	P01857 homo sapien
31	146.5	26.5	105	1 LAC5 MOUSE	P20764 mus musculu
32	145	26.2	336	1 GCB MOUSE	P01866 mus musculu
33	145	26.2	405	1 GCBV MOUSE	P01867 mus musculu

ALIGNMENTS

RESULT 1

ID	KAC_HUMAN	STANDARD;	PRT;	106 AA.
AC	P01834;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	Ig kappa chain C region.			
GN	IGKC.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
CX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE (MYELOMA PROTEIN EU).			
RX	MEDLINE=71064023; PubMed=5489770;			
RA	Gottlieb P.D., Cunningham B.A., Rutishauser U., Edelman G.M.;			
RT	"The covalent structure of a human gamma G-immunoglobulin. VI. Amino acid sequence of the light chain.";			
RL	Biochemistry 9:3155-3161(1970).			
RN	[2]			
RP	DISULFIDE BONDS.			
RX	MEDLINE=71064027; PubMed=4923144;			
RA	Gall W.E., Edelman G.M.;			
RT	"The covalent structure of a human gamma G-immunoglobulin. X. Intrachain disulfide bonds.";			
RL	Biochemistry 9:3188-3196(1970).			
RN	[3]			
RP	SEQUENCE (BENCE-JONES PROTEIN TI).			
RX	MEDLINE=72188439; PubMed=5027703;			
RA	Suter L., Barnikol H.U., Watanabe S., Hilschmann N.;			
RT	"Rule of antibody structure. The primary structure of a monoclonal immunoglobulin L-chain of kappa-type, subgroup 3 (Bence-Jones protein Ti). IV. The complete amino acid sequence and its significance for the mechanism of antibody production.";			
RL	Hoppe-Seyler's Z. Physiol. Chem. 353:189-208(1972).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=81042304; PubMed=6775618;			
RA	Hietter P.A., Max E.E., Seidman J.G., Maizel J.V. Jr., Leder P.;			
RT	"Cloned human and mouse kappa immunoglobulin constant and J region genes conserve homology in functional segments.";			
RL	Cell 22:197-207(1980).			
RN	[5]			
RP	SEQUENCE (BENCE-JONES PROTEIN ROY).			
RA	Hilschmann N., Barnikol H.U., Hess M., Langer B., Ponstingl H., Steinmetz-Kayne M., Suter L., Watanabe S.;			
RA	(In) Fraeek F., Shugar D. (eds.);			
RL	Gamma globulins: structure and function, pp.57-74, Academic Press, New York (1969).			
RN	[6]			
RP	SEQUENCE (BENCE-JONES PROTEIN CUM).			
RX	MEDLINE=68242259; PubMed=5586923;			
RA	Hilschmann N.;			
RT	"The complete amino acid sequence of Bence Jones protein Cum (kappa-type).";			

P01870 oryctolagus  
P06337 mesocricetu  
P20768 suncus muri  
P01855 rattus norv  
P20762 rattus norv  
P01858 mus musculu  
P01869 mus musculu  
P01873 mus musculu  
P20760 rattus norv  
P22436 mus musculu  
P03987 mus musculu

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KACA RAT
ID _KACA_RAT STANDARD; PRT; 106 AA.
AC P01836;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE IG kappa chain C region, A allele.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]_TaxID=10116;
RN SEQUENCE FROM N.A.
RX MEDLINE=82082587; PubMed=6273908;
RX STRAIN=DA;
RA Sheppard H.W., Gutman G.A.;
RT "Allelic forms of rat kappa chain genes: evidence for strong
RT selection at the level of nucleotide sequence.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:7064-7068(1981).
CC -I- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02118; KIRCA.
DR HSSP; P01842; 2MCG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00407; IGcl; 1.
DR PROSITE; PS00835; IG LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1
FT DOMAIN 5 102 IG-LIKE.
FT DISULFID 26 86
FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
SQ SEQUENCE 106 AA; 11732 MW; B7E120D9700DD66 CRC64;

Query Match 64.9%; Score 359; DB 1; Length 106;
Best Local Similarity 63.5%; Pred. No. 3.3e-29;
Matches 66; Conservative 16; Mismatches 22; Indels 0; Gaps 0;

QY 4 AASVFIFFPSDQLSGASVCLNNFYPREAKVQWKNALQSGNSQESVTVQDSKD 63
DB 3 AAPTQIFPPSMQLTSGGATVCFVNFYPRDISVKWKIDGSEQRDGVLDVTDQDSKD 62
QY 64 STVSLSTLTSLKADYKHKVACEVTHQGLSPVTKSNRGEC 107
DB 63 STYSMSSTLSLTKVEYERHNLVTCVVKHTSSPVPVKSFRNEC 106

RESULT 4
KAC_MOUSE
ID _KAC_MOUSE STANDARD; PRT; 106 AA.
AC P01937;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE IG kappa chain C region.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_TaxID=10090;
RN SEQUENCE (MOPC 21).
RX MEDLINE=73053310; PubMed=4638343;
RA Svasti J., Milstein C.;
RT "The complete amino acid sequence of a mouse kappa light chain.";
RL Biochem. J. 128:427-444(1972).
RN [2]
RN DISULFIDE BONDS (MOPC 21).
RX MEDLINE=73008889; PubMed=5073237;
RA Svasti J., Milstein C.;
RT "The disulphide bridges of a mouse immunoglobulin G1 protein.";
RL Biochem. J. 126:837-850(1972).

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RN RP SEQUENCE FROM N.A., AND REVISIONS TO 53-59.
RX MEDLINE=79084137; PubMed=103625;
RA Hamlyn P.H., Brownlee G.G., Cheng C.-C., Gait M.J., Milstein C.;
RT "Complete sequence of constant and 3' noncoding regions of an
RT immunoglobulin mRNA using the dideoxynucleotide method of RNA
RT sequencing.";
RL Cell 15:1067-1075(1978).
RN [4]
RN SEQUENCE FROM N.A.
RX MEDLINE=82059477; PubMed=6170937;
RA Hamlyn P.H., Gait M.J., Milstein C.;
RT "Complete sequence of an immunoglobulin mRNA using specific priming
RT and the dideoxynucleotide method of RNA sequencing.";
RL Nucleic Acids Res. 9:4485-4494(1981).
RN [5]
RN SEQUENCE FROM N.A.
RX MEDLINE=81191915; PubMed=6262318;
RA Max E.E., Maizel J.V. Jr., Leder P.;
RT "The nucleotide sequence of a 5.5-kilobase DNA segment containing the
RT mouse kappa immunoglobulin J and C region genes.";
RL J. Biol. Chem. 256:5116-5120(1981).
RN [6]
RN SEQUENCE FROM N.A.
RX MEDLINE=81198949; PubMed=6785724;
RA Altenburger W., Neumaier P.S., Steinmetz M., Zachau H.G.;
RT "DNA sequence of the constant gene region of the mouse immunoglobulin
RT kappa chain.";
RL Nucleic Acids Res. 9:971-981(1981).
RN [7]
RN SEQUENCE FROM N.A.
RX MEDLINE=88329081; PubMed=3138116;
RA de Waale P., Feys V., van de Voorde A., Molemans F., Fiers W.;
RT "Expression in non-lymphoid cells of mouse recombinant immunoglobulin
RT directed against the tumour marker human placental alkaline
RT phosphatase.";
RL Eur. J. Biochem. 176:287-295(1988).
RN CC -I- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC -----
CC EMBL; V00807; CAA24189.1; --
CC PIR; B90262; KIMS.
CC PDB; 1AIF; 01-FEB-97.
CC PDB; 1FSK; 02-OCT-00.
CC PDB; 1IGC; 03-JUN-95.
CC PDB; 1KBS; 08-APR-98.
CC PDB; 1KCB; 11-MAY-02.
CC PDB; 1KCS; 11-MAY-02.
CC PDB; 1KCU; 11-MAY-02.
CC PDB; 1KCV; 11-MAY-02.
CC PDB; 25C8; 09-JUL-99.
CC MGD; MGI:96495; IGK-C.
CC InterPro; IPR007110; IG-like.
CC InterPro; IPR003597; IG-cl.
CC InterPro; IPR003006; IG_MHC.
CC Pfam; PF00047; Ig; 1.
CC SMART; SM00407; IGcl; 1.
CC PROSITE; PS00835; IG LIKE; 1.
CC PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; 3D-structure.
FT NON_TER 1
FT DOMAIN 5 102 IG-LIKE.
FT DISULFID 26 86 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 106 106
SQ SEQUENCE 106 AA; 11778 MW; 4B51FF5EF49BAE5 CRC64;

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RT immunoglobulin lambda-chains.";
RL Biochem. J. 197;177-183(1981).
CC -I- MISCELLANEOUS: THIS LAMBDA CHAIN EXPRESSES THE C7 ALLOTYPIC
CC SPECIFICITY.
CC -I- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR HSP; P01842; 7FAB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00407; Igcl; 1.
DR PROSITE; PSS0835; IG-LIKE; 1.
DR PROSITE; PS00290; IG_MHC; FALSE NEG.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1
FT DOMAIN 6 100 IG-LIKE.
FT DISULFID 27 86
FT DISULFID 104 104 INTERCHAIN (WITH HEAVY CHAIN).
FT SEQUENCE 105 AA; 11484 MW; B427513272E8663D CRC64;

Query Match 36.8%; Score 203.5; DB 1; Length 105;
Best Local Similarity 44.3%; Pred. No. 1.1e-13;
Matches 47; Conservative 15; Mismatches 33; Indels 11; Gaps 4;

QY 6 PSVIFPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNS--QESVTEQDSK 63
DB 6 PSVILFPPSSEELKDKATLVCLISDFIPRTVKVWKAD-----GNSVTQGVDTTPSKQ 60

QY 64 ST--YSLSTLTLSKADYEKKHYACEVTHQGLSSPVTKSFNRGEC 107
DB 61 SNKYAASSFLHTANQWKSQSVTCQVTHG--HTVEKSLAPABC 104

RESULT 15
LACI.RAT STANDARD; PRT; 104 AA.
AC P20766;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig lambda-1 chain C region.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]_
RP SEQUENCE FROM N.A.
RX MEDLINE=8730594; PubMed=3114047;
RA Steen M.L., Hellman L., Pettersson U.;
RT "The immunoglobulin lambda locus in rat consists of two C lambda
RT genes and a single V lambda gene.";
RL Gene 55:75-84(1987).
CC -I- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M22520; AAA41419.1; ALT_INIT.
DR HSP; P01842; 7FAB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00407; Igcl; 1.
DR PROSITE; PSS0835; IG-LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1

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```

FT DOMAIN 6 99 IG-LIKE.
FT DISULFID 27 85
FT DISULFID 103 103 INTERCHAIN (WITH HEAVY CHAIN).
SQ SEQUENCE 104 AA; 11565 MW; CBF71811F4BC978A CRC64;

Query Match 34.4%; Score 190; DB 1; Length 104;
Best Local Similarity 39.0%; Pred. No. 2.4e-12;
Matches 41; Conservative 20; Mismatches 38; Indels 6; Gaps 3;

QY 4 AAPSVEIFPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNA-LQSGNSQSVTEQDSK 62
DB 4 ATPSVTLFPPSSEELKDKATLVCMVTDYFGVMTVMKADGTPITQGVETTQPFKQNNK 63

QY 63 DSTYLSLSTLTLSKADYEKKHYACEVTHQGLSSPVTKSFNRGEC 107
DB 64 ---YNATSYLLLTAKAWETHSNYSQOVTHE--ENTVEKSLRAEC 103

Search completed: January 13, 2004, 12:39:27
Job time : 5.67249 secs

```

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 13, 2004, 12:20:44 ; Search time 19.1572 Seconds  
(without alignments)  
1441.318 Million cell updates/sec

Title: US-09-990-586-97

Perfect score: 553

Sequence: 1 RTVAAPSVFIPPSDEQLKS.....EVTHQGLSSPVTKSFNRGEC 107

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SEPREMBL\_23:\*

1: sp\_archaea:\*

2: sp\_bacteria:\*

3: sp\_fungi:\*

4: sp\_human:\*

5: sp\_invertebrate:\*

6: sp\_mammal:\*

7: sp\_mhc:\*

8: sp\_organelle:\*

9: sp\_phase:\*

10: sp\_plant:\*

11: sp\_todent:\*

12: sp\_virus:\*

13: sp\_vertebrate:\*

14: sp\_unclassified:\*

15: sp\_rvirus:\*

16: sp\_bacteriap:\*

17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	553	100.0	234	4 Q8NEK1	Q8nek1 homo sapien
2	553	100.0	239	4 Q8TCD0	Q8tcd0 homo sapien
3	549	99.3	239	4 Q8NEK0	Q8nek0 homo sapien
4	352	63.7	233	11 Q91WS9	Q91ws9 mus musculu
5	352	63.7	234	11 Q8R028	Q8r028 mus musculu
6	352	63.7	234	11 Q91W88	Q91w88 mus musculu
7	352	63.7	234	11 Q8R062	Q8r062 mus musculu
8	352	63.7	234	11 Q8VC80	Q8vc80 mus musculu
9	352	63.7	235	11 Q91W12	Q91w12 mus musculu
10	352	63.7	238	11 Q8VC16	Q8vc16 mus musculu
11	352	63.7	238	11 Q99M37	Q99m37 mus musculu
12	352	63.7	239	11 Q8VC55	Q8vc55 mus musculu
13	352	63.7	239	11 Q8K058	Q8k058 mus musculu
14	347	62.7	214	11 Q9R1A5	Q9r1a5 mus musculu
15	211.5	38.2	106	4 Q8TCJ5	Q8tcj5 homo sapien
16	211.5	38.2	233	4 Q8TBC9	Q8tbc9 homo sapien

17	211.5	38.2	236	4 Q8NEJ1	Q8nej1 homo sapien
18	210.5	38.1	130	11 Q9D8W4	Q9d8w4 mus musculu
19	208.5	37.7	233	4 Q8N3F4	Q8n3f4 homo sapien
20	208.5	37.7	233	4 Q8N355	Q8n355 homo sapien
21	208.5	37.7	237	4 Q8WUK4	Q8wuk4 homo sapien
22	208.5	37.7	237	4 Q8WTU6	Q8wtu6 homo sapien
23	208.5	37.7	240	4 Q8WUK3	Q8wuk3 homo sapien
24	199.5	36.1	235	11 Q99M11	Q99m11 mus musculu
25	192.5	34.8	233	4 Q96I69	Q96i69 homo sapien
26	192.5	34.8	236	4 Q96E61	Q96e61 homo sapien
27	174	31.5	105	11 Q99JCI	Q99jci mus musculu
28	159.5	28.8	473	11 Q9D8L4	Q9d8l4 mus musculu
29	153.5	27.8	468	11 Q99L31	Q99l31 mus musculu
30	153.5	27.8	473	11 Q99L25	Q99l25 mus musculu
31	151	27.3	473	4 Q8TC63	Q8tc63 homo sapien
32	149	26.9	509	4 Q8NF17	Q8nf17 homo sapien
33	149	26.9	521	4 Q8N4Y9	Q8n4y9 homo sapien
34	148	26.8	471	4 Q8TC77	Q8tc77 homo sapien
35	148	26.8	701	4 Q96PQ8	Q96pq8 homo sapien
36	144	26.0	473	11 Q91Z05	Q91z05 mus musculu
37	144	26.0	474	11 Q8R3H6	Q8r3h6 mus musculu
38	143	25.9	463	11 Q99LC4	Q99lc4 mus musculu
39	142	25.7	437	11 Q9R1A4	Q9r1a4 mus musculu
40	142	25.7	469	11 Q8R3V9	Q8r3v9 mus musculu
41	139.5	25.2	337	6 Q95M34	Q95m34 equus cabal
42	136	24.6	613	11 Q8VCX7	Q8vcx7 mus musculu
43	134	24.2	684	13 Q90544	Q90544 ginglymosto
44	127.5	23.1	267	13 Q90529	Q90529 ginglymosto
45	127.5	23.1	268	13 Q90524	Q90524 ginglymosto

#### ALIGNMENTS

##### RESULT 1

Q8NEK1 PRELIMINARY; PRT; 234 AA.

AC Q8NEK1;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lung;  
RA Strausberg R.;  
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  
DR ENBL; BC030813; AAH30813.1; -  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003597; IG\_c1.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_v.  
DR Pfam; PF00047; IG\_2.  
DR SMART; SM00407; IGI; 1.  
DR SMART; SM00406; IGI; 1.  
DR PROSITE; PS00835; IG\_LIKE; 2.  
DR PROSITE; PS00290; IG\_MHC; 1.  
KW Hypothetical protein.

SEQUENCE 234 AA; 25530 MW; 6316E8DEF8D132F8 CRC64;

Query Match 100.0%; Score 553; DB 4; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.7e-49;  
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFIPPSDEQLKSGTASVVCLNNFYPPREAKVQWKVDNALQSGNSQESVTEQD 60

Db 128 RTVAAPSVFIPPSDEQLKSGTASVVCLNNFYPPREAKVQWKVDNALQSGNSQESVTEQD 187

Qy 61 SKDSTVLSSTLTLSKADYKHKVACEVTHOGLSPVTKSFNRGEC 107



RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC028540; AAH28540.1; --  
 DR InterPro; IPR003006; IG\_MHC.  
 DR Pfam; PF00047; IG\_2.  
 DR SMART; SM00406; IGv; 1.  
 DR PROSITE; PS00290; IG\_MHC; 1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 234 AA; 25702 MW; 148377F9C1CDOAEE CRC64;

Query Match 63.7%; Score 352; DB 11; Length 234;  
 Best Local Similarity 60.7%; Pred. No. 1.3e-28;  
 Matches 65; Conservative 15; Mismatches 27; Indels 0; Gaps 0;

QY 1 RTVAAPSVFPPSPDEQLKSGTASVVCLLNNFYPRKAVQWKVDNALQSGNSQESVTEQD 60  
 DB 128 RADAAPTQSVIFPPSPSEQLTSGGASVVCFLNNFYPKDINVKKIDGSRQNGVLSWTDQD 187

QY 61 SKDSTYSLSTLTLSKADYKHKVYACEVTHQGLSPVTKSFNRGEC 107

DB 188 SKDSTYSMSSTLTLTDEYERHNSYTCETHTKTSTSPIVKSFNRNEC 234

# RESULT 6

ID Q91WF8 PRELIMINARY; PRT; 234 AA.  
 AC Q91WF8;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Hypothetical 25.9 kDa protein.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Colon;  
 RA Strausberg R.;  
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC015292; AAH15292.1; --  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_v.  
 DR InterPro; IPR001865; Ribosomal\_S2.  
 DR Pfam; PF00047; IG\_2.  
 DR SMART; SM00406; IGv; 1.  
 DR PROSITE; PS00290; IG\_MHC; 1.  
 DR PROSITE; PS00962; RIBOSOMAL\_S2\_1; 1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 234 AA; 25929 MW; B0D0B056EB7812D2 CRC64;

Query Match 63.7%; Score 352; DB 11; Length 234;  
 Best Local Similarity 60.7%; Pred. No. 1.3e-28;  
 Matches 65; Conservative 15; Mismatches 27; Indels 0; Gaps 0;

QY 1 RTVAAPSVFPPSPDEQLKSGTASVVCLLNNFYPRKAVQWKVDNALQSGNSQESVTEQD 60  
 DB 128 RADAAPTQSVIFPPSPSEQLTSGGASVVCFLNNFYPKDINVKKIDGSRQNGVLSWTDQD 187

QY 61 SKDSTYSLSTLTLSKADYKHKVYACEVTHQGLSPVTKSFNRGEC 107

DB 188 SKDSTYSMSSTLTLTDEYERHNSYTCETHTKTSTSPIVKSFNRNEC 234

Query Match 63.7%; Score 352; DB 11; Length 234;  
 Best Local Similarity 60.7%; Pred. No. 1.3e-28;  
 Matches 65; Conservative 15; Mismatches 27; Indels 0; Gaps 0;

QY 1 RTVAAPSVFPPSPDEQLKSGTASVVCLLNNFYPRKAVQWKVDNALQSGNSQESVTEQD 60  
 DB 128 RADAAPTQSVIFPPSPSEQLTSGGASVVCFLNNFYPKDINVKKIDGSRQNGVLSWTDQD 187

QY 61 SKDSTYSLSTLTLSKADYKHKVYACEVTHQGLSPVTKSFNRGEC 107

DB 188 SKDSTYSMSSTLTLTDEYERHNSYTCETHTKTSTSPIVKSFNRNEC 234

# RESULT 7

ID Q8R062 PRELIMINARY; PRT; 234 AA.  
 AC Q8R062;  
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Hypothetical 25.9 kDa protein.  
 OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Colon;  
 RA Strausberg R.;  
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC027418; AAH27418.1; --  
 DR InterPro; IPR007110; IG\_LIKE.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_v.  
 DR Pfam; PF00047; IG\_2.  
 DR SMART; SM00406; IGv; 1.  
 DR PROSITE; PS00835; IG\_LIKE; 2.  
 DR PROSITE; PS00290; IG\_MHC; 1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 234 AA; 25857 MW; 4EB08C81426AEB1 CRC64;

Query Match 63.7%; Score 352; DB 11; Length 234;  
 Best Local Similarity 60.7%; Pred. No. 1.3e-28;  
 Matches 65; Conservative 15; Mismatches 27; Indels 0; Gaps 0;

QY 1 RTVAAPSVFPPSPDEQLKSGTASVVCLLNNFYPRKAVQWKVDNALQSGNSQESVTEQD 60  
 DB 128 RADAAPTQSVIFPPSPSEQLTSGGASVVCFLNNFYPKDINVKKIDGSRQNGVLSWTDQD 187

QY 61 SKDSTYSLSTLTLSKADYKHKVYACEVTHQGLSPVTKSFNRGEC 107

DB 188 SKDSTYSMSSTLTLTDEYERHNSYTCETHTKTSTSPIVKSFNRNEC 234

# RESULT 8

ID Q8VCP0 PRELIMINARY; PRT; 234 AA.  
 AC Q8VCP0;  
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Hypothetical 25.7 kDa protein.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Colon;  
 RA Strausberg R.;  
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC019474; AAH19474.1; --  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_v.  
 DR Pfam; PF00047; IG\_2.  
 DR SMART; SM00406; IGv; 1.  
 DR PROSITE; PS00290; IG\_MHC; 1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 234 AA; 25702 MW; 102551C58AC2FA9F CRC64;

Query Match 63.7%; Score 352; DB 11; Length 234;  
 Best Local Similarity 60.7%; Pred. No. 1.3e-28;  
 Matches 65; Conservative 15; Mismatches 27; Indels 0; Gaps 0;

QY 1 RTVAAPSVFPPSPDEQLKSGTASVVCLLNNFYPRKAVQWKVDNALQSGNSQESVTEQD 60  
 DB 128 RADAAPTQSVIFPPSPSEQLTSGGASVVCFLNNFYPKDINVKKIDGSRQNGVLSWTDQD 187

QY 61 SKDSTYSLSTLTLSKADYKHKVYACEVTHQGLSPVTKSFNRGEC 107

DB 188 SKDSTYSMSSTLTLTDEYERHNSYTCETHTKTSTSPIVKSFNRNEC 234

# RESULT 9

Q91W12

```
Matches 65; Conservative 15; Mismatches 27; Indels 0; Gaps 0;
QY 1 RTVAAPSVFPPSPDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
DB 133 RADAAPTIVSIPPSSQLTSGGASVVCFLNFPKIDINVKWIDGSRQNGVLSWTDQD 192
QY 61 SKDSTYSLSTLTLSKADYKHKVYACEVTHOGLSSPVTKSFNRGEC 107
DB 193 SKDSTYMSSTLTLTDEYERHNSYTCETHKTSPIVKSFNRNEC 239

RESULT 13
Q8K0F8 PRELIMINARY; PRT; 239 AA.
ID Q8K0F8
AC Q8K0F8
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC Tissue=Breast tumor;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC031498; AAH31498.1; -.
DR InterPro; IPR002198; ADH_short.
DR InterPro; IPR003599; IG.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00409; IG1; 1.
DR SMART; SM00406; IG1; 1.
DR PROSITE; PS00061; ADH_SHORT; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 239 AA; 26366 MW; D7BE84398AA341F0 CRC64;

Query Match 63.7%; Score 352; DB 11; Length 239;
Best Local Similarity 60.7%; Pred. No. 1.4e-28;
Matches 65; Conservative 15; Mismatches 27; Indels 0; Gaps 0;
QY 1 RTVAAPSVFPPSPDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
DB 133 RADAAPTIVSIPPSSQLTSGGASVVCFLNFPKIDINVKWIDGSRQNGVLSWTDQD 192
QY 61 SKDSTYSLSTLTLSKADYKHKVYACEVTHOGLSSPVTKSFNRGEC 107
DB 193 SKDSTYMSSTLTLTDEYERHNSYTCETHKTSPIVKSFNRNEC 239

RESULT 14
Q9RIA5 PRELIMINARY; PRT; 214 AA.
ID Q9RIA5
AC Q9RIA5
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Kappa light chain of Mab7 (fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Wilde K.G.; Yu X.; Ekramoddoullah A.K.M.; Misra S.;
RT "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
antibody (Mab 7, its light and heavy chains) and construction of a
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single chain antibody (scFV).";
Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
EMBL; AF152371; AAD40242.1; -.
HSP; P01679; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00406; IG1; 1.
DR PROSITE; PS00835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
FT NON_TER 1 214
FT NON_TER 214 214
SQ SEQUENCE 214 AA; 23922 MW; 52BA205FDE995E2A CRC64;

Query Match 62.7%; Score 347; DB 11; Length 214;
Best Local Similarity 59.8%; Pred. No. 3.9e-28;
Matches 64; Conservative 15; Mismatches 28; Indels 0; Gaps 0;
QY 1 RTVAAPSVFPPSPDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
DB 108 RADAAPTIVSIPPSSQLTSGGASVVCFLNFPKIDINVKWIDGSRQNGVLSWTDQD 167
QY 61 SKDSTYSLSTLTLSKADYKHKVYACEVTHOGLSSPVTKSFNRGEC 107
DB 168 SKDSTYMSSTLTLTDEYERHNSYTCETHKTSPIVKCFNRNEC 214

RESULT 15
Q8TCJ5 PRELIMINARY; PRT; 106 AA.
ID Q8TCJ5
AC Q8TCJ5;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein (fragment).
GN DKFP667J0810.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC Tissue=Lymph node;
RA Duetscherhoef A.; Lauber J.; Mewes H.W.; Weil B.; Wiemann S.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL713800; CAD28551.1; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00407; IG1; 1.
DR PROSITE; PS00835; IG LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
FT NON_TER 1
FT NON_TER 106
SQ SEQUENCE 106 AA; 11265 MW; 145272BBE65F4565 CRC64;

Query Match 38.2%; Score 211.5; DB 4; Length 106;
Best Local Similarity 41.0%; Pred. No. 2e-14;
Matches 43; Conservative 26; Mismatches 31; Indels 5; Gaps 3;
QY 4 AAPSFTVFPSPDQLKSGTASVVCLLNNFYPREAKVQWKVDNA-LOGNSQESVTEQDSK 62
DB 5 AAPSFTVFPSPSEBELQKATLVCLISDFYFGAVTVANKADSPFKAG--VETTPSKQS 62
QY 63 DSTYSLSTLTLSKADYKHKVYACEVTHOGLSSPVTKSFNRGEC 107
DB 63 NKYAASSYLSLTPEQWKSHKSYSCQVTHEG--STVEKTVAPTEC 105

Search completed: January 13, 2004, 12:43:08
Job time : 20.1572 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 13, 2004, 12:18:44 ; Search time 24.9511 Seconds  
(without alignments)  
680.681 Million cell updates/sec

Title: US-09-990-586-97

Perfect score: 553

Sequence: 1 RTVAAPSVFIPPPSEQLKS.....EVTHQGLSSPVTKSPNRGEC 107

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A\_Geneseq 15Jun03.\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	553	100.0	107	AAW40578	Human kappa CL dom
2	553	100.0	107	AAW50152	Human kappa light
3	553	100.0	107	AAW08745-	Human kappa-CL dom
4	553	100.0	107	AAW92425	Human kappa protei
5	553	100.0	107	AAW27000	Human kappa CL dom
6	553	100.0	107	ABG31883	Human kappa CL dom
7	553	100.0	107	ABB98755	Human kappa light
8	553	100.0	143	RAP93559	Sequence of human
9	553	100.0	193	AAW52145	Humanised HMFG1 li

10	553	100.0	201	20	AAW29770	P-selectin ligand
11	553	100.0	212	23	ABP51955	Humanised anti-CD1
12	553	100.0	213	17	AAW04301	Antibody fusion pr
13	553	100.0	213	22	AAE10510	Humanised high pot
14	553	100.0	213	22	AAE10512	Humanised high pot
15	553	100.0	213	22	AAE10514	Humanised high pot
16	553	100.0	213	22	AAE10516	Humanised high pot
17	553	100.0	213	22	AAE10518	Humanised high pot
18	553	100.0	213	22	AAE10520	Humanised high pot
19	553	100.0	213	22	AAE10522	Humanised high pot
20	553	100.0	213	22	AAE10524	Humanised high pot
21	553	100.0	213	22	AAE10526	Humanised high pot
22	553	100.0	213	22	AB83157	Ganglioside GM2 an
23	553	100.0	213	23	ABP65663	Human RSV antibody
24	553	100.0	213	23	ABP65665	Human RSV antibody
25	553	100.0	213	23	ABP65667	Human RSV antibody
26	553	100.0	213	23	ABP65669	Human RSV antibody
27	553	100.0	213	23	ABP65671	Human RSV antibody
28	553	100.0	213	23	ABP65673	Human RSV antibody
29	553	100.0	213	23	ABP65675	Human RSV antibody
30	553	100.0	213	23	ABP65677	Human RSV antibody
31	553	100.0	213	23	ABP65679	Human RSV antibody
32	553	100.0	213	23	ABP65681	Human RSV antibody
33	553	100.0	213	23	ABP65683	Human RSV antibody
34	553	100.0	213	23	ABP65685	Human RSV antibody
35	553	100.0	213	23	ABP65687	Human RSV antibody
36	553	100.0	213	23	ABP65689	Human RSV antibody
37	553	100.0	213	23	ABP65691	Human RSV antibody
38	553	100.0	213	23	ABP65693	Human RSV antibody
39	553	100.0	213	23	ABP65695	Human RSV antibody
40	553	100.0	213	23	ABP65697	Human RSV antibody
41	553	100.0	213	23	ABP65699	Human RSV antibody
42	553	100.0	213	23	ABP6601	Human RSV antibody
43	553	100.0	213	23	ABP6605	Human RSV antibody
44	553	100.0	213	23	ABP6607	Human RSV antibody
45	553	100.0	213	23	ABP66609	Human RSV antibody

#### ALIGNMENTS

#### RESULT 1

AAW40578

ID AAW40578 standard; protein; 107 AA.

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AC

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DT

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KW

KW

KW

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PD

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XX Disclosure; Fig 4A-B; 25pp; English.

PS This invention describes a method for improving the clinical outcome in

CC focal ischaemic stroke by administering novel anti-CD18 antibody which

CC has cerebroprotective properties. The invention particularly describes a

CC method of treating focal ischaemic stroke caused by the obstruction of a

CC main cerebral artery which comprises administering an anti-CD18 antibody

CC to increase the blood flow or reduce the infarct size, where: (1) the

CC antibody binds to an extracellular domain of CD18 and inhibits or reduces

CC the ability of the cell expressing CD18 to bind to endothelium, (2) the

CC antibody binds CD18 with an affinity of less than 4 nm, or (3) the

CC antibody dissociates CD18/CD18 complex. This sequence represents the

CC human kappa-CL domain which is used to illustrate the method of the

CC invention.

XX Sequence 107 AA;

XX Query Match 100.0%; Score 553; DB 20; Length 107;

XX Best Local Similarity 100.0%; Pred. No. 6.4e-49; Indels 0; Gaps 0;

XX Matches 107; Conservative 0; Mismatches 0;

QY 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

DB 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

QY 61 SKDSTYLSSTLTLSKADYKHKVYACEVTHQGLSPVTKSFNRGEC 107

DB 61 SKDSTYLSSTLTLSKADYKHKVYACEVTHQGLSPVTKSFNRGEC 107

RESULT 4

AAW92425

ID AAW92425 standard; peptide; 107 AA.

AC AAW92425;

XX 23-APR-1999 (first entry)

XX Human Kappa protein CL domain.

XX Antibody; salvage receptor binding epitope; Fab; F(ab')<sub>2</sub>; immunoglobulin;

XX CH region; CL region; kidney; Fc region; CH1 domain; CH2 domain; IGG;

XX kappa protein; renal clearance rate; circulatory half-life.

XX Homo sapiens.

XX US5869046-A.

XX 09-FEB-1999.

XX 14-APR-1995; 95US-0422092.

XX 14-APR-1995; 95US-0422092.

XX (GETH ) GENENTECH INC.

XX Presta LG, Snedecor BR;

XX WPI; 1999-152694/13.

XX Production of antibody fragments with reduced renal clearance - by

XX introducing salvage receptor binding epitope into CH1 or CL region

XX Disclosure; Column 55-58; 38pp; English.

XX This invention describes a method for preparing a variant Fab or F(ab')<sub>2</sub>

XX polypeptide having increased half-life in vivo, where the polypeptide

XX contains an Ig or Ig-like domain comprising a CH1 and/or CL region, is

XX cleared from the kidneys and does not contain an IGG Fc region. The

XX method involves altering the polypeptide within the CH1 or CL region to

XX incorporate a salvage receptor binding epitope taken from two loops of

XX a CH2 domain of an IGG Fc region. The polypeptides have a reduced renal

CC clearance rate and an increased circulatory half-life. This sequence

CC represents a human kappa protein CL domain used in the method of the

CC invention.

XX Sequence 107 AA;

XX Query Match 100.0%; Score 553; DB 20; Length 107;

XX Best Local Similarity 100.0%; Pred. No. 6.4e-49; Indels 0; Gaps 0;

XX Matches 107; Conservative 0; Mismatches 0;

QY 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

DB 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

QY 61 SKDSTYLSSTLTLSKADYKHKVYACEVTHQGLSPVTKSFNRGEC 107

DB 61 SKDSTYLSSTLTLSKADYKHKVYACEVTHQGLSPVTKSFNRGEC 107

RESULT 5

AAW27000

ID AAW27000 standard; Protein; 107 AA.

AC AAW27000;

XX 25-JAN-2001 (first entry)

XX Human kappa CL domain.

XX Salvage receptor binding epitope; immunomodulator; LFA-1 agonist;

XX mutagenesis; anti-CD18 Fab H52; immunoglobulin; Ig; Crohn's disease;

XX psoriasis; meningitis; allergy; eczema; B-cell lymphoma; wound repair;

XX inflammation; vaccine.

XX Homo sapiens.

XX US6121022-A.

XX 19-SEP-2000.

XX 14-APR-1995; 95US-0422112.

XX 14-APR-1995; 95US-0422112.

XX (GETH ) GENENTECH INC.

XX Presta LG, Snedecor BR;

XX WPI; 2000-610925/58.

XX New nucleic acid encoding new modified polypeptides with increased

XX circulatory half-life useful for preventing/treating LFA-1-mediated

XX disorders, e.g. reducing inflammatory responses or inducing tolerance

XX to immunostimulants -

XX Disclosure; Fig 2; 38pp; English.

XX The present sequence was used in a method for improving the in vivo

XX half-life of polypeptides. The polypeptides comprise an Ig constant

XX domain or an Ig-like constant domain, and a salvage receptor binding

XX epitope within the Ig or Ig-like domain. The salvage receptor epitope is

XX taken from two loops of the CH2 domain of an Fc region of an Ig molecule.

XX The modified polypeptides are useful for preventing or treating

XX LFA-1-mediated disorders, e.g. Crohn's disease, psoriasis, meningitis,

XX allergic conditions (e.g. eczema), antigen-antibody complex mediated

XX diseases, B-cell lymphomas. They are also useful for wound repair,

XX reducing inflammatory responses and inducing tolerance to

XX immunostimulants. They may also be used in diagnostic assays. The nucleic

XX acids and modified polypeptides are useful for the passive immunisation

XX of patients, as well as for affinity purification of an antigen from

XX recombinant cell culture or natural sources.

XX Sequence 107 AA;

QY 61 SKDSTVSLSTLTLSKADYERKHVKYACEVTHQGLSSPVTKSFNRGEC 107  
 DB 61 SKDSTVSLSTLTLSKADYERKHVKYACEVTHQGLSSPVTKSFNRGEC 107

## RESULT 8

AAP93559  
 ID AAP93559 standard; protein; 143 AA.

AC AAP93559;  
 XX 25-MAR-2003 (updated)  
 DT 28-JAN-1991 (first entry)  
 XX Sequence of human kappa light chain fragment.

XX HIV; antiviral; therapy; diagnosis.

KW Homo sapiens.

XX Key Location/Qualifiers

PH Region 1..37

FT /label=

FT /note="light variable and joining"

FT Region 38..38

FT /note="light constant"

FT Region 37..38

FT /note="insert site"

FT W08902922-A.

PN 06-APR-1989.

XX 03-OCT-1988; 88WO-US03414.

XX 02-OCT-1987; 87US-0104329.

XX 28-SEP-1986; 88US-0250785.

XX (GETH ) GENENTECH INC.

PA Capon DJ, Gregory TJ;

XX WPI; 1989-114397/15.

XX P-PSDB; AAP93559.

XX New nucleic acid sequences encoding adhesin, esp. CD4, variants -

PT partic. with trans-membrane domain inactivated or fused to other

PT peptide, useful esp. for treating HIV infections

XX Example; Figure Fig 5; 79pp; English.

XX It is employed in the prepn. of CD4 fusions. The insert site is

XX given in the Features Table. CD4 fusion proteins can have antiviral and

XX immunomodulatory activity are esp. useful for treating HIV infections,

XX regardless of genetic variation within the virus. They and antibodies

XX raised against them can also be used diagnostically for assaying adhesins

XX and their ligands.

XX (Updated on 25-MAR-2003 to correct PR field.)

XX (Updated on 25-MAR-2003 to correct PA field.)

XX Sequence 143 AA;

SQ Query Match 100.0%; Score 553; DB 10; Length 143;  
 Best Local Similarity 100.0%; Pred. No. 9.2e-49;  
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIFFPSDEQLKSGTASVIVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60  
 DB 37 RTVAAPSVFIFFPSDEQLKSGTASVIVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 96

## RESULT 9

AAM52145  
 ID AAM52145 standard; Protein; 193 AA.

AC AAM52145;  
 XX 05-FEB-2002 (first entry)

DT Humanised HMFG1 light chain.

XX Humanised monoclonal antibody; polymorphic epithelial mucin; PEM1;

XX cytotoxic; endonuclease; DNase I; human; cytostatic; cancer; apoptosis.

XX Synthetic.

XX WO200174905-A1.

XX 11-OCT-2001.

XX 26-MAR-2001; 2001WO-GB01324.

XX 03-APR-2000; 2000GB-0008049.

XX 02-OCT-2000; 2000US-237159P.

XX (ANTI-) ANTISOMA RES LTD.

XX Young RJ;

XX WPI; 2001-662969/76.

XX Novel compound used to treat cancer has target cell-specific portion

XX comprising humanised monoclonal antibody having specificity for

XX polymorphic epithelial mucin, and cytotoxic portion having

XX endonucleolytic activity

XX Claim 20; Figure 3; 176pp; English.

XX The invention relates to a compound which comprises a target

XX cell-specific portion, comprising an humanised monoclonal antibody,

XX having specificity for polymorphic epithelial mucin (PEM) or its antigen

XX binding fragment and a cytotoxic portion having endonucleolytic activity,

XX exemplified by AAM52154-AAM52168 and encoded by ABA02682-ABA02728. The

XX compound has cytostatic activity useful for treating cancer and acting as

XX a potential inducer of apoptosis.

XX Sequence 193 AA;

SQ Query Match 100.0%; Score 553; DB 22; Length 193;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-48;  
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIFFPSDEQLKSGTASVIVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60  
 DB 87 RTVAAPSVFIFFPSDEQLKSGTASVIVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 146

## RESULT 10

AAY29770  
 ID AAY29770 standard; Protein; 201 AA.

AC AAY29770;  
 XX 04-NOV-1999 (first entry)

DT P-selectin ligand and kappa chain constant region fusion protein.

XX Human; P-selectin ligand; glycoprotein; fusion protein; infection;

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Db 106 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 165

Qy 61 SKDSTYSLSSLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107

Db 166 SKDSTYSLSSLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 212

RESULT 12

AAW04301

ID AAW04301 standard; Protein; 213 AA.

AC AAW04301;

XX

XX

DT 25-MAR-2003 (updated)

DT 14-FEB-1997 (first entry)

XX

DE Antibody fusion protein.

XX

XX Antibody; fusion protein; recombinant antibody; tumour therapy; prodrug.

KW

XX

OS Synthetic.

OS

XX

PN BP737747-A2.

XX

XX

PD 16-OCT-1996.

XX

XX

PF 13-MAR-1996; 96EP-0103913.

XX

XX

PR 11-APR-1995; 95DE-1013676.

XX

PA (BEHW ) BEHRINGWERKE AG.

XX

PI Bosslet K, Czech J, Oppen M;

XX

XX WPI; 1996-457328/46.

DR N-PSDB; AAT38397.

XX

XX

PT Prodn. of recombinant antibody (Ab), Ab fragment or Ab/enzyme fusion

PT protein - by cytoplasmic expression in thio:redoxin:reductase

PT deficient E. coli

XX

PS Example 1; Figure 5a; 12pp; German.

XX

CC Production of recombinant antibodies (Ab), Ab fragments or Ab

CC fragment/enzyme fusion proteins can be used for tumour therapy,

CC especially when the fusion protein comprises a tumour-specific

CC Ab fragment and an enzyme capable of converting a non-toxic prodrug

CC to a toxic drug. The fusion proteins are constructed in expression

CC vectors and expressed in thio:redoxin:reductase deficient E.coli,

CC allowing expression products to be isolated in soluble functional

CC form without renaturation. The Ab fragment is an Fab fragment or an

CC antigen binding region. In the fusion protein, the Ab component is

CC humanised and the enzyme component is a human cytoplasmic enzyme.

CC This fusion protein comprises the antibody constant and variable

CC light chain regions.

CC (Updated on 25-MAR-2003 to correct PR field.)

XX

XX

Qy 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

Db 107 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 166

Qy 61 SKDSTYSLSSLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107

Db 167 SKDSTYSLSSLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 213

RESULT 14

AAE10512

ID AAE10512 standard; Protein; 213 AA.

XX

AC AAE10512;

XX

RESULT 13

AAE10510

ID AAE10510 standard; Protein; 213 AA.

XX

AC AAE10510;

XX

DT 10-DEC-2001 (first entry)

XX

XX

DE Humanised high potency antibody clone 25 full length light chain.

XX

XX Human; light chain; respiratory syncytial virus infection; virucide;

KW parainfluenza virus; therapy; high potency antibody; drug; cocaine;

KW cancer cell; toxic substance.

XX

OS Homo sapiens.

OS Synthetic.

XX

PN WO200164751-A2.

XX

PD 07-SEP-2001.

XX

XX

PF 01-MAR-2001; 2001WO-US06815.

XX

XX

PR 01-MAR-2000; 2000US-0186252.

XX

PA (MEDI-) MEDIMUNE INC.

XX

PI Young JF, Koenig S, Johnson LS, Huse WD, Wu H, Watkins JD;

XX

XX WPI; 2001-582150/65.

XX

XX High potency recombinant antibody, useful for preventing and treating

PT diseases induced or caused by viruses, especially respiratory syncytial

PT virus and parainfluenza virus, has high kinetic association rate

PT constant -

XX

XX

PS Claim 23; Page 75-76; 98pp; English.

XX

CC The invention relates to a high potency antibody including its

CC immunologically active portions, fragments and segments other than

CC vitamin. The antibody has increased potency, high rate constant for

CC antibody-antigen complex formation and high affinity for any desired

CC antigen. The high potency antibody is also useful for nullifying or

CC ameliorating the effects of addictive drugs, such as cocaine. The high

CC potency has specificity for antigenic determinants found on microbes

CC such as viruses, bacteria or fungi, antigens found on cancer cells and

CC toxic substances or product of toxic substances. The high potency

CC antibody is useful for preventing or treating a disease caused by a

CC virus such as respiratory syncytial virus (RSV) and parainfluenza

CC virus (PIV). The present sequence is humanised high potency antibody

CC full length light chain variable region.

XX

XX

Qy 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

Db 107 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 166

Qy 61 SKDSTYSLSSLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107

Db 167 SKDSTYSLSSLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 213

Query Match 100.0%; Score 553; DB 22; Length 213;

Best Local Similarity 100.0%; Pred. No. 1.5e-48;

Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

Db 107 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 166

Qy 61 SKDSTYSLSSLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107

Db 167 SKDSTYSLSSLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 213

RESULT 14

AAE10512

ID AAE10512 standard; Protein; 213 AA.

XX

AC AAE10512;

XX

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 13, 2004, 12:43:20 ; Search time 17.1013 Seconds  
(without alignments)  
1260.812 Million cell updates/sec

Title: US-09-990-586-97  
Perfect score: 553  
Sequence: 1 RTVAAPSVFIPPPDEQLKS.....EVTHQGLSSPVTKSFNRGEC 107

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 747907 seqs, 201509753 residues

Total number of hits satisfying chosen parameters: 747907

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:\*

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4:	/cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5:	/cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6:	/cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
7:	/cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
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9:	/cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
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11:	/cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
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15:	/cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16:	/cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
17:	/cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
18:	/cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES				Description	
Result No.	Score	Query Match	Length DB ID		
1	553	100.0	107	9	US-09-811-384-5
2	553	100.0	107	11	US-09-990-586-97
3	553	100.0	107	11	US-09-990-586-99
4	553	100.0	107	12	US-10-159-006-20
5	553	100.0	107	12	US-10-310-113-156
6	553	100.0	107	12	US-10-310-113-168
7	553	100.0	107	12	US-10-230-880-97
8	553	100.0	107	12	US-10-230-880-99
9	553	100.0	107	15	US-10-366-709-54
10	553	100.0	107	15	US-10-121-464-18
11	553	100.0	107	15	US-10-269-805-67
12	553	100.0	212	12	US-10-320-231A-77
13	553	100.0	212	14	US-10-011-125-5
14	553	100.0	213	9	US-09-796-848A-38
15	553	100.0	213	9	US-09-796-848A-40

RESULT 1  
US-09-811-384-5  
; Sequence 5, Application US/09811384  
; Patent No. US20020081294A1  
; GENERAL INFORMATION:  
; APPLICANT: Bednar, Martin M.  
; Thomas, G. Roger  
; Gross, Cordell E.  
; TITLE OF INVENTION: ANTI-CD18 ANTIBODIES IN STROKE  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/811,384  
; FILING DATE: 20-Dec-2000  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/251652  
; FILING DATE: 17-FEB-2000  
; APPLICATION NUMBER: 08/788800  
; FILING DATE: 22-JAN-1997  
; APPLICATION NUMBER: 60/093038  
; FILING DATE: 23-JAN-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Love, Richard B.  
; REGISTRATION NUMBER: 34,659  
; REFERENCE/DOCKET NUMBER: PI729C1  
; TELECOMMUNICATION INFORMATION:

Sequence 42, Appl	9	US-09-796-848A-42
Sequence 44, Appl	213	9
Sequence 46, Appl	213	9
Sequence 48, Appl	213	9
Sequence 50, Appl	213	9
Sequence 52, Appl	213	9
Sequence 54, Appl	213	9
Sequence 209, App	213	10
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Sequence 215, App	213	10
Sequence 217, App	213	10
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ALIGNMENTS

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; FILE REFERENCE: 58122(71758)
; CURRENT APPLICATION NUMBER: US/10/310,113
; CURRENT FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: 09/990,586
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/343,306
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/293,854
; PRIOR FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: 08/814,806
; PRIOR FILING DATE: 1997-03-10
; NUMBER OF SEQ ID NOS: 169
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 166
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-310-113-166

Query Match      100.0%; Score 553; DB 12; Length 107;
Best Local Similarity 100.0%; Pred. No. 6.5e-53;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RTVAAPSVFIFFPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
DB      1 RTVAAPSVFIFFPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

QY      61 SKDSTYLSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107
DB      61 SKDSTYLSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107

RESULT 6
US-10-310-113-168
; Sequence 168, Application US/10310113
; Publication No. US20030176664A1
; GENERAL INFORMATION:
; APPLICANT: JIAO, JIN-AN
; APPLICANT: NIEVES, ESPERANZA LILIANA
; APPLICANT: MOSQUERA, LUIS A.
; TITLE OF INVENTION: USE OF ANTI-TISSUE FACTOR ANTIBODIES FOR TREATING
; FILE REFERENCE: 58122(71758)
; CURRENT APPLICATION NUMBER: US/10/310,113
; CURRENT FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: 09/990,586
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/343,306
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/293,854
; PRIOR FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: 08/814,806
; PRIOR FILING DATE: 1997-03-10
; NUMBER OF SEQ ID NOS: 169
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 168
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-310-113-168

Query Match      100.0%; Score 553; DB 12; Length 107;
Best Local Similarity 100.0%; Pred. No. 6.5e-53;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RTVAAPSVFIFFPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
DB      1 RTVAAPSVFIFFPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

QY      61 SKDSTYLSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107
DB      61 SKDSTYLSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107
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RESULT 7
US-10-230-880-97
; Sequence 97, Application US/10230880
; Publication No. US20030190705A1
; GENERAL INFORMATION:
; APPLICANT: WONG, HING C.
; APPLICANT: STINSON, JEFFREY L.
; APPLICANT: MOSQUERA, LUIS A.
; TITLE OF INVENTION: METHOD OF HUMANIZING IMMUNE SYSTEM MOLECULES
; FILE REFERENCE: 71758/58066
; CURRENT APPLICATION NUMBER: US/10/230,880
; CURRENT FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: 09/990,586
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/343,306
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/293,854
; PRIOR FILING DATE: 1999-04-16
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 97
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-230-880-97

Query Match      100.0%; Score 553; DB 12; Length 107;
Best Local Similarity 100.0%; Pred. No. 6.5e-53;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RTVAAPSVFIFFPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
DB      1 RTVAAPSVFIFFPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

QY      61 SKDSTYLSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107
DB      61 SKDSTYLSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107

RESULT 8
US-10-230-880-99
; Sequence 99, Application US/10230880
; Publication No. US20030190705A1
; GENERAL INFORMATION:
; APPLICANT: WONG, HING C.
; APPLICANT: STINSON, JEFFREY L.
; APPLICANT: MOSQUERA, LUIS A.
; TITLE OF INVENTION: METHOD OF HUMANIZING IMMUNE SYSTEM MOLECULES
; FILE REFERENCE: 71758/58066
; CURRENT APPLICATION NUMBER: US/10/230,880
; CURRENT FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: 09/990,586
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/343,306
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/293,854
; PRIOR FILING DATE: 1999-04-16
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 99
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-230-880-99

Query Match      100.0%; Score 553; DB 12; Length 107;
Best Local Similarity 100.0%; Pred. No. 6.5e-53;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RTVAAPSVFIFFPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
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Db 106 RTVAAPSVFIIPPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 165  
Qy 61 SKDSTYSLSTLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 107  
Db 166 SKDSTYSLSTLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 212

RESULT 13  
US-10-011-125-5  
; Sequence 5, Application US/10011125  
; Publication No. US20020142388A1  
; GENERAL INFORMATION:  
; APPLICANT: Chen, Christina Yu-Ching  
; TITLE OF INVENTION: BACTERIAL HOST STRAINS  
; FILE REFERENCE: P1804R1  
; CURRENT APPLICATION NUMBER: US/10/011.125  
; CURRENT FILING DATE: 2001-12-07  
; PRIOR APPLICATION NUMBER: US 60/256,162  
; PRIOR FILING DATE: 2000-12-14  
; NUMBER OF SEQ ID NOS: 10  
; SEQ ID NO 5  
; LENGTH: 212  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Sequence is synthesized.  
US-10-011-125-5

Query Match 100.0%; Score 553; DB 14; Length 212;  
Best Local Similarity 100.0%; Pred. No. 1.5e-52;  
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFIIPPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60  
Db 106 RTVAAPSVFIIPPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 165

Qy 61 SKDSTYSLSTLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 107  
Db 166 SKDSTYSLSTLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 212

RESULT 14  
US-09-796-848A-38  
; Sequence 38, Application US/09796848A  
; Patent No. US20020098189A1  
; GENERAL INFORMATION:  
; APPLICANT: Young, James F.  
; APPLICANT: Johnson, Leslie S.  
; APPLICANT: Huse, William D.  
; APPLICANT: Wu, Hexren  
; APPLICANT: Watkins, Jeffrey D.  
; TITLE OF INVENTION: High Potency Recombinant Antibodies and Methods of  
; FILE REFERENCE: 469201-526  
; CURRENT APPLICATION NUMBER: US/09/796,848A  
; CURRENT FILING DATE: 2001-10-30  
; PRIOR APPLICATION NUMBER: U.S. 60/186,252  
; PRIOR FILING DATE: 2000-03-01  
; NUMBER OF SEQ ID NOS: 59  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 38  
; LENGTH: 213  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Light chain of  
; OTHER INFORMATION: high potency antibody.  
US-09-796-848A-38

Query Match 100.0%; Score 553; DB 9; Length 213;  
Best Local Similarity 100.0%; Pred. No. 1.5e-52;  
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFIIPPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60  
Db 107 RTVAAPSVFIIPPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 166

Qy 61 SKDSTYSLSTLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 107  
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RESULT 15  
US-09-796-848A-40  
; Sequence 40, Application US/09796848A  
; Patent No. US20020098189A1  
; GENERAL INFORMATION:  
; APPLICANT: Young, James F.  
; APPLICANT: Johnson, Leslie S.  
; APPLICANT: Huse, William D.  
; APPLICANT: Wu, Hexren  
; APPLICANT: Watkins, Jeffrey D.  
; TITLE OF INVENTION: High Potency Recombinant Antibodies and Methods of  
; FILE REFERENCE: 469201-526  
; CURRENT APPLICATION NUMBER: US/09/796,848A  
; CURRENT FILING DATE: 2001-10-30  
; PRIOR APPLICATION NUMBER: U.S. 60/186,252  
; PRIOR FILING DATE: 2000-03-01  
; NUMBER OF SEQ ID NOS: 59  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 40  
; LENGTH: 213  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Light chain of  
; OTHER INFORMATION: high potency antibody.  
US-09-796-848A-40

Query Match 100.0%; Score 553; DB 9; Length 213;  
Best Local Similarity 100.0%; Pred. No. 1.5e-52;  
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFIIPPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60  
Db 107 RTVAAPSVFIIPPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 166

Qy 61 SKDSTYSLSTLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 107  
Db 167 SKDSTYSLSTLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 213

Search completed: January 13, 2004, 13:13:44  
Job time : 18.1013 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 13, 2004, 12:33:50 ; Search time 9.25133 Seconds  
(without alignments)  
489.353 Million cell updates/sec

Title: US-09-990-586-97

Perfect score: 553

Sequence: 1 RTVAAPSVFIFFPSDEQLKS.....EVTHQGLSPVTKSFNRGRC 107

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep.\*  
2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	553	100.0	107	1	US-08-422-101-8
2	553	100.0	107	1	US-08-422-091-8
3	553	100.0	107	2	US-08-422-092-8
4	553	100.0	107	2	US-08-788-800-5
5	553	100.0	107	3	US-08-422-093-8
6	553	100.0	107	3	US-08-422-112-8
7	553	100.0	107	4	US-09-301-593-20
8	553	100.0	213	3	US-08-630-820-6
9	553	100.0	213	3	US-08-397-411-12
10	553	100.0	214	1	US-08-456-516-12
11	553	100.0	214	2	US-07-934-373C-24
12	553	100.0	214	2	US-07-934-373C-39
13	553	100.0	214	2	US-07-934-373C-40
14	553	100.0	214	2	US-08-480-753-6
15	553	100.0	214	2	US-08-788-800-11
16	553	100.0	214	3	US-09-041-889-11
17	553	100.0	214	3	US-08-437-642B-24
18	553	100.0	214	3	US-08-437-642B-39
19	553	100.0	214	3	US-08-437-642B-40
20	553	100.0	214	3	US-08-837-058B-11
21	553	100.0	214	3	US-09-097-309-2
22	553	100.0	214	3	US-08-397-411-5
23	553	100.0	214	3	US-09-097-171A-2
24	553	100.0	214	4	US-09-247-352-4
25	553	100.0	214	4	US-09-460-587-2
26	553	100.0	214	4	US-09-679-397-1
27	553	100.0	214	4	US-08-146-206C-24

28	553	100.0	214	4	US-09-456-635-4	Sequence 4, Appli
29	553	100.0	214	4	US-09-680-148-1	Sequence 1, Appli
30	553	100.0	214	4	US-09-289-942A-6	Sequence 6, Appli
31	553	100.0	214	4	US-09-304-465A-1	Sequence 1, Appli
32	553	100.0	214	4	US-09-417-264-11	Sequence 11, Appli
33	553	100.0	214	5	PCT-US93-07832-24	Sequence 24, Appli
34	553	100.0	214	5	PCT-US93-07832-39	Sequence 39, Appli
35	553	100.0	214	5	PCT-US93-07832-40	Sequence 40, Appli
36	553	100.0	215	2	US-08-480-753-8	Sequence 8, Appli
37	553	100.0	218	2	US-08-887-352B-13	Sequence 13, Appli
38	553	100.0	218	2	US-08-887-352B-15	Sequence 15, Appli
39	553	100.0	218	2	US-08-887-352B-17	Sequence 17, Appli
40	553	100.0	218	2	US-08-887-352B-19	Sequence 19, Appli
41	553	100.0	218	2	US-08-887-352B-24	Sequence 24, Appli
42	553	100.0	218	3	US-08-466-151-9	Sequence 9, Appli
43	553	100.0	218	3	US-09-109-207C-13	Sequence 13, Appli
44	553	100.0	218	3	US-09-109-207C-15	Sequence 15, Appli
45	553	100.0	218	3	US-09-109-207C-17	Sequence 17, Appli

ALIGNMENTS

RESULT 1  
US-08-422-101-8  
; Sequence 8, Application US/08422101  
; Patent No. 5739277  
; GENERAL INFORMATION:  
; APPLICANT: Leonard Presta  
; APPLICANT: Brad Snedecor  
; TITLE OF INVENTION: Altered Polypeptides with Increased  
; NUMBER OF SEQUENCES: Half-Life  
; CORRESPONDENCE ADDRESS: 31  
; ADDRESS: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/422.101  
; FILING DATE: 14-APR-1995  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lee, Wendy M.  
; REGISTRATION NUMBER:  
; REFERENCE/DOCKET NUMBER: 932-3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415/225-1994  
; TELEFAX: 415/952-9881  
; TELEX: 910/371-7168  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 107 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
US-08-422-101-8

Query Match 100.0%; Score 553; DB 1; Length 107;  
Best Local Similarity 100.0%; Pred. No. 4.9e-57;  
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 RTVAAPSVFIFFPSDEQLKS...EVTHQGLSPVTKSFNRGRC...VTEQD 60

CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Lee, Wendy M.  
REGISTRATION NUMBER: 40,378  
REFERENCE/DOCKET NUMBER: P098711  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-1994  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 107 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-08-788-800-5

Query Match 100.0%; Score 553; DB 2; Length 107;  
Best Local Similarity 100.0%; Pred. No. 4.9e-57;  
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIFFPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60  
DB 1 RTVAAPSVFIFFPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60  
QY 61 SKDSTYLSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107  
DB 61 SKDSTYLSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107

RESULT 5  
US-08-422-093-8  
Sequence 8, Application US/08422093  
Patent No. 6056871  
GENERAL INFORMATION:  
APPLICANT: Leonard Presta  
APPLICANT: Brad Snedecor  
TITLE OF INVENTION: Altered Polypeptides with Increased  
TITLE OF INVENTION: Half-Life  
NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080

COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patin (Genentech)  
CURRENT APPLICATION DATA:  
FILING DATE: 14-APR-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION NUMBER:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Lee, Wendy M.  
REGISTRATION NUMBER:  
REFERENCE/DOCKET NUMBER: 932-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-1994  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 107 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-422-093-8

Query Match 100.0%; Score 553; DB 2; Length 107;  
Best Local Similarity 100.0%; Pred. No. 4.9e-57;  
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIFFPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60  
DB 1 RTVAAPSVFIFFPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60  
QY 61 SKDSTYLSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107  
DB 61 SKDSTYLSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107

US-08-422-093-8  
Sequence 8, Application US/08422093  
Patent No. 6056871  
GENERAL INFORMATION:  
APPLICANT: Leonard Presta  
APPLICANT: Brad Snedecor  
TITLE OF INVENTION: Altered Polypeptides with Increased  
TITLE OF INVENTION: Half-Life  
NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080

COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patin (Genentech)  
CURRENT APPLICATION DATA:  
FILING DATE: 14-APR-1995  
CLASSIFICATION: 536  
PRIOR APPLICATION NUMBER:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Lee, Wendy M.  
REGISTRATION NUMBER: 932  
REFERENCE/DOCKET NUMBER: 932  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-1994  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 107 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-422-093-8

Query Match 100.0%; Score 553; DB 3; Length 107;  
Best Local Similarity 100.0%; Pred. No. 4.9e-57;  
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIFFPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60  
DB 1 RTVAAPSVFIFFPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60  
QY 61 SKDSTYLSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107  
DB 61 SKDSTYLSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107

RESULT 6  
US-08-422-112-8  
Sequence 8, Application US/08422112  
Patent No. 6121022  
GENERAL INFORMATION:  
APPLICANT: Leonard Presta  
APPLICANT: Brad Snedecor  
TITLE OF INVENTION: Altered Polypeptides with Increased  
TITLE OF INVENTION: Half-Life  
NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080

COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/422,112  
FILING DATE: 14-APR-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Lee, Wendy M.  
REGISTRATION NUMBER:  
REFERENCE/DOCKET NUMBER: 932-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-1994  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 107 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-422-112-8

Query Match 100.0%; Score 553; DB 3; Length 107;  
Best Local Similarity 100.0%; Pred. No. 4.9e-57;  
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIFFPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60  
DB 1 RTVAAPSVFIFFPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60  
QY 61 SKDSTYLSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107  
DB 61 SKDSTYLSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107

RESULT 7  
US-09-301-593-20  
Sequence 20, Application US/09301593A



QY 61 SKDSTYLSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSNRGE 107  
 |||||  
 Db 168 SKDSTYLSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSNRGE 214  
 |||||

## RESULT 15

US-08-788-800-11  
 ; Sequence 11, Application US/08788800  
 ; Patent No. 5914112  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bednar, Martin M.  
 ; APPLICANT: Thomas, G. Roger  
 ; APPLICANT: Gross, Cordell E.  
 ; TITLE OF INVENTION: ANTI-CD18 ANTIBODIES IN STROKE  
 ; NUMBER OF SEQUENCES: 15  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Genentech, Inc.  
 ; STREET: 460 Point San Bruno Blvd  
 ; CITY: South San Francisco  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 94080  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: WinPatIn (Genentech)  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/788,800  
 ; FILING DATE: 22-Jan-1997  
 ; CLASSIFICATION: 424  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Lee, Wendy M.  
 ; REGISTRATION NUMBER: 40,378  
 ; REFERENCE/DOCKET NUMBER: P0987r1  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 415/225-1994  
 ; TELEFAX: 415/952-9881  
 ; TELEX: 910/371-7168  
 ; INFORMATION FOR SEQ ID NO: 11:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 214 amino acids  
 ; TYPE: Amino Acid  
 ; TOPOLOGY: Linear  
 ; US-08-788-800-11

Query Match 100.0%; Score 553; DB 2; Length 214;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-56;  
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIFFPSDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQGNLSQESVTEQD 60  
 |||||  
 Db 108 RTVAAPSVFIFFPSDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQGNLSQESVTEQD 167  
 |||||

QY 61 SKDSTYLSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSNRGE 107  
 |||||  
 Db 168 SKDSTYLSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSNRGE 214  
 |||||

Search completed: January 13, 2004, 12:46:33  
 Job time: 9.25153 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM: protein - protein search, using sw model

Run on: January 13, 2004, 12:22:35 ; Search time 24.0664 Seconds  
(without alignments)  
1326.564 Million cell updates/sec

Title: US-09-990-586-98

Perfect score: 1778

Sequence: 1 EFASKTGPVFLAPSSKST.....MHEALHNHYTKSLSPGK 332

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 76:\*

1: PIR1:\*

2: PIR2:\*

3: PIR3:\*

4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1767	99.4	330	1 GHU	Ig gamma-1 chain C
2	1630.5	91.7	377	2 A23511	Ig gamma-3 chain C
3	1628.5	91.6	377	2 A60764	Ig gamma-3 chain C
4	1604	90.2	326	1 G2HU	Ig gamma-2 chain C
5	1590.5	89.5	327	1 G4HU	Ig gamma-4 chain C
6	1263.5	71.1	374	2 S69339	Ig heavy chain V r
7	1263	71.0	328	2 I47159	Ig gamma 2a chain
8	1260	70.9	255	4 S31866	Ig gamma-1 chain C
9	1257	70.7	328	2 I47160	Ig gamma 2b chain
10	1254	70.5	234	2 PT0207	Ig gamma chain C r
11	1231	69.2	328	2 I47158	Ig gamma 1 chain c
12	1230.5	69.2	323	1 GHKB	Ig gamma 3 chain c
13	1227	69.0	328	2 I47161	Ig gamma-2 chain C
14	1212.5	68.2	329	1 G2GP	Ig gamma-1 chain -
15	1199.5	67.5	472	2 S31459	Ig heavy chain pre
16	1180.5	66.4	470	2 S22080	Ig heavy chain C r
17	1161.5	65.3	308	2 C30554	Ig heavy chain C r
18	1154	64.9	444	2 FC4436	monoclonal antibody
19	1152	64.8	326	2 PS0017	Ig gamma-1 chain C
20	1151	64.7	289	1 G3HUI	Ig gamma-3 heavy c
21	1146.5	64.5	333	2 PS0018	Ig gamma-2b chain C
22	1142	64.2	324	1 G1MS	Ig gamma-1 chain C
23	1141	64.2	329	1 G3MSC	Ig gamma-3 chain C
24	1137	63.9	393	1 G1MSM	Ig gamma-1 chain C
25	1130	63.6	398	1 G3MSM	Ig gamma-3 chain C
26	1126	63.3	330	1 G2MSA	Ig gamma-2a chain
27	1126	63.3	469	2 S37483	Ig gamma-2a chain
28	1123.5	63.2	335	1 G2MSAB	Ig gamma-2a chain
29	1121	63.0	399	1 G2MSAM	Ig gamma-2a chain

## ALIGNMENTS

### RESULT 1

GHU

Ig gamma-1 chain C region - human

C:Species: Homo sapiens (man)

C:Date: 31-Jan-1981 #sequence revision 18-Aug-1982 #text change 16-Jul-1999

C:Accession: A93433; S36861; S33887; B90563; A90564; B91568; A91723; A02146

R:Ellison, J.W.; Berson, B.J.; Hood, L.E.

Nucleic Acids Res. 10, 4071-4079, 1982

A:Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.

A:Reference number: A93433; MUID:82274238; PMID:6287432

A:Accession: A93433

A:Molecule type: DNA

A:Residues: 1-330 <ELL>

A:Cross-references: EMBL:Z17370

A:Note: this sequence has the Gln(17) allotypic marker, 97-Lys, and the Gln(1) markers, A:Note: Lys-330 is removed after translation

R:Harris, L.J.

submitted to the EMBL Data Library, October 1992

A:Reference number: S33904

A:Accession: S36861

A:Molecule type: DNA

A:Residues: 2-330 <HAR>

A:Cross-references: EMBL:Z17370

R:Takahashi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Honjo, T.

Cell 29, 671-679, 1982

A:Title: Structure of human immunoglobulin gamma genes: implications for evolution of a

A:Reference number: S33887; MUID:83001943; PMID:6811139

A:Accession: S33887

A:Molecule type: DNA

A:Residues: 88-113;235-330 <TAK>

A:Cross-references: EMBL:Z17370

R:Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman,

Biochemistry 9, 3161-3170, 1970

A:Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid sequer.

A:Reference number: A90563; MUID:71064024; PMID:5489771

A:Contents: myeloma protein Eu

A:Accession: B90563

A:Molecule type: protein

A:Residues: 1-96,'R',98-135 <CUN>

A:Note: this sequence has the Gln(3) marker, 97-Arg

R:Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.

Biochemistry 9, 3171-3181, 1970

A:Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid sequer

A:Reference number: A90564; MUID:71064025; PMID:5530842

A:Contents: Eu

A:Accession: A90564

A:Molecule type: protein

A:Residues: 136-154,'Q',156-165,'Q',167-176,'Q',178-194,'N',196-197,'D',199-238,'E',240,

A:Note: this sequence has the Gln(non-1) markers, 239-Glu and 241-Met

R:Ponstingl, H.; Hilschmann, N.

Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976

A:Title: Die Primarstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Nie),

Query Match 91.6%; Score 1628.5; DB 2; Length 377;  
Best Local Similarity 82.0%; Pred. No. 9e-107;  
Matches 309; Conservative 10; Mismatches 11; Indels 47; Gaps 1;

QY 3 ASTKGPSVPELPAPSSKSTSGTAALGCLVKDYFPEPTVTVSNWNGALTSVHTFPAVLQSS 62  
DB 1 ASTKGPSVPELPAPSSKSTSGTAALGCLVKDYFPEPTVTVSNWNGALTSVHTFPAVLQSS 60

QY 63 GLYSLSVTVTPSSSLGTQTYICNVNHPKSNTPKVDKKV----- 100  
DB 61 GLYSLSVTVTPSSSLGTQTYICNVNHPKSNTPKVDKKVPLGDTHTTCRCPEPKSC 120

QY 101 -----EPKSCDKTHICPPCPAPELGPGPSVFLFPKPKDT 135  
DB 121 DTPPPCPCPEPKSCDTPPPCPCPEPKSCDTPPPCPCPEPKSGVFLFPKPKDT 180

QY 136 LMSRTPVETCVVDVSHEDPEVKFNWYDGVGVHNAKTKPREEQYNSTYRVSVLTVLH 195  
DB 181 LMSRTPVETCVVDVSHEDPEVKFNWYDGVGVHNAKTKPREEQYNSTYRVSVLTVLH 240

QY 196 QDWLNKEYKCKVSNKALPAPIEKTISKAKGQRPQVYTLPPSRDELTKQVSLTCLVK 255  
DB 241 QDWLNKEYKCKVSNKALPAPIEKTISKAKGQRPQVYTLPPSRDELTKQVSLTCLVK 300

QY 256 GFVPSDIAVWESNGQPNNTKTPVLDSDGSLYSLYKLVKSRWQGNVFCVSMHE 315  
DB 301 GFVPSDIAVWESNGQPNNTKTPVLDSDGSLYSLYKLVKSRWQGNVFCVSMHE 360

QY 316 ALHNYTKQSLSPGK 332  
DB 361 ALHNRTPQSLSPGK 377

RESULT 4  
G2HU  
Ig gamma-2 chain C region - human  
C:Species: Homo sapiens (man)  
C:Date: 30-Apr-1981 #sequence revision 13-Jun-1983 #text\_change 21-Jul-2000  
C:Accession: A93906; A92809; A90752; A93132; A02148  
R:Ellison, J.; Hood, L.  
Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982  
A:Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain con  
A:Reference number: A93906; MUID:82197621; PMID:6904948  
A:Accession: A93906  
A:Molecule type: DNA  
A:Residues: 1-326 <ELL>  
A:Cross-references: GB:V00554; GB:J00230; NID:932759; PIDN:CAB58438.1; PID:96066056  
A:Note: Lys-326 is probably removed posttranslationally  
R:Wang, A.C.; Tung, E.; Fudenberg, H.H.  
J. Immunol. 125, 1048-1054, 1980  
A:Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and f  
A:Reference number: A92809; MUID:81007873; PMID:6774012  
A:Contents: myeloma protein T11  
A:Accession: A92809  
A:Molecule type: protein  
A:Residues: 1-19, 'Q', 21-57, 'Z', 59, 'A', 61-193, 'D', 195-325 <WAN>  
A:Note: Trp-156 is at or near the complement-binding site  
R:Connell, G.E.; Parr, D.M.; Hofmann, T.  
Can. J. Biochem. 57, 758-767, 1979  
A:Title: The amino acid sequences of the three heavy chain constant region domains of a  
A:Reference number: A90752; MUID:80001357; PMID:113060  
A:Contents: myeloma protein Zie  
A:Accession: A90752  
A:Molecule type: protein  
A:Residues: 1-24, 'E', 26-57, 'EV', 60-85, 132-171, 'ZZZ', 175, 'B', 177-193, 'D', 195-196, 'Q', 198-  
A:Note: This sequence has since been revised  
R:Hofmann, T.; Parr, D.M.  
Mol. Immunol. 16, 923-925, 1979  
A:Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin g  
A:Reference number: A93132; MUID:80114419; PMID:118920  
A:Contents: Zie  
A:Accession: A93132

A:Molecule type: protein  
A:Residues: 238-275 <HOF>  
R:Hofmann, T.; Parr, D.M.  
Submitted to the Atlas, March 1980  
A:Reference number: A94591  
A:Contents: annotation; Zie, revisions to residues 25, 59, 60, and 264-268  
A:Note: The revised sequence differs from that shown in having 60-Ala and in the amidat  
ned  
R:Milstein, C.; Frangione, B.  
Biochem. J. 121, 217-225, 1971  
A:Title: Disulphide bridges of the heavy chain of human immunoglobulin G2.  
A:Reference number: A90253; MUID:72033500; PMID:4940472  
A:Contents: annotation; myeloma protein Sa, disulfide bonds  
R:Frangione, B.; Milstein, C.; Pink, J.R.L.  
Nature 221, 145-148, 1969  
A:Title: Structural studies of immunoglobulin G.  
A:Reference number: A93157; MUID:69064124; PMID:5782707  
A:Contents: annotation; Sa, disulfide bonds  
C:Genetics:  
A:Gene: GDB:IGHG2  
A:Cross-references: GDB:119338; OMIM:147110  
A:Map position: 14q32.33-14q32.33  
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (ka  
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin  
F:20-85/Domain: immunoglobulin homology <IM1>  
F:123-202/Domain: immunoglobulin homology <IM2>  
F:233-306/Domain: immunoglobulin homology <IM3>  
F:14/Disulfide bonds: interchain (to light chain) #status experimental  
F:27-83,140-200,246-304/Disulfide bonds: #status experimental  
F:102,103,106,109/Disulfide bonds: interchain (to heavy chain) #status experimental  
F:176/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 90.2%; Score 1604; DB 1; Length 326;  
Best Local Similarity 91.2%; Pred. No. 3.9e-105;  
Matches 301; Conservative 12; Mismatches 13; Indels 4; Gaps 2;

QY 3 ASTKGPSVPELPAPSSKSTSGTAALGCLVKDYFPEPTVTVSNWNGALTSVHTFPAVLQSS 62  
DB 1 ASTKGPSVPELPAPSSKSTSGTAALGCLVKDYFPEPTVTVSNWNGALTSVHTFPAVLQSS 60

QY 63 GLYSLSVTVTPSSSLGTQTYICNVNHPKSNTPKVDKVPKSCDKTHCPCPELPG 122  
DB 61 GLYSLSVTVTPSSSLGTQTYICNVNHPKSNTPKVDKVPKSCDKTHCPCPELPG 116

QY 123 PSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVGVHNAKTKPREEQYN 182  
DB 117 PSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVGVHNAKTKPREEQYN 176

QY 183 STYRWVSVLTVLHODWLNKEYKCKVSNKALPAPIEKTISKAKGQRPQVYTLPPSRDE 242  
DB 177 STYRWVSVLTVLHODWLNKEYKCKVSNKALPAPIEKTISKAKGQRPQVYTLPPSRDE 236

QY 243 LTKQVSLTCLVKGFPYPSDIAVWESNGQPNNTKTPVLDSDGSLYSLYKLVKSRW 302  
DB 237 MTKQVSLTCLVKGFPYPSDIAVWESNGQPNNTKTPVLDSDGSLYSLYKLVKSRW 296

QY 303 QQGNVFCVSMHEALHNYTKQSLSPGK 332  
DB 297 QQGNVFCVSMHEALHNYTKQSLSPGK 326

RESULT 5  
G4HU  
Ig gamma-4 chain C region - human  
C:Species: Homo sapiens (man)  
C:Date: 02-Apr-1982 #sequence revision 02-Apr-1982 #text\_change 16-Jul-1999  
C:Accession: A90933; A90249; A02150  
R:Ellison, J.; Buxbaum, J.; Hood, L.  
DNA 1, 11-18, 1981  
A:Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.  
A:Reference number: A90933; MUID:83157104; PMID:6299662

Db 177 STYRVSVLPVPIQHDWLNKGFCKVNNKDLPAPIITRIISKAKGQTRPQVYTLPPHAE 236  
 QY 243 LTKNOVSLCLVKGFPSPDIAVWESNGQ--PNNYKTTTPPVLDSDGSPFLYKSLTVDKS 300  
 Db 237 LSRKSVITCLVIGFPPDIDVWQNGQPEPEGNRYRTTPQODVGTGYLYSKFSVDKA 296  
 QY 301 RWQGNVFCSCVMHEALHNYHTQKSLSPGK 332  
 Db 297 SWGGGIFQCAVMHEALHNYHTQKSLTPGK 328

## RESULT 8

S31866  
 Ig gamma-1 chain C region - synthetic  
 A:Species: synthetic  
 A:Note: Homo sapiens (man) gene engineered and expressed in Escherichia coli  
 C:Date: 06-Jan-1995 #sequence\_revision 17-Mar-1997 #text\_change 19-May-2000  
 C:Accession: S31866  
 R:Filipula, D.  
 Submitted to the EMBL Data Library, February 1993  
 A:Description: Screening method for protein-protein interactions of cloned gene products.  
 A:Reference number: S31866  
 A:Accession: S31866  
 A:Molecule type: mRNA  
 A:Residues: 1-255 <FIL>  
 A:Cross-references: EMBL:X70421; NID:G33068; PIDN:CAA49866.1; PID:G33069  
 C:Keywords: immunoglobulin  
 F:1-22/Region: Escherichia coli outer membrane protein A precursor  
 F:23-255/Region: human Ig gamma-1 chain C region

Query Match 70.9%; Score 1260; DB 4; Length 255;  
 Best Local Similarity 97.5%; Pred. No. 3.6e-81;  
 Matches 233; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
 QY 94 TKVDKVEPKSCDKTHTCCPAPELLGGPSVFLPPPKDFTLMISRTPEVTCVVVDYSH 153  
 Db 17 TAAQADVESKCDKTHCTCPAPELLGGPSVFLPPPKDFTLMISRTPEVTCVVVDYSH 76  
 QY 154 EPEVKFNWYVDGVEVHNATKPREQYNSTYRVVSVLTVLHQDWLNGKEYCKCKVSKNAL 213  
 Db 77 EPEVKFNWYVDGVEVHNATKPREQYNSTYRVVSVLTVLHQDWLNGKEYCKCKVSKNAL 136  
 QY 214 PAPIETISKAGQPREPOVYTLPPSRDELTKNOVSLCLVKGFPSPDIAVWESNGQPE 273  
 Db 137 PAPIETISKAGQPREPOVYTLPPSRDELTKNOVSLCLVKGFPSPDIAVWESNGQPE 196  
 QY 274 NNYKTTTPVLDSDGSPFLYKSLTVDKSRWQGNVFCSCVMHEALHNYHTQKSLSPGK 332  
 Db 197 NNYKTTTPVLDSDGSPFLYKSLTVDKSRWQGNVFCSCVMHEALHNYHTQKSLSPGK 255

## RESULT 9

I47160  
 Ig gamma 2b chain constant region - pig (fragment)  
 C:Species: Sus scrofa domestica (domestic pig)  
 C:Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 21-Jan-2000  
 C:Accession: I47160  
 R:Kacskovics, I.; Sun, J.; Butler, J.E.  
 J. Immunol. 153, 3565-3573, 1994  
 A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a  
 A:Reference number: I47158; MUID:95015845; PMID:7930579  
 A:Accession: I47160  
 A>Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-328 <KAC>  
 A:Cross-references: EMBL:U03780; NID:G433125; PIDN:AAA52218.1; PID:G433126  
 C:Genetics:  
 A:Gene: IgG2b  
 C:Superfamily: immunoglobulin C region; immunoglobulin homology  
 F:133-202/Domain: immunoglobulin homology <IMM>

Query Match 70.7%; Score 1257; DB 2; Length 328;  
 Best Local Similarity 69.3%; Pred. No. 8e-81;

Matches 230; Conservative 42; Mismatches 54; Indels 6; Gaps 2;  
 QY 3 ASTKGPVFLAPLASKSTSGTAALCLVXDYFPPEVTVVSNWNGALTSVHTTPAVLQSS 62  
 Db 1 AKTAPLVYFLAPCGRTDGTGPNVALGLASSYFPPEVTVVSNWNGALTSVHTTPAVLQSS 60  
 QY 63 GLYSLSVTVTPSSSLGTQYICNVNHNKPSNTKVDKVEPKSCDKTHTCCPAPELLGG 122  
 Db 61 GLYSLSVTVTPASSLSKSYTCNVNHPATITKVDKRVGKTKPPCPDICACPSP----G 116  
 QY 123 PSVELFPKPKDFTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREQYN 182  
 Db 117 PSVFIKPKDFTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREQYN 176  
 QY 183 STYRVSVLTVLHQDWLNGKEYCKCKVSKNALPAPIETISKAGQPREPOVYTLPPSRDE 242  
 Db 177 STYRVSVLTVLHQDWLNGKEYCKCKVSKNALPAPIETISKAGQPREPOVYTLPPHAE 236  
 QY 243 LTKNOVSLCLVKGFPSPDIAVWESNGQ--PNNYKTTTPPVLDSDGSPFLYKSLTVDKS 300  
 Db 237 LSRKSVITCLVIGFPPDIDVWQNGQPEPEGNRYRTTPQODVGTGYLYSKFSVDKA 296  
 QY 301 RWQGNVFCSCVMHEALHNYHTQKSLSPGK 332  
 Db 297 SWGGGIFQCAVMHEALHNYHTQKSLTPGK 328

RESULT 10  
 PT0207  
 Ig gamma chain C region - chimpanzee  
 C:Species: Pan troglodytes (chimpanzee)  
 C:Date: 23-Nov-1991 #sequence\_revision 23-Nov-1991 #text\_change 16-Jul-1999  
 C:Accession: PT0207  
 R:Ehrlich, P.H.; Moustafa, Z.A.; Oestberg, L.  
 Mol. Immunol. 28, 319-322, 1991  
 A:Title: Nucleotide sequence of chimpanzee Cc and hinge regions.  
 A:Reference number: PT0207; MUID:91287716; PMID:2062315  
 A:Accession: PT0207  
 A:Molecule type: mRNA  
 A:Residues: 1-234 <EHR>  
 C:Superfamily: immunoglobulin C region; immunoglobulin homology  
 C:Keywords: immunoglobulin  
 F:48-117/Domain: immunoglobulin homology <IMM>

Query Match 70.5%; Score 1254; DB 2; Length 234;  
 Best Local Similarity 98.7%; Pred. No. 8.5e-81;  
 Matches 231; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 92 SNTKVDKVEPKSCDKTHTCCPAPELLGGPSVFLPPPKDFTLMISRTPEVTCVVVDV 151  
 Db 1 SNTKVDKVEPKSCDKTHTCCPAPELLGGPSVFLPPPKDFTLMISRTPEVTCVVVDV 60  
 QY 152 SHEDPEVKFNWYVDGVEVHNATKPREQYNSTYRVVSVLTVLHQDWLNGKEYCKCKVSKN 211  
 Db 61 SHEDPEVKFNWYVDGVEVHNATKPREQYNSTYRVVSVLTVLHQDWLNGKEYCKCKVSKN 120  
 QY 212 ALPAIETISKAGQPREPOVYTLPPSRDELTKNOVSLCLVKGFPSPDIAVWESNGQ 271  
 Db 121 ALPAIETISKAGQPREPOVYTLPPSRDELTKNOVSLCLVKGFPSPDIAVWESNGQ 180  
 QY 272 PENNYKTTTPVLDSDGSPFLYKSLTVDKSRWQGNVFCSCVMHEALHNYHTQKS 325  
 Db 181 PENNYKTTTPVLDSDGSPFLYKSLTVDKSRWQGNVFCSCVMHEALHNYHTQKS 234

## RESULT 11

I47158  
 Ig gamma 1 chain constant region - pig (fragment)  
 C:Species: Sus scrofa domestica (domestic pig)  
 C:Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 21-Jan-2000  
 C:Accession: I47158  
 R:Kacskovics, I.; Sun, J.; Butler, J.E.  
 J. Immunol. 153, 3565-3573, 1994



QY 3 ASTKGSVPFLAPSSKSTSGGTAALGCLVKDYFPEPVTWNSGALTSVHTFPAVLQSS 62  
 Db 1 AKTAPSVYPLAPCGRDIGENVALGCLASSYFPPEVTWNSGALTSVHTFPAVLQPS 60  
 QY 63 GLYSLSVVTVPPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHTCPCPAPELLGG 122  
 Db 61 GLYSLSVVTVPPSSSLKSYTCNVNHPKSNTKVDKVEPKSCDKTHTCPCPAPELLGG 116  
 QY 123 PSVFLFPPPKDITLMISRTPEVTCVVVDVSHEDPEVKENFVVDGVEVHNATKPREQYN 182  
 Db 117 PSVFLFPPPKDITLMISRTPEVTCVVVDVSHEDPEVKENFVVDGVEVHNATKPREQYN 176  
 QY 183 STYRVSVTLVHODWLNKGKCYKCKVSNKALPAPIETIKTSKAKQPREPQVYTLPPSRDE 242  
 Db 177 STYRVSVTLVHODWLNKGKCYKCKVSNKALPAPIETIKTSKAKQPREPQVYTLPPSRDE 236  
 QY 243 LTKNOVSLTCLVKGYFSPDIAVEWESNGQ--PENNYKTTTPVLSDSGDSFFLYSKLTVDKS 300  
 Db 237 LRSKVTYVTLVIGFYPPDIIHVEWKSNGQPEPEGNRYRTTPQDQVDGTFELYSKLAVDKA 296  
 QY 301 RMOQGNVFSVSMHEALHNHYTQKSLSLSPGK 332  
 Db 297 RWDHGETFECAVWHEALHNHYTQKSLSLSPGK 328

## RESULT 14

G2GP

IG gamma-2 chain C region - guinea pig  
 C/Species: Cavia porcellus (guinea pig)  
 C/Date: 07-May-1981 #sequence\_revision 07-May-1981 #text\_change 16-Jul-1999  
 C/Accession: A94553; A90352; A90359; A90384; A90385; A02151  
 R.Frischmann, T.M.  
 submitted to the Atlas, April 1975  
 A/Reference number: A94553  
 A/Accession: A94553  
 A/Molecule type: protein  
 A/Residues: 1-3 <TRI>  
 R.Bischoff, B.K.; Hussain, Q.Z.; Cebra, J.J.  
 Biochemistry 10, 18-25, 1971  
 A/Title: Structure of heavy chain from strain 13 guinea pig immunoglobulin-G(2). III. Am  
 A/Reference number: A90352; MUID:71058471; PMID:5538606  
 A/Accession: A90352  
 A/Molecule type: protein  
 A/Residues: 4-68 <BIR>  
 R.Furner, K.J.; Cebra, J.J.  
 Biochemistry 10, 9-17, 1971  
 A/Title: Structure of heavy chain from strain 13 guinea pig immunoglobulin-G(2). II. Am  
 A/Reference number: A90359; MUID:71058486; PMID:5538616  
 A/Accession: A90359  
 A/Molecule type: protein  
 A/Residues: 69-133/312-329 <TUR>  
 R.Furner, K.J.; Cebra, J.J.  
 Biochemistry 13, 4796-4803, 1974  
 A/Title: Primary structure of the C-H2 homology region from guinea pig IgG2 antibodies.  
 A/Reference number: A90384; MUID:75036072; PMID:4429665  
 A/Accession: A90384  
 A/Molecule type: protein  
 A/Residues: 134-226 <TRA>  
 R.Frischmann, T.M.; Cebra, J.J.  
 Biochemistry 13, 4804-4811, 1974  
 A/Title: Primary structure of the C-H3 homology region from guinea pig IgG2 antibodies.  
 A/Reference number: A90385; MUID:75036073; PMID:4609467  
 A/Accession: A90385  
 A/Molecule type: protein  
 A/Residues: 227-311 <TR2>  
 R.Oliveira, B.; Lamm, M.E.  
 Biochemistry 10, 26-31, 1971  
 A/Title: Interchain disulfide bridges of guinea pig gamma-2- immunoglobulin.  
 A/Reference number: A90354; MUID:71058474; PMID:4922544  
 A/Contents: annotation: disulfide bonds  
 A/Note: Cys-16 is involved in a heavy-light chain bond  
 A/Note: Cys-105, Cys-107, and Cys-110 form inter-heavy chain bonds

C/Comment: This chain was isolated from pooled serum of strain 13 inbred guinea pigs.  
 C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (L) and two identical heavy (H) chains. In some cases, such as IgA and IgM, the subunits associate into a dimer.  
 C/Superfamily: immunoglobulin C region; immunoglobulin homology  
 C/Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin  
 F/21-81/Domain: immunoglobulin homology <IM1>  
 F/135-204/Domain: immunoglobulin homology <IM2>  
 F/241-310/Domain: immunoglobulin homology <IM3>  
 F/28-79/Disulfide bonds: #status experimental  
 F/142-202/Disulfide bonds: #status experimental  
 F/178/Binding site: carbohydrate (Asn) (covalent) #status experimental  
 F/248-308/Disulfide bonds: #status experimental

Query Match 68.2%; Score 1212.5; DB 1; Length 329;

Best Local Similarity 70.3%; Pred. No. 1.1e-77;

Matches 234; Conservative 28; Mismatches 62; Indels 9; Gaps 4;

QY 3 ASTKGSVPFLAPSSKSTSGGTAALGCLVKDYFPEPVTWNSGALTSVHTFPAVLQSS 62

Db 2 ARTAPSVFPLAASCVDTSNNMTLGLVKGYPPEPVTWNSGALTSVHTFPAVLQ-S 60

QY 63 GLYSLSVVTVPPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTH--TCPPCPAPELL 120

Db 61 GLYSLSVVTVPPSSSLKSYTCNVNHPKSNTKVDKVEPKSCDKTH--TCPPCPAPELL 116

QY 121 GGPVSFLFPPPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQ 180

Db 117 GGPVSFLFPPPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQ 176

QY 181 YNSTRVSVTLVHODWLNKGKCYKCKVSNKALPAPIETIKTSKAKQPREPQVYTLPPSR 240

Db 177 YNSTRVSVTLVHODWLNKGKCYKCKVSNKALPAPIETIKTSKAKQPREPQVYTLPPSR 236

QY 241 DELTKNOVSLTCLVKGYFSPDIAVEWESNGQ--ENNYKTTTPVLSDSGDSFFLYSKLTVD 298

Db 237 DELTKNOVSLTCLVKGYFSPDIAVEWESNGQ--ENNYKTTTPVLSDSGDSFFLYSKLTVD 296

QY 299 KSRWQGNVFSVSMHEALHNHYTQKSLSLSPG 331

Db 297 KSRWQGNVFSVSMHEALHNHYTQKSLSLSPG 329

## RESULT 15

S31459

IG gamma-1 chain - sheep (fragment)

C/Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C/Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 16-Jul-1999

C/Accession: S31459

R.Patri, S.; Nau, F.

submitted to the EMBL Data Library, December 1992

A/Reference number: S31459

A/Accession: S31459

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-472 &lt;PAT&gt;

A/Cross-references: EMBL:X69797

C/Superfamily: immunoglobulin C region; immunoglobulin homology

C/Keywords: immunoglobulin

F/277-346/Domain: immunoglobulin homology &lt;IM&gt;

Query Match 67.5%; Score 1199.5; DB 2; Length 472;

Best Local Similarity 67.5%; Pred. No. 1.3e-76;

Matches 224; Conservative 38; Mismatches 67; Indels 3; Gaps 2;

QY 3 ASTKGSVPFLAPSSKSTSGGTAALGCLVKDYFPEPVTWNSGALTSVHTFPAVLQSS 62

Db 142 ASTTTPKVPYPLTSCCGDTSSTSVTLGLCLVSSYFPEPVTWNSGALTSVHTFPAVLQSS 201

QY 63 GLYSLSVVTVPPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHTCPCPAPELLGG 122

Db 202 GLYSLSVVTVPPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHTCPCPAPELLGG 260

QY 123 PSVFLFPPPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREQYN 182

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 13, 2004, 12:19:34 ; Search time 14.4378 Seconds  
(without alignments)  
1076.912 Million cell updates/sec

Title: US-09-990-586-98

Perfect score: 1778

Sequence: 1 EFATKGSVPFLAPSSKST.....MHEALHNHYTKSLSPGK 332

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1767	99.4	330	1 GCI_HUMAN	P01857 homo sapien
2	1604	90.2	326	1 GCI_HUMAN	P01859 homo sapien
3	1590.5	89.5	327	1 GCI_HUMAN	P01861 homo sapien
4	1230.5	69.2	323	1 GC_RABIT	P01870 oryctolagus
5	1212.5	68.2	329	1 GC2_CAVPO	P01862 cavia porce
6	1156	65.0	290	1 GCI_HUMAN	P01860 homo sapien
7	1152	64.8	326	1 GCI_RAT	P02059 rattus norv
8	1146.5	64.5	333	1 GCI_RAT	P02061 rattus norv
9	1142	64.2	324	1 GCI_MOUSE	P01868 mus musculu
10	1141	64.2	329	1 GCI_MOUSE	P22436 mus musculu
11	1137	63.9	393	1 GCI_MOUSE	P01869 mus musculu
12	1130	63.6	398	1 GCI_MOUSE	P03987 mus musculu
13	1126	63.3	330	1 GCAA_MOUSE	P01863 mus musculu
14	1123.5	63.2	335	1 GCB_MOUSE	P01864 mus musculu
15	1121	63.0	399	1 GCM_MOUSE	P01865 mus musculu
16	1118.5	62.9	329	1 GCC_RAT	P02062 rattus norv
17	1112	62.5	322	1 GCA_RAT	P20760 rattus norv
18	1087	61.1	336	1 GCB_MOUSE	P01866 mus musculu
19	1082	60.9	405	1 GCB_MOUSE	P01867 mus musculu
20	492	27.7	428	1 EPC_HUMAN	P01854 homo sapien
21	483.5	27.2	429	1 EPC_RAT	P01855 rattus norv
22	468	26.3	421	1 EPC_MOUSE	P06336 mus musculu
23	444	25.0	454	1 MUC_HUMAN	P01871 homo sapien
24	439.5	24.7	458	1 MUC_RABIT	P03988 oryctolagus
25	429.5	24.2	455	1 MUC_MOUSE	P01872 mus musculu
26	429	24.1	479	1 MUC_RABIT	P04221 oryctolagus
27	422	23.7	457	1 MUC_SUNMU	P020768 suncus muri
28	419.5	23.6	476	1 MUC_MOUSE	P01873 mus musculu
29	417	23.5	450	1 MUC_CANFA	P01874 canis famil
30	415.5	23.4	454	1 MUC_MESAU	P06337 mesocricetu
31	402	22.6	391	1 MUCB_HUMAN	P04220 homo sapien
32	395	22.2	438	1 HVCB_HETFR	P23087 heterodontu
33	386	21.7	461	1 HVCB_HETFR	P23088 heterodontu

## ALIGNMENTS

### RESULT 1

ID	GCI_HUMAN	STANDARD	PRT	330 AA
AC	P01857	1986 (Rel. 01, Created)		
DT	21-JUL-1986	(Rel. 01, Last sequence update)		
DT	15-SEP-2003	(Rel. 42, Last annotation update)		
DE	IG gamma-1 chain C region.			
GN	IGHG1			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=82274238; PubMed=6287432;			
RA	Ellison J.W., Berson B.J., Hood L.E.;			
RT	"The nucleotide sequence of a human immunoglobulin C gamma1 gene."			
RL	Nucleic Acids Res. 10:4071-4079(1982).			
RN	[2]			
RP	SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).			
RX	MEDLINE=71064024; PubMed=5489771;			
RA	Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,			
RA	Maxdal M.J., Edelman G.M.;			
RT	"The covalent structure of a human gamma G-immunoglobulin. VII. Amino acid sequence of heavy-chain cyanogen bromide fragments H1-H4."			
RL	Biochemistry 9:3161-3170(1970).			
RN	[3]			
RP	SEQUENCE OF 136-329 (EU).			
RX	MEDLINE=71064025; PubMed=5530842;			
RA	Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,			
RA	Edelman G.M.;			
RT	"The covalent structure of a human gamma G-immunoglobulin. 8. Amino acid sequence of heavy-chain cyanogen bromide fragments H5-H7."			
RL	Biochemistry 9:3171-3181(1970).			
RN	[4]			
RP	SEQUENCE (MYELOMA PROTEIN NIE).			
RX	MEDLINE=77070289; PubMed=828475;			
RA	Ponstingl H., Hilschmann N.;			
RT	"The rule of antibody structure. The primary structure of a monoclonal IgG1 immunoglobulin (myeloma protein NIE). III. The chymotryptic peptides of the H-chain, alignment of the tryptic peptides and discussion of the complete structure."			
RL	Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).			
RN	[5]			
RP	SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS.			
RX	MEDLINE=83289131; PubMed=6884994;			
RA	Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;			
RT	"Three-dimensional structure determination of antibodies. Primary structure of crystallized monoclonal immunoglobulin IgG1 KOL, I."			
RL	Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).			
RN	[6]			
RP	DISULFIDE BONDS.			
RX	MEDLINE=71064027; PubMed=4923144;			
RA	Gall W.E., Edelman G.M.;			
RT	"The covalent structure of a human gamma G-immunoglobulin. X.			

34	385.5	21.7	438	1 HVC2_HETFR	P23085 heterodontu
35	384.5	21.6	353	1 ALC1_HUMAN	P01876 homo sapien
36	381.5	21.5	353	1 ALC1_GORGO	P20758 gorilla gor
37	380	21.4	370	1 HVC1_HETFR	P23084 heterodontu
38	379	21.3	340	1 ALC2_HUMAN	P01877 homo sapien
39	363	20.4	393	1 HVC3_HETFR	P23086 heterodontu
40	348	19.6	344	1 ALC_MOUSE	P01878 mus musculu
41	329	18.5	446	1 MUC_CHICK	P01875 gallus gall
42	320	18.0	299	1 ALC_RABIT	P01879 oryctolagus
43	290.5	16.3	481	1 MUCM ICTPU	P23735 ictalurus p
44	223.5	12.6	383	1 DTC_HUMAN	P01880 homo sapien
45	194.5	10.9	513	1 SHS1_MOUSE	P97797 m protein-t



QY 303 OQGNVFSVSMHEALHNYHTQKSLSPCK 332  
 DB 301 OQGNVFSVSMHEALHNYHTQKSLSPCK 330

RESULT 2  
 GC2\_HUMAN  
 ID GC2\_HUMAN STANDARD; PRT; 326 AA.  
 AC P01859;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE IG gamma-2 chain C region.  
 GN IGHG2

OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE OF 2-326 FROM N.A.  
 RX MEDLINE=82197621; PubMed=6804948;  
 RA Ellison J.W., Hood L.E.;  
 RT "Linkage and sequence homology of two human immunoglobulin gamma  
 heavy chain constant region genes.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 79:1984-1988(1982).  
 RN [2]  
 RP SEQUENCE OF 88-115 FROM N.A.  
 RX TISSUE-Petal liver;  
 RC MEDLINE=83001943; PubMed=6811139;  
 RA Takahashi N., Ueda S., Obata M., Nikaido T., Nakai S., Honjo T.;  
 RT "Structure of human immunoglobulin gamma genes: implications for  
 evolution of a gene family.";  
 RL Cell 29:671-679(1982).  
 RN [3]  
 RP SEQUENCE OF 99-177 AND 310-326 FROM N.A.  
 RC TISSUE-Fetal liver;  
 RX MEDLINE=84235992; PubMed=6329676;  
 RA Krawinkel U., Rabbitts T.H.;  
 RT "Comparison of the hinge-coding segments in human immunoglobulin gamma  
 heavy chain genes and the linkage of the gamma 2 and gamma 4 subclass  
 genes";  
 RL EMBO J. 1:403-407(1982).  
 RN [4]  
 RP SEQUENCE OF 1-325 (MYELOMA PROTEIN TIL).  
 RX MEDLINE=81007873; PubMed=6774012;  
 RA Wang A.-C., Tung E., Fudenberg H.H.;  
 RT "The primary structure of a human IGH2 heavy chain: genetic,  
 evolutionary, and functional implications.";  
 RL J. Immunol. 125:1048-1054(1980).  
 RN [5]  
 RP SEQUENCE OF 1-85 AND 132-325 (MYELOMA PROTEIN ZIE).  
 RX MEDLINE=80001357; PubMed=113060;  
 RA Connell G.E., Parr D.M., Hofmann T.;  
 RT "The amino acid sequences of the three heavy chain constant region  
 domains of a human IGH2 myeloma protein.";  
 RL Can. J. Biochem. 57:758-767(1979).  
 RN [6]  
 RP SEQUENCE OF 238-275 (ZIE).  
 RX MEDLINE=80114419; PubMed=118920;  
 RA Hofmann T., Parr D.M.;  
 RT "A note of the amino acid sequence of residues 381-391 of human  
 immunoglobulin gamma chains.";  
 RL Mol. Immunol. 16:923-925(1979).  
 RN [7]  
 RP REVISIONS TO 25; 59; 60 AND 264-268 (ZIE).  
 RA Hofmann T., Parr D.M.;  
 RL Submitted (MAR-1980) to the PIR data bank.  
 RN [8]  
 RP SEQUENCE OF 1-121 (DOT).  
 RX MEDLINE=95255298; PubMed=7737190;  
 RA Stoppini M., Bellotti V., Negri A., Merlini G., Garver F., Ferri G.;  
 RT "Characterization of the two unique human anti-flavin monoclonal  
 immunoglobulins.";

RL Eur. J. Biochem. 228:886-893(1995).  
 RN [9]  
 RP DISULFIDE BONDS.  
 RX MEDLINE=72033500; PubMed=4940472;  
 RA Milstein C., Frangione B.;  
 RT "Disulfide bridges of the heavy chain of human immunoglobulin G2.";  
 RL Biochem. J. 121:217-225(1971).  
 RN [10]  
 RP DISULFIDE BONDS.  
 RX MEDLINE=69064124; PubMed=5782707;  
 RA Frangione B., Milstein C., Pink J.R.L.;  
 RT "Structural studies of immunoglobulin G.";  
 RL Nature 221:145-148(1969).  
 CC  
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 CC  
 CC EMBL; J00230; AAB59393.1; -.  
 DR PIR; A93906; G2HU.  
 DR HSP; P01857; IFC1.  
 DR Genew; HGNC:5526; IGHG2.  
 DR MIM; 147110; -.  
 DR GO; GO:0005624; C:membrane fraction; NAS.  
 DR GO; GO:0003823; F:antigen binding activity; TAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003597; IG\_c1.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR Pfam; PF00047; IG; 3.  
 DR SMART; SM00407; IGC1; 2.  
 DR PROSITE; PS00835; IG\_LIKE; 3.  
 DR PROSITE; PS00290; IG\_MHC; 2.  
 KW Immunoglobulin domain; Immunoglobulin C region.  
 FT NON\_TER 1 98  
 FT DOMAIN 1 98  
 FT DOMAIN 99 110  
 FT DOMAIN 111 219  
 FT DOMAIN 220 326  
 FT DISULFID 14 14  
 FT DISULFID 27 83  
 FT DISULFID 102 102  
 FT DISULFID 103 103  
 FT DISULFID 106 106  
 FT DISULFID 109 109  
 FT DISULFID 140 200  
 FT DISULFID 246 304  
 FT SITE 156 156  
 FT MOD\_RES 326 326  
 FT VARIANT 60 60  
 FT CONFLICT 109 109  
 FT SEQUENCE 326 AA; 35884 MW; 8310878C6879C CRC64;  
 SQ  
 Query Match 90.2%; Score 1604; DB 1; Length 326;  
 Best Local Similarity 91.2%; Pred. No. 1.2e-113;  
 Matches 301; Conservative 12; Mismatches 13; Indels 4; Gaps 2;  
 QY 3 ASTKGFSVFPLAPSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 62  
 DB 1 ASTKGFSVFPLAPSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60  
 QY 63 GLYSLSSVTVTPSSSLGTQITICNVNKPSTKVDKVKPEKSCDKTHTCPCPAPPELLGG 122  
 DB 61 GLYSLSSVTVTPSSSLGTQITICNVNKPSTKVDKVKPEKSCDKTHTCPCPAPPELLGG 116  
 QY 123 PSVFLFPKPKDITLMISRTPEVTCVVDVSHEDPEVQFNWYVDGVGVNATKPKREEQYN 182  
 DB 117 PSVFLFPKPKDITLMISRTPEVTCVVDVSHEDPEVQFNWYVDGVGVNATKPKREEQFN 176



RL Biochem. J. 116:249-259 (1970).  
 RN [5]  
 RP SEQUENCE OF 129-131 AND 155-322.  
 RA Hill R.L., Lebovitz H.E., Fellows R.E. Jr., Delaney R.;  
 RL (in) Killander J. (eds.);  
 RL Gamma globulins, Nobel symp. 3, pp.109-127, Almqvist and Wiksell,  
 RL Stockholm (1967).  
 CC -1- MISCELLANEOUS: REF.1 SEQUENCE HAS THE D12 ALLOTYPIC MARKER,  
 CC 104-THR, AND THE E14 MARKER, 185-THR. REF.3 HAS THE D11 AND E15  
 CC MARKERS AND REF.5 THE E15 MARKER.  
 CC -1- SIMILARITY: Contains 3 immunoglobulin-like domains.  
 CC  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL: M16426; AAA31289.1; -;  
 DR PIR: A91749; GHRB.  
 DR HSSP: P01857; IFC1.  
 DR InterPro: IPR007110; IG-like.  
 DR InterPro: IPR003597; IG\_C1.  
 DR InterPro: IPR003006; IG\_MHC.  
 DR Pfam: PF00047; Ig; 2.  
 DR SMART: SM00407; Igc1; 2.  
 DR PROSITE: PS00835; IG-LIKE; 3.  
 DR PROSITE: PS00290; IG\_MHC; 1.  
 DR Immunoglobulin domain; Immunoglobulin C region; Repeat.  
 FT NON TER 1 96  
 FT DOMAIN 6 1  
 FT 114 213 IG-LIKE 1.  
 FT 222 318 IG-LIKE 2.  
 FT 104 104 T -> M (IN D11 MARKER).  
 FT 185 185 T -> A (IN E15 MARKER).  
 FT 48 48 N -> E (IN REF. 2).  
 FT 71 71 V -> VPV (IN REF. 2).  
 FT 144 144 Q -> E (IN REF. 3 AND 4).  
 FT 173 173 N -> D (IN REF. 5).  
 FT 187 187 Q -> D (IN REF. 5).  
 FT 201 201 N -> D (IN REF. 5).  
 FT 218 218 Q -> E (IN REF. 5).  
 FT 233 233 E -> Q (IN REF. 5).  
 FT 246 246 N -> D (IN REF. 5).  
 FT 256 256 E -> G (IN REF. 5).  
 FT 260 260 N -> D (IN REF. 5).  
 FT 266 266 N -> D (IN REF. 5).  
 FT 280 280 Y -> W (IN REF. 5).  
 FT 284 284 N -> S (IN REF. 5).  
 SQ SEQUENCE 323 AA; 35404 MW; 69E8AA118D579A8B CRC64;  
  
 Query Match 59.28; Score 1230.5; DB 1; Length 323;  
 Best Local Similarity 70.08; Pred. No. 1.5e-85;  
 Matches 229; Conservative 34; Mismatches 57; Indels 7; Gaps 2;  
  
 QY 6 KGPSVFLAPSSKSTSGTAAALGCLVDFPFPVTVSWNSGALTSVHTFPVAVLQSSGLY 65  
 DB 4 KAPSVFLAPCCGTPSPSTVTLGCLVKGYPFPVTVTWSGTLTNGVTFPVSQSSGLY 63  
  
 QY 66 SLSSVWTVFSSSLGTQYICNVNHPKNTKVKKPEKSCDKTHTCPCPAPELLGGPSV 125  
 DB 64 SLSSVWTVFSSS---QPVTCNVNHPATNTKVDKTVAPSTCSK---FTCPPELLGGPSV 116  
  
 QY 126 FLFPFKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVVHNAKPKPEQVNSTY 185  
 DB 117 FIFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVVHNAKPKPEQVNSTY 176  
  
 QY 186 RVSVLTVLQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYTLPPSRDELTK 245  
 DB 177 RVSVLTVLQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYTLPPSRDELTK 236

QY 246 NOVSLTCLYKGFPSDIAVWESNGQPENNYKTTPFVLDSDGSFFLYSKLTVDKRWQOG 305  
 DB 237 RVSLTCLMNGFSPDISVWENKNGKAEDNYKTTPAVLDSGDSYFLYKNKLSVPTSEWQRG 296  
  
 QY 306 NYFSCSVWHEALHNHYTKSLSLSPGK 332  
 DB 297 DVFTCSVWHEALHNHYTKSLSLSPGK 323  
  
 RESULT 5  
 GC2\_CAVPO STANDARD; PRT; 329 AA.  
 AC P01862;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig gamma-2 chain C region.  
 DE Cavia porcellus (Guinea pig).  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Myricognathi; Caviidae; Cavia.  
 ON NCBI\_TaxID=10141;  
 RX MEDLINE=71058471; PubMed=5538606;  
 RA Birshstein B.K., Huseain Q.Z., Cebra J.J.;  
 RT "Structure of heavy chain from strain 13 guinea pig  
 RT immunoglobulin-G(2). 3. Amino acid sequence of the region around the  
 RT half-cystine joining heavy and light chains.";  
 RL Biochemistry 10:18-25(1971).  
 RN [3]  
 RP SEQUENCE OF 69-133 AND 312-329.  
 RX MEDLINE=71058486; PubMed=5538616;  
 RA Turner K.J., Cebra J.J.;  
 RT "Structure of heavy chain from strain 13 guinea pig  
 RT immunoglobulin-G(2). II. Amino acid sequence of the carboxyl-terminal  
 RT and hinge region cyanogen bromide fragments.";  
 RL Biochemistry 10:9-17(1971).  
 RN [4]  
 RP SEQUENCE OF 134-226.  
 RX MEDLINE=75036072; PubMed=4429665;  
 RA Tracey D.E., Cebra J.J.;  
 RT "Primary structure of the CH2 homology region from guinea pig IgG2  
 RT antibodies.";  
 RL Biochemistry 13:4796-4803(1974).  
 RN [5]  
 RP SEQUENCE OF 227-311.  
 RX MEDLINE=75036073; PubMed=4609467;  
 RA Trischmann T.M., Cebra J.J.;  
 RT "Primary structure of the CH3 homology region from guinea pig IgG2  
 RT antibodies.";  
 RL Biochemistry 13:4804-4811(1974).  
 RN [6]  
 RP DISULFIDE BONDS.  
 RX MEDLINE=71058474; PubMed=4922544;  
 RA Oliveira B., Lamm M.E.;  
 RT "Interchain disulfide bridges of guinea pig gamma-2-immunoglobulin.";  
 RL Biochemistry 10:26-31(1971).  
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM POOLED SERUM OF STRAIN  
 CC 13 INBRED GUINEA PIGS.  
 DR PIR: A94553; G2GF.  
 DR HSSP: P01842; 7FAB.  
 DR InterPro: IPR007110; IG-like.  
 DR InterPro: IPR003597; IG\_C1.  
 DR InterPro: IPR003006; IG\_MHC.  
 DR Pfam: PF00047; Ig; 2.  
 DR SMART: SM00407; Igc1; 2.  
 DR PROSITE: PS00835; IG-LIKE; 3.  
 DR PROSITE: PS00290; IG\_MHC; 1.  
 KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.

```
FT NON_TER 1 1 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 16 16
FT DISULFID 28 79
FT DISULFID 105 105 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 110 110 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 142 202
FT CARBOHYD 178 178 N-LINKED (GLCNAC. . .).
FT DISULFID 248 308
SQ SEQUENCE 329 AA; 36074 MW; 5D231B7164D1FBA9 CRC64;

Query Match 68.2%; Score 1212.5; DB 1; Length 329;
Best Local Similarity 70.3%; Pred. No. 3.5e-84;
Matches 234; Conservative 28; Mismatches 62; Indels 9; Gaps 4;

QY 3 ASTKGPSVFLPAPSSKSTGGTAAALCGLVKDYFPEPTVWNSGALTSVHTFFPAVLQSS 62
DB 2 ARTAPSVFLPAAASCVDTSGSMMLTCLGLVKGYFPEPTVWNSGALTSVHTFFPAVLQ-S 60
QY 63 GLYSLSVTVPRSSSLGTQYICNVNHNKSNKTVKDKVPEKSCDKTH--TCPPCAPPELL 120
DB 61 GLYSLTSMVTPVPSQKAT----CNVAHPASSSTKVDTVEPIPTPZBPCTCPCPCPPENL 116
QY 121 GSPSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVFNFNVDGVEVHNNAKTKPREEQ 180
DB 117 GSPSVFLFPKPKDTLMISLTPRTVCVVDVSDPEVQFTFVDNKPVGNAETKPRVEQ 176
QY 181 YNSTYRVSVLVTHQDWLNGKEYKCKVSNKALPAPIETISKAKGQPREPOVYTLPPSR 240
DB 177 YNTTFRVSVLPIHQDNLRGKFEKCKVYNKALPAPIETISKAKGPMPPVYTLPPSR 236
QY 241 DELTKNQSVTLCLVKGYFSDIAVESNGQP--ENNYKTPPVLDSDGSFELYSKLTV 298
DB 237 DELSKKSVTVCLIIINFFPADIHVENASNPVSEKEYKNTPIEDADGSFELYSKLTV 296
QY 299 KSRWQQNVFSCVMHEALHNHYTKSLSPG 331
DB 297 KSAWDOQTVTCVSMHEALHNHYTKAISRSPG 329

RESULT 6
GC3_HUMAN STANDARD; PRT; 290 AA.
AC P01860;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ig gamma-3 chain C region (heavy chain disease protein) (HDC).
GN IGHG3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE (DISEASE PROTEIN WIS).
RX MEDLINE=81021548; PubMed=6774747;
RA Frangione B., Rosenwasser E., Prelli F., Franklin E.C.;
RT "Primary structure of human gamma 3 immunoglobulin deletion mutant:
RL gamma 3 heavy-chain disease protein WIS.";
RN [2]
RP Biochemistry 19:4304-4308(1980).
RX REVISIONS TO 12-97 (PROTEIN WIS).
RA MEDLINE=77118561; PubMed=402363;
RA Michaelson T.E., Frangione B., Franklin E.C.;
RT "Primary structure of the 'hinge' region of human IgG3. Probable
RL quadruplication of a 15-amino acid residue basic unit.";
RN [3]
RP J. Biol. Chem. 252:883-889(1977).
RX REVISIONS TO 59-289 (PROTEIN WIS/DISEASE PROTEIN ZUC).
RA MEDLINE=77021516; PubMed=823945;
RA Wolfenstein-Rodriguez C., Frangione B., Prelli F., Franklin E.C.;
RT "The amino acid sequence of 'heavy chain disease' protein ZUC.
RL Structure of the FC fragment of immunoglobulin G3.";
RN [4]
RP Biochem. Biophys. Res. Commun. 71:907-914(1976).
RX SEQUENCE FROM N.A. (DISEASE PROTEIN OMM).
RA Alexander A., Steinmetz M., Barritault D., Frangione B.,
RA Franklin E.C., Hood L., Buxbaum J.N.;
RT "Gamma heavy chain disease in man: cDNA sequence supports partial
RL gene deletion model.";
RN [5]
RP Proc. Natl. Acad. Sci. U.S.A. 79:3260-3264(1982).
RX INTERCHAIN DISULFIDE BOND AT POSITION 7 IN ADDITION TO THE 11
CC -1- SUBUNIT: DIMER LINKED BY 12 DISULFIDE BONDS; IT HAS AN EXTRA
CC -1- INTERCHAIN DISULFIDE BOND AT POSITION 7 IN ADDITION TO THE 11
CC -1- NORMALLY PRESENT IN THE HINGE REGION.
CC -1- MISCELLANEOUS: THE HEAVY CHAIN DISEASE PROTEIN WIS IS SHOWN.
CC -1- MISCELLANEOUS: THE SEQUENCE OF RESIDUES 42-76 WAS TAKEN FROM THE
CC -1- REF.2.
CC -1- MISCELLANEOUS: DISEASE PROTEIN WIS IS LACKING MOST OF THE V REGION
CC -1- AND ALL OF THE CH1 REGION.
CC -1- MISCELLANEOUS: DISEASE PROTEIN ZUC LACK MOST OF THE V REGION, ALL
CC -1- OF THE CH1 REGION, AND PART OF THE HINGE COMPARED WITH NORMAL
CC -1- GAMMA-3 HEAVY CHAINS.
CC -1- MISCELLANEOUS: DISEASE PROTEIN OMM MAY REPRESENT AN ALLELIC FORM
CC -1- OR ANOTHER GAMMA CHAIN SUBCLASS.
CC -1- MISCELLANEOUS: THE HINGE REGION IN GAMMA-3 CHAINS IS ABOUT FOUR
CC -1- TIMES AS LONG AS IN OTHER GAMMA CHAINS AND CONTAINS THREE
CC -1- IDENTICAL 15-RESIDUE SEGMENTS PRECEDED BY A SIMILAR 17-RESIDUE
CC -1- SEGMENT (12-28).
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CC HSSP; P01857; 1FC1.
CC Genew; HGNC:5527; IGHG3.
CC MIM; 147120; -.
CC GO; GO:0005624; C:membrane fraction; NAS.
CC GO; GO:0003823; P:antigen binding activity; TAS.
CC GO; GO:0006955; P:immune response; NAS.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003597; Ig_C1.
CC Pfam; PF00047; Ig_2.
CC SMART; SM00407; IGc1; 1.
CC PROSITE; PS00835; IG_LIKE; 2.
CC PROSITE; PS00290; IG_MHC; 1.
CC Immunoglobulin domain; Immunoglobulin C region; Glycoprotein; Repeat;
KW Pyroliidone carboxylic acid.
FT DOMAIN 12 73 HINGE.
FT DOMAIN 74 183 CH2.
FT DOMAIN 184 289 CH3.
FT REPEAT 29 43
FT REPEAT 44 58
FT REPEAT 59 73
FT MOD_RES 1 1
FT CARBOHYD 6 6
FT DISULFID 7 7 PYROLIDONE CARBOXYLIC ACID.
FT DISULFID 24 24 INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT DISULFID 27 27 INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT DISULFID 33 33 INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT DISULFID 39 39 INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT DISULFID 42 42 INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT DISULFID 48 48 INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT DISULFID 54 54 INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT DISULFID 57 57 INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT DISULFID 63 63 INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT DISULFID 69 69 INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT DISULFID 72 72 INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT CARBOHYD 140 140 N-LINKED (GLCNAC. . .).
FT MOD_RES 230 290 REMOVED POST-TRANSLATIONALLY.
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FT VARIANT 126 127 QV -> EB (IN ZUC).  
 FT VARIANT 134 134 /FTID=VAR 003890.  
 FT F -> L (IN OMM).  
 FT VARIANT 139 139 /FTID=VAR 003891.  
 FT F -> Y (IN OMM).  
 FT VARIANT 182 182 /FTID=VAR 003892.  
 FT T -> A (IN OMM).  
 FT VARIANT 227 227 /FTID=VAR 003893.  
 FT S -> N (IN OMM).  
 FT VARIANT 227 227 /FTID=VAR 003894.  
 FT MISSING (IN ZUC).  
 FT VARIANT 279 279 /FTID=VAR 003895.  
 FT F -> Y (IN OMM).  
 FT /FTID=VAR 003896.  
 SQ SEQUENCE 290 AA; 32331 MW; E69CB957052F46 CRC64;

Query Match 65.0%; Score 1156; DB 1; Length 290;  
 Best Local Similarity 90.5%; Pred. No. 5.3e-80;  
 Matches 210; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

QY 101 EPKSCDTHTCPPCPAPPELLGSPVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKF 160  
 DB 59 EPKSCDTPPPCPAPPELLGSPVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKF 118

QY 161 NWYDGVGVHNAKTKPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 220  
 DB 119 KWIYDGVGVHNAKTKPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 178

QY 221 ISKAKQPREQVYTLPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 280  
 DB 179 ISKTKGQPREQVYTLPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 238

QY 281 PVLDSGSGFFLYSKLTVDKSRWQGNVFCSCWMEALHNHYTKSLSPGK 332  
 DB 239 PVLDSGSGFFLYSKLTVDKSRWQGNVFCSCWMEALHNHYTKSLSPGK 290

RESULT 7  
 GC1\_RAT ID GC1\_RAT STANDARD; PRT; 326 AA.  
 AC P20759;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig gamma-1 chain C region.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89232738; PubMed=3149946;  
 RA Brueggemann M.;  
 RT "Evolution of the rat immunoglobulin gamma heavy-chain gene family."  
 RL Gene 74:473-482(1988).  
 DR PIR; PS0017; PS0017.  
 DR HSSP; P01842; 7FAB.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig\_c1.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR Pfam; PF00047; Ig\_3.  
 DR SMART; SM00407; IGc1; 2.  
 DR PROSITE; PS00835; IG\_LIKE; 3.  
 DR PROSITE; PS00290; IG\_MHC; 1.  
 KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.  
 FT NON\_TER 1 1  
 FT DOMAIN 1 97 CH1.  
 FT DOMAIN 98 112 HINGE.  
 FT DOMAIN 113 219 CH2.  
 FT DOMAIN 220 326 CH3.  
 FT DISULFID 27 82  
 FT DISULFID 102 102 INTERCHAIN (WITH A HEAVY CHAIN).  
 FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).

FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).  
 FT DISULFID 111 111 INTERCHAIN (WITH A HEAVY CHAIN).  
 FT DISULFID 140 200  
 FT DISULFID 246 304  
 FT CARBOHYD 176 176 N-LINKED (GLCNAC. .) (POTENTIAL).  
 SQ SEQUENCE 326 AA; 35946 MW; 013BAB45EF49B9DA CRC64;

Query Match 64.8%; Score 1152; DB 1; Length 326;  
 Best Local Similarity 63.1%; Pred. No. 1.2e-79;  
 Matches 210; Conservative 53; Mismatches 60; Indels 10; Gaps 4;

QY 3 ASTKGPSVFPLAPSSKSTSGGTAALGLCLVKDYFPPPVTVSNKSGALTSGVHTFPAVLQSS 62  
 DB 1 AETAPSVPLAPAGTALKNSMTLGLCLVKGFPPPVTVSNKSGALTSGVHTFPAVLQ-S 59

QY 63 GLYSLSVVTVPSLSLGTQYICNVNHPKSNKVKPEKSCDKHTHTCPPCPAPPELLGG 122  
 DB 60 GLYTLTSSVTVPSLSPSTWPSQTVTCNVAHPASSTKVDKIVPRNCG--GDCKPC---ICTG 113

QY 123 ---PSVLEPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYDGVGVHNAKTKPRE 179  
 DB 114 SEVSSVFIIPPCKKDTLITLPKVTCTVVDVLSQDDPEVHFWFVDDVEVHTAQRPEE 173

QY 180 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 239  
 DB 174 QNSIFRSVSELPILHQDWLNGRTFRCVKVTSAAFPSPIEKTIKPEGRQVPHVYTMSP 233

QY 240 RELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDK 299  
 DB 234 KEEMTQNEVSIICMVKGFYPPDIYVWQNGQPQENYKNTPTMDTDSGYFLYSLNVRK 293

QY 300 SRWQGNVFCSCWMEALHNHYTKSLSPGK 332  
 DB 294 EKWQGNFTCSVLHLEGLHNHTKSLSPGK 326

RESULT 8  
 GCB\_RAT ID GCB\_RAT STANDARD; PRT; 333 AA.  
 AC P20761;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Ig gamma-2B chain C region.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89232738; PubMed=3149946;  
 RA Brueggemann M.;  
 RT "Evolution of the rat immunoglobulin gamma heavy-chain gene family."  
 RL Gene 74:473-482(1988).  
 CC -1- SIMILARITY: Contains 3 immunoglobulin-like domains.  
 DR PIR; PS0018; PS0018.  
 DR HSSP; P01842; 7FAB.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig\_c1.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR Pfam; PF00047; Ig\_3.  
 DR SMART; SM00407; IGc1; 2.  
 DR PROSITE; PS00835; IG\_LIKE; 3.  
 DR PROSITE; PS00290; IG\_MHC; 1.  
 KW Immunoglobulin domain; Immunoglobulin C region; Repeat.  
 FT NON\_TER 1 1  
 FT DOMAIN 6 96 IG-LIKE 1.  
 FT DOMAIN 124 223 IG-LIKE 2.  
 FT DOMAIN 232 328 IG-LIKE 3.  
 FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).  
 FT DISULFID 27 80  
 FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).  
 FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).



FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).  
 FT DISULFID 115 115 INTERCHAIN (WITH A HEAVY CHAIN).  
 FT DISULFID 147 207  
 FT DISULFID 253 311  
 SQ SEQUENCE 333 AA; 36497 MW; 55FBB64D48D460A6 CRC64;  
 Query Match  
 Best Local Similarity 64.58; Score 1146.5; DB 1; Length 333;  
 Matches 215; Conservative 44; Mismatches 68; Indels 9; Gaps 3;  
 QY 3 ASTKGSVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVWNSGALTSVGHVFFPAVLQSS 62  
 Db 1 AQTAPSVYPLAPGCGDTTSTVTLCGLVKGYFPEPTVWNSGALSSDVHFFPAVLQ-S 59  
 QY 63 GLYSLSVTVVPSSISLGTQYICNVHKSNTKVDKKVPKS-----CDKTHTCPPCPA 116  
 Db 60 GLYTLTSSVT--SSTVPQVTCNVAPASSTKVDKKVERNGGKHCPTCTCKKCPV 117  
 QY 117 PELLGGSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNAKTKP 176  
 Db 118 PELLGGSVFIFFPKPKDILLISQNAKVCVVVDVSEEPDVFQSFVNNVEVHTAQTP 177  
 QY 177 REQYNSTYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIETKISKAKGQPREPQVYTL 236  
 Db 178 REQYNSTYRVSALPIQHODWNSGKEFKCKVNNKALPSPIEKTISKPKGLVRKPKQVYM 237  
 QY 237 PPRDELTKQVSLTCLVKGYFSPDIAVEWESNGQPENNYKTPPVLDSDGSFELYSLKT 296  
 Db 238 GPTEQLTEGTVSLTCLTSLFNDLGVENTSGHIEKRYKNTEPVWDSGDSGFFMYSKLN 297  
 QY 297 VDKSRWQGNVFCVSNVHEALHNHYTQKSLSLSPGK 332  
 Db 298 VERSRWDSRAPFVCSVYVHEGLNHNHYEKSISRPPGK 333  
 RESULT 9  
 CCL\_MOUSE  
 ID\_GCL\_MOUSE STANDARD; PRT; 324 AA.  
 AC P01868;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Ig gamma-1 chain C region secreted form.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=80045036; PubMed=115593;  
 RA Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,  
 RA Takahashi N., Mano Y.,  
 RT "Cloning and complete nucleotide sequence of mouse immunoglobulin  
 gamma 1 chain gene."  
 RL Cell 18:559-568(1979).  
 RN [2]  
 RP SEQUENCE OF 76-324 FROM N.A. (MYELOMA PROTEIN MOPC 31C).  
 RX MEDLINE=8022559; PubMed=6769752;  
 RA Obata M., Yamawaki-Kataoka Y., Takahashi N., Kataoka T., Shimizu A.,  
 RA Mano Y., Seidman J.G., Peterlin B.M., Leder P., Honjo T.;  
 RT "Immunoglobulin gamma 1 heavy chain gene: structural gene sequences  
 cloned in a bacterial plasmid."  
 RL Gene 9:87-97(1980).  
 RN [3]  
 RP SEQUENCE OF 70-322 FROM N.A. (MYELOMA PROTEIN MOPC 21).  
 RX MEDLINE=80012837; PubMed=113776;  
 RA Rogers J., Clarke P., Salsner W.;  
 RT "Sequence analysis of cloned cDNA encoding part of an immunoglobulin  
 heavy chain."  
 RL Nucleic Acids Res. 6:3305-3321(1979).  
 RN [4]  
 RP SEQUENCE (MYELOMA PROTEIN MOPC 21).  
 RX MEDLINE=78242286; PubMed=98524;

RA Adetudbo K.;  
 RT "Evolution of immunoglobulin subclasses. Primary structure of a  
 murine myeloma gamma1 chain."  
 RL J. Biol. Chem. 253:6068-6075(1978).  
 RN [5]  
 RP DISULFIDE BONDS (MOPC 21).  
 RX MEDLINE=7300889; PubMed=5073237;  
 RA Svasti J., Milstein C.;  
 RT "The disulphide bridges of a mouse immunoglobulin G1 protein."  
 RL Biochem. J. 126:837-850(1972).  
 CC 1- SUBCELLULAR LOCATION: Secreted.  
 CC 1- ALTERNATIVE PRODUCTS:  
 CC Event-Alternative splicing; Named isoforms=2;  
 CC Name=Secreted;  
 CC IsoId=P01868-1; Sequence=Displayed;  
 CC Note=May be the major isoform;  
 CC Name=Membrane-bound;  
 CC IsoId=P01869-1; Sequence=External;  
 CC -----  
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 or send an email to license@sib-sib.ch).  
 CC -----  
 CC EMBL; V00793; CAA24172.1; -;  
 DR EMBL; V00793; CAA24173.1; -;  
 DR EMBL; V00793; CAA24174.1; -;  
 DR EMBL; V00793; CAA24175.1; -;  
 DR EMBL; V00795; CAA24176.1; -;  
 DR PIR; A02159; G1MS.  
 DR PDB; 1IGC; 03-JUN-95.  
 DR GlycoSuiteDB; P01868;  
 DR MGD; MGI:96446; Igh-4.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig cl.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR Pfam; PF00047; Ig; 3.  
 DR SMART; SMC0407; IGH1; 2.  
 DR PROSITE; PS50835; IG\_LIKE; 3.  
 DR PROSITE; PS00290; IG\_MHC; 1.  
 DR Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;  
 KW Alternative splicing; 3D-structure.  
 FT NON TER 1 1  
 FT DOMAIN 1 97  
 FT DOMAIN 98 110  
 FT HINGE 111 217  
 FT DOMAIN 218 324  
 FT DOMAIN 27 82  
 FT DISULFID 102 102  
 FT DISULFID 104 104  
 FT DISULFID 107 107  
 FT DISULFID 109 109  
 FT DISULFID 138 198  
 FT CARBOHYD 174 174  
 FT N-LINKED (GLCNAC. . .)  
 FT FTIG=CAR\_000055.  
 FT DISULFID 244 302  
 FT MOD RES 324 324  
 FT CONFLICT 276 276 N -> D (IN REF. 3).  
 FT CONFLICT 278 278 N -> D (IN REF. 3).  
 SQ SEQUENCE 324 AA; 35704 MW; A338812F3D1F2C93 CRC64;  
 Query Match 64.2%; Score 1142; DB 1; Length 324;  
 Best Local Similarity 62.0%; Pred. No. 6.9e-79;  
 Matches 206; Conservative 56; Mismatches 60; Indels 10; Gaps 4;  
 QY 3 ASTKGSVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVWNSGALTSVGHVFFPAVLQSS 62  
 Db 1 AKTTPSVYPLAPGCGDTTSTVTLCGLVKGYFPEPTVWNSGALSSDVHFFPAVLQSD 60  
 QY 63 GLYSLSVTVVPSSISLGTQYICNVHKSNTKVDKKVPKS-----CDKTHTCPP--CPAPELL 120

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Db 61 -LYTSSSVTPSSRRPSETTCNVAHPASTKVDKIVPRDCG-----CRPICITVPEV- 114
QY 121 GGPVFLFPKPKKOTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 180
Db 115 --SSVFIFFPKPKDVLITLTPKVTCCVVVDISKDDPEVQFQSFVDDVEVHTAQTPREEQ 172
QY 181 YNSTVRVSVLTVLHODWLNKEVKCKVSNKALPAPIETIKISKAKGQPREPQVYTLPPSR 240
Db 173 FNSITFRSVSELPFIHQDWLNKEFKCRVNSAAFPAPIETIKISKAKGQPREPQVYTIIPPK 232
QY 241 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKS 300
Db 233 EQAKDKVSLCMTIDFPEDITVEWQNGQPAENYKNTQPIWNTNGSYFVSKLVQKS 292
QY 301 RWQGNVFCSCVMHEALHNHYTKQSLSPGK 332
Db 293 NWEAGNTFTCSVLHSEGLHNHHTKSLSPGK 324

RESULT 10
GC3_MOUSE STANDARD; PRT; 329 AA.
AC P22436;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ig gamma-3 chain C region, secreted form.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85027161; PubMed=6092053;
RA Kels J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,
RA Tucker P.W., Blattner F.R.;
RT "Structural analysis of the murine IgG3 constant region gene.";
RL EMBO J. 3:2041-2046 (1984).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: J00451; -- NOT_ANNOTATED_CDS.
CC PIR: B02156; G3MSC.
CC HSP: P01857; IFC1.
CC InterPro: IPR007110; Ig-like.
CC InterPro: IPR003597; Ig cl.
CC InterPro: IPR003006; Ig_MHC.
CC Pfam: PF00047; Ig; 3.
CC SMART: SM00407; Igc1; 2.
CC PROSITE: PS00835; IG_LIKE; 3.
CC PROSITE: PS00290; IG_MHC; 1.
CC Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW Transmembrane; Alternative splicing.
FT NON_TER 1 1
FT DOMAIN 1 97 CH1.
FT DOMAIN 98 113 HINGE.
FT DOMAIN 114 223 CH2.
FT DOMAIN 224 327 CH3.
SQ SEQUENCE 329 AA; 36228 MW; F45827174182BAD6 CRC64;

Query Match 64.2%; Score 1141; DB 1; Length 329;
Best Local Similarity 64.0%; Pred No. 8.1e-79;
Matches 212; Conservative 47; Mismatches 68; Indels 4; Gaps 3;

QY 4 STKGPSVFLPAPSKSTSGTALGCLVKDYFPEPTVWVSNKALPAPIETIKISKAKGQPREPQVYTLPPSR 63

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Db 1 TTAPSVFLPVCSDTSGSSVTLGCLVKGYFPEPTVWVSNKALPAPIETIKISKAKGQPREPQVYTLPPSR 59
QY 64 LYSLSGVTVTPSSSLGCTQYICNVNHNKPSNTKVDKVPKSCDKHTCTP--PCPAPELLG 121
Db 60 FYSLSLVTPSGTSPQTVICNVNHPASKTELKIEPR-TPKSTPGSSCPGNILG 118
QY 122 GPSVFLFPKPKKOTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 181
Db 119 GPSVFIFFPKPKDALMISLTTPKVTCCVVVDVSDDDPDVHVSFVDDVHTAMTQPREAQ 178
QY 182 NSTVRVSVLTVLHODWLNKEVKCKVSNKALPAPIETIKISKAKGQPREPQVYTLPPSRD 241
Db 179 NTFRVVSLPQHODWLNKEVKCKVSNKALPAPIETIKISKAKGQPREPQVYTIIPPRE 238
QY 242 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSR 301
Db 239 QMSKKVSLTCLVTNFFSEALISVEWENGELEQDYKNTTPILDSDGTFLYSLKLTVDTS 298
QY 302 WQGNVFCSCVMHEALHNHYTKQSLSPGK 332
Db 299 WLQGEIFTCVVHEALHNHHTQKLSRSPGK 329

RESULT 11
GC1M_MOUSE STANDARD; PRT; 393 AA.
AC P01869;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DE 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig gamma-1 chain C region, membrane-bound form.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=80045036; PubMed=115593;
RA Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,
RA Takahashi N., Maro Y.;
RT "Cloning and complete nucleotide sequence of mouse immunoglobulin
RT gamma 1 chain gene.";
RL Cell 18:559-568 (1979).
RN [2]
RP SEQUENCE OF 323-393 FROM N.A.
RX MEDLINE=82197626; PubMed=6804950;
RA Tyler B.M., Cowman A.F., Gerondakis S.D., Adams J.M., Bernard O.;
RT "mRNA for surface immunoglobulin gamma chains encodes a highly
RT conserved transmembrane sequence and a 28-residue intracellular
RT domain.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:2008-2012 (1982).
RN [3]
RP SEQUENCE OF 323-366 FROM N.A.
RX MEDLINE=82115295; PubMed=6799207;
RA Rogers J., Choi E., Souza L., Carter C., Word C.J., Kuehl M.,
RA Eisenberg D., Wall R.;
RT "Gene segments encoding transmembrane carboxyl termini of
RT immunoglobulin gamma chains.";
RL Cell 26:19-27 (1991).
RN [4]
RP SEQUENCE OF 1-44 FROM N.A.
RX MEDLINE=8222190; PubMed=6283537;
RA Yamawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;
RT "Nucleotide sequences of gene segments encoding membrane domains of
RT immunoglobulin gamma chains.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627 (1982).
CC -!- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=2;
CC Name=Membrane-bound;
CC IsoId=P01869-1; Sequence=Displayed;
CC Name=Secreted;
CC IsoId=P01868-1; Sequence=External;
CC Note=May be the major isoform;

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EMBL; V00793; CAA24172.1; -
EMBL; V00793; CAA24173.1; -
EMBL; V00793; CAA24174.1; -
PIR; B02159; GIMSM.
DR PDB; 15C8; 23-MAR-99.
DR PDB; 1AB6; 18-MAR-98.
DR PDB; 1CL7; 12-JAN-00.
DR PDB; 1F11; 06-FEB-01.
DR PDB; 1F58; 29-DEC-99.
DR PDB; 1K25; 24-JUL-02.
DR PDB; 1KCR; 11-MAY-02.
DR PDB; 25C8; 09-JUL-99.
DR MGD; MGI:96446; Igh-4.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00407; Igc1; 2.
DR PROSITE; PS00835; IG_LIKE; 3.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW Alternative splicing; Transmembrane; 3D-structure.
FT NON_TER 1 97
FT DOMAIN 1 97 CHI.
FT DOMAIN 98 110 HINGE.
FT DOMAIN 111 217 CH2.
FT DOMAIN 218 324 CH3.
FT DISULFID 27 82
FT DISULFID 102 102 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 104 104 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 138 198
FT CARBOHYD 174 174 N-LINKED (GLCNAC. . .).
FT DISULFID 244 302
FT TRANSMEM 340 357 POTENTIAL.
FT DOMAIN 358 393 CYTOPLASMIC (POTENTIAL).
SQ SEQUENCE 393 AA; 43386 MW; 4C688343B7A1CE27 CRC64;

Query Match 63.9%; Score 1137; DB 1; Length 393;
Best Local Similarity 61.9%; Pred. No. 2.1e-78;
Matches 205; Conservative 56; Mismatches 60; Indels 10; Gaps 4;

QY 3 ASTKGSVPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 62
DB 1 AKTTPSPVPLAPGSAAGNSMTVLGCLVKGFPEPVTVTWSGSLSSGVHTFPAVLQSD 60
QY 63 GLYSLSSVTVFSSSLGCTQYICNVNHFPSNTKVKKEPKSCDKTHTCPP--CPAPELL 120
DB 61 -LYTLSSVTVFSSPRSETVTCNVAHPASSITKDKIVPRDCG---CKPCICTVPEV- 114
QY 121 GGSVFLFPKPKDMLMISRTVEVTCVVDVSHEDPEVKFNVDGVVHNAKTKPREQ 180
DB 115 --SSVFIFFPKPKDVLITLTPEVTCVVDVDSKDDPEVQFSFVDDVAVHTAQTPREQ 172
QY 181 YNSTRVSWVLTVHDLWNGKEYKCKVSNKALPAPIETIKAKGQPREPOVYTLPPSR 240
DB 173 FNSFTRSVSELPIMHQDLWNGKEPKCRVNSAPPAPIETIKTKGRKAPQVITPPK 232
QY 241 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKS 300
DB 233 EQMAKDKVSLTCLMIDFFEDITVEWQNGQPAENYKNTQIPMTNGSVFYVSKLVQKS 292
QY 301 RWQGGVFCSSVWHEALHNHYTQKSLSLSPG 331

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293 NWEAGNTFTCSVLHLEGLHNHHHTKSLSHSPG 323
DB 293 NWEAGNTFTCSVLHLEGLHNHHHTKSLSHSPG 323
RESULT 12
GC3M MOUSE STANDARD; PRT; 398 AA.
AC P03987;
DT 23-OCT-1986 (Rel. 02, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-3 chain C region, membrane-bound form.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85027161; PubMed=6092053;
RA Wels J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,
RA Tucker P.W., Blattner F.R.;
RT "Structural analysis of the murine IgG3 constant region gene.";
RL EMBO J. 3:2041-2046(1984).
RN [2]
RP SEQUENCE OF 328-398 FROM N.A.
RX MEDLINE=84041483; PubMed=6314258;
RA Komaromy M., Clayton L., Rogers J., Robertson S., Kettman J.,
RA Wall R.;
RT "The structure of the mouse immunoglobulin in gamma 3 membrane gene
segment.";
RL Nucleic Acids Res. 11:6775-6785(1983).
CC -----
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CC -----
EMBL; J00451; AAB59655.1; -.
EMBL; V01526; CAA24767.1; ALT_SEQ.
PIR; A02156; GIMSM.
HSP; P01857; IFC1.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00407; Igc1; 2.
DR PROSITE; PS00835; IG_LIKE; 3.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW Transmembrane; Alternative splicing.
FT NON_TER 1 97
FT DOMAIN 1 97 CHI.
FT DOMAIN 98 113 HINGE.
FT DOMAIN 114 223 CH2.
FT DOMAIN 224 327 CH3.
FT TRANSMEM 346 362
FT DOMAIN 363 398 POTENTIAL.
FT DOMAIN 393 398 CYTOPLASMIC (POTENTIAL).
FT CONFLICT 333 333 E -> G (IN REF. 2).
FT CONFLICT 342 342 E -> Q (IN REF. 2).
FT CONFLICT 388 388 P -> F (IN REF. 2).
SQ SEQUENCE 398 AA; 43929 MW; CF7F264B50A41B95 CRC64;

Query Match 63.6%; Score 1130; DB 1; Length 398;
Best Local Similarity 63.8%; Pred. No. 7.2e-78;
Matches 210; Conservative 47; Mismatches 68; Indels 4; Gaps 3;

QY 4 STKGPSVPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG 63
DB 1 TTTAPSVYPLVPGCSDTSGSSVTLGCLVKGFPEPVTVKVNYSGLSSGVRTVSSVLQ-SG 59

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QY 64 LYSLSVTVVPSVSSSLGTQYICNVNHPKNTKVDKVKPKSCDKTHTCP--CPAPELLG 121
Db 60 FYSLSLVTVVPSVSSSLGTQYICNVNHPKNTKVDKVKPKSCDKTHTCP--CPAPELLG 118
QY 122 GPSVFLFPKPKDMLISRTPEVTCVVVDVSHEDPEVKENWYVDGVEVHNATKPREEQY 181
Db 119 GPSVFLFPKPKDMLISRTPEVTCVVVDVSHEDPEVKENWYVDGVEVHNATKPREEQY 178
QY 182 NSYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 241
Db 179 NSYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 238
QY 242 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFPLYSKLVTDKSR 301
Db 239 QMSKKVSLTCLVNFSEALSVEWERNGELEQDYKNTTPILDSGTYFLYSLKLVTDKSR 298
QY 302 WQGNVPSVCSVMHEALHNHYTQKSLSLSP 330
Db 299 WLOGEIFTCSVWHEALHNHYTQKSLSLSP 327

RESULT 13
GCAB MOUSE STANDARD; PRT; 330 AA.
ID GCAB MOUSE STANDARD; PRT; 330 AA.
AC P01863;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig gamma-2A chain C region, A allele.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81076554; PubMed=6777755;
RA Skokorav J.-L., Auffray C., Rougeon F.;
RT "Structure of the constant and 3' untranslated regions of the murine
RL Balb/c gamma 2a heavy chain messenger RNA.";
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=81198976; PubMed=6262729;
RA Yamawaki-Kataoka Y., Miyata T., Honjo T.;
RT "The complete nucleotide sequence of mouse immunoglobulin gamma 2a gene
RL and evolution of heavy chain genes: further evidence for intervening
RL sequence-mediated domain transfer.";
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=81232894; PubMed=6787604;
RA Ollio R., Auffray C., Mochamps C., Rougeon F.;
RT "Comparison of mouse immunoglobulin gamma 2a and gamma 2b chain genes
RL suggests that exons can be exchanged between genes in a multigenic
RL family.";
RN [4]
RP MYELOMA PROTEIN MOPC 173.
RX MEDLINE=74175517; PubMed=4831970;
RA Bourgois A., Fougereau M., Rocca-Serra J.;
RT "Determination of the primary structure of a mouse IgG2a
RL immunoglobulin amino-acid sequence of the Fc fragment. Implications
RL for the evolution of immunoglobulin structure and function.";
RN [5]
RP DISULFIDE BONDS.
RX MEDLINE=73056887; PubMed=4565406;
RA de Preval C., Fougereau M.;
RT "Determination of the primary structure of a mouse gamma G2a
RL immunoglobulin. Identification of the disulfide bridges.";
RN [6]
RP SIMILARITY: Contains 3 immunoglobulin-like domains.
CC -1- SIMILARITY: Contains 3 immunoglobulin-like domains.

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CC -----
DR EMBL; V00798; CAA24178.1; -.
DR PIR; A02152; G2MSA.
DR PDB; 1E4W; 12-JUL-01.
DR PDB; 1E4X; 12-JUL-01.
DR PDB; 1WNU; 06-MAY-99.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig ci.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00407; IGc1; 2.
DR PROSITE; PS00835; IG LIKE; 3.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; 3D-structure; Repeat.
FT NON_TER 1
FT DOMAIN 6 98 IG-LIKE 1.
FT DOMAIN 121 220 IG-LIKE 2.
FT DOMAIN 229 325 IG-LIKE 3.
FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 82 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 110 110 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 144 204 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 250 308
FT MOD_RES 330 330 REMOVED POST-TRANSLATIONALLY.
SQ SEQUENCE 330 AA; 36389 MW; B84361C545A6864 CRC64;

Query Match 63.3%; Score 1126; DB 1; Length 330;
Best Local Similarity 63.6%; Pred. No. 1.1e-77;
Matches 211; Conservative 44; Mismatches 73; Indels 4; Gaps 3;

QY 3 ASTKGPSVFPLAPSSKSTSGTAAALGLCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 62
Db 1 AKTTAPSVYPLAPVCGDTTGTSSVTLGCLVKGYFPEPVTLTWNSGSLSSGVHTFPAVLQSD 60
QY 63 GLYSLSVTVVPSVSSSLGTQYICNVNHPKNTKVDKVKPKSCDKTHTCP--CPAPELL 120
Db 61 -LYTSLSSVTVVPSVSSSLGTQYICNVNHPKNTKVDKVKPKSCDKTHTCP--CPAPELL 118
QY 121 GPSVFLFPKPKDMLISRTPEVTCVVVDVSHEDPEVKENWYVDGVEVHNATKPREEQ 180
Db 119 GPSVFLFPKPKDMLISRTPEVTCVVVDVSHEDPEVKENWYVDGVEVHNATKPREEQ 178
QY 181 NSYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 240
Db 179 NSYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 238
QY 241 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFPLYSKLVTDK 300
Db 239 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFPLYSKLVTDK 298
QY 301 WQGNVPSVCSVMHEALHNHYTQKSLSLSPGK 332
Db 299 WQGNVPSVCSVMHEALHNHYTQKSLSLSPGK 330

RESULT 14
GCAB MOUSE STANDARD; PRT; 335 AA.
ID GCAB MOUSE STANDARD; PRT; 335 AA.
AC P01864;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig gamma-2A chain C region secreted form (B allele).
OS Mus musculus (Mouse).

```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6;  
RA MEDLINE=82037861; PubMed=6170065;  
RX Dognin M.J., Lauwereys M., Strosberg A.D.;  
RT "Multiple amino acid substitutions between murine gamma 2a heavy  
chain Fc regions of Ig1a and Ig1b allotypic forms.";  
RL Proc. Natl. Acad. Sci. U.S.A. 78:4031-4035(1981).  
CC -1- SUBCELLULAR LOCATION: Secreted (Potential).  
CC -1- ALTERNATIVE PRODUCTS:  
CC Event-Alternative splicing; Named isoforms=2;  
CC Name=Secreted;  
CC IsoId=P01864-1; Sequences=Displayed;  
CC Notes-Probably the major isoform;  
CC Name=Membrane-bound;  
CC IsoId=P01865-1; Sequences=External;  
CC MISCELLANEOUS: THE SEQUENCE DIFFERS FROM THAT OF THE A ALLELE,  
FROM BALB/C MICE, AT 15% OF THE POSITIONS.  
CC -1- SIMILARITY: Contains 3 immunoglobulin-like domains.  
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CC EMBL; J00479; -; NOT\_ANNOTATED\_CDS.  
DR PIR; A02153; G2MSAB.  
DR PDB; 1B0G; 23-MAR-99.  
DR PDB; 1HH6; 26-JAN-01.  
DR PDB; 1HH9; 12-JAN-01.  
DR PDB; 1HI6; 08-FEB-01.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig\_c1.  
DR InterPro; IPR003006; Ig\_MHC.  
DR Pfam; PF00047; Ig; 3.  
DR SMART; SM00407; Igcl; 2.  
DR PROSITE; PS00835; IG\_LIKE; 3.  
DR InterPro; IPR00290; IG\_MHC; 1.  
DR Immunoglobulin domain; Immunoglobulin C region; Alternative splicing;  
3D-structure; Repeat.  
KW 3D-structure; Repeat.  
FT NON\_TER 1 1  
FT DOMAIN 6 98 IG-LIKE 1.  
FT DOMAIN 126 225 IG-LIKE 2.  
FT DOMAIN 234 330 IG-LIKE 3.  
SQ SEQUENCE 335 AA; 36596 MW; FA3382792CBB13C6 CRC64;  
  
Query Match 63.2%; Score 1123.5; DB 1; Length 335;  
Best Local Similarity 61.3%; Pred. No. 1.8e-77;  
Matches 206; Conservativity 53; Mismatches 70; Indels 7; Gaps 2;  
  
QY 3 ASTKGPSVFLPAPSSKSTSGGTAALGCLVKGYFPEPVTVVNSGALTSGVHTFPAVLQSS 62  
DB 1 AKTTAPSVPLPVCGGTTGSSVTLGCLVKGYFPEPVTLTWNSSGSLSSGVHTFPALLQ-S 59  
  
QY 63 GLYSLSVVTVSSSLGQTYICNVNHPKSNTKDKKVEPK-----SCDTHTCPCPA 116  
DB 60 GYLTLSVVTVTSNTPSQTICNVNHPASSPKVDKKEPRVPTQNCPQHPQVPPCAA 119  
  
QY 117 PBLGSGPSVFLPFPKPKDPLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKP 176  
DB 117 PBLGSGPSVFLPFPKPKDPLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKP 176

DB 120 PBLGSGPSVFIIPPCKIKDVLMIISLPMVTGVVVDVSDDDPQVQISFVNNVHTAQQT 179  
QY 177 REEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYTL 236  
DB 180 HREDYNSLTREVVSALPIQHODMWSGKEFKCKVNNALPSPIEKTIISKRGPVRAQVYVL 239  
QY 237 PPSRDELTKQVSLCLVKGFPYSPDIADVWESNGGFPENNYKTPPVLDSDGSGFFLYSKLT 296  
DB 240 PPAEEMTKKFSLTGMITGFLPAEIAVDWTSNGRTEQNYKNTATVLDSDGSGFYFYSKLR 299  
QY 297 VDKSRWQCGNVFSCSVNHEALNNHYTKQSLSPGK 332  
DB 300 VQKSTWERSLFCACSVVHEVNLHTTKTISRSLGK 335  
  
RESULT 15  
GCAM MOUSE  
ID GCAM\_MOUSE STANDARD; PRT; 399 AA.  
AC P01865;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 01-AUG-1991 (Rel. 19, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE IG gamma-2A chain C region, membrane-bound form.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=82221190; PubMed=6283537;  
RA Yamawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;  
RT "Nucleotide sequences of gene segments encoding membrane domains of  
immunoglobulin gamma chains";  
RL Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).  
CC -1- ALTERNATIVE PRODUCTS:  
CC Event-Alternative splicing; Named isoforms=2;  
CC Name=Membrane-bound;  
CC IsoId=P01865-1; Sequences=Displayed;  
CC Name=Secreted;  
CC IsoId=P01864-1; Sequences=External;  
CC Notes-Probably the major isoform;  
CC -1- SIMILARITY: Contains 3 immunoglobulin-like domains.  
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CC EMBL; J00471; AAB59661.1; ALT\_INIT.  
DR PIR; A02154; G2MSAM.  
DR PDB; 1K35; 08-APR-98.  
DR PDB; 1YEE; 15-OCT-97.  
DR MGD; MGI:96443; Igh-1.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig\_c1.  
DR InterPro; IPR003006; Ig\_MHC.  
DR Pfam; PF00047; Ig; 2.  
DR SMART; SM00407; Igcl; 2.  
DR PROSITE; PS00835; IG\_LIKE; 3.  
DR PROSITE; PS00290; IG\_MHC; 1.  
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;  
Transmembrane; Alternative splicing; 3D-structure; Repeat.  
FT NON\_TER 1 1  
FT DOMAIN 6 98 IG-LIKE 1.  
FT DOMAIN 121 220 IG-LIKE 2.  
FT DOMAIN 229 335 IG-LIKE 3.  
FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).  
FT DISULFID 27 82 INTERCHAIN (WITH A HEAVY CHAIN).  
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).  
FT DISULFID 110 110 INTERCHAIN (WITH A HEAVY CHAIN).

Search completed: January 13, 2004, 12:39:28  
Job time : 15.4978 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 13, 2004, 12:20:44 ; Search time 59.441 Seconds  
(without alignments)  
1441.318 Million cell updates/sec

Title: US-09-990-586-98

Perfect score: 1778

Sequence: 1 EFASIKGPSVFLPSSKST.....MHEALNHVTKSLSPCK 332

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 23:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phase:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_rvirus:\*
- 16: sp\_bacteriap:\*
- 17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1767	99.4	471	Q8TC77	Q8tc77 homo sapien
2	1626.5	91.5	521	Q8N4Y9	Q8n4y9 homo sapien
3	1615.5	90.9	509	Q8NF17	Q8nf17 homo sapien
4	1590.5	89.5	473	Q8TC63	Q8tc63 homo sapien
5	1266.5	71.2	337	Q9SM34	Q9sm34 equus caball
6	1264	71.1	701	Q9SPQ8	Q9spq8 homo sapien
7	1161	65.3	469	Q9R3V9	Q9r3v9 mus musculus
8	1155	65.0	463	Q9RLC4	Q9rlc4 mus musculus
9	1151	64.7	437	Q9RIA4	Q9ria4 mus musculus
10	1137.5	64.0	473	Q9D8L4	Q9d8l4 mus musculus
11	1122	63.1	468	Q9RL31	Q9rl31 mus musculus
12	1122	63.1	473	Q9SL25	Q9sl25 mus musculus
13	1088	61.2	473	Q9L205	Q9l205 mus musculus
14	1088	61.2	474	Q9R3H6	Q9r3h6 mus musculus
15	444.5	25.0	597	Q9BU10	Q9bu10 homo sapien
16	444.5	25.0	597	Q9BQ88	Q9bq88 homo sapien

17	444.5	25.0	597	4	Q96BB9	Q96bb9 homo sapien
18	436.5	24.6	278	11	Q921K1	Q921k1 mus musculus
19	434.5	24.4	588	4	Q8WUX4	Q8wux4 homo sapien
20	434.5	24.4	613	4	Q96EY0	Q96ey0 homo sapien
21	434.5	24.4	613	4	Q8WUK1	Q8wuk1 homo sapien
22	434.5	24.4	614	4	Q96GA6	Q96ga6 homo sapien
23	434.5	24.4	614	4	Q96AA6	Q96aa6 homo sapien
24	434.5	24.6	613	11	Q8VCX7	Q8vcx7 mus musculus
25	398	22.4	375	4	Q9BSZ1	Q9bsz1 homo sapien
26	384.5	21.6	384	4	Q9UP60	Q9up60 homo sapien
27	384.5	21.6	493	4	Q8NCL6	Q8nc16 homo sapien
28	384.5	21.6	494	4	Q96K68	Q96k68 homo sapien
29	384.5	21.5	495	4	Q96KX8	Q96kx8 homo sapien
30	381.5	21.5	496	4	Q96DK0	Q96dk0 homo sapien
31	381.5	21.5	499	4	Q8NSK4	Q8nsk4 homo sapien
32	379.5	21.3	497	4	Q8WY24	Q8wy24 homo sapien
33	379.5	21.3	500	4	Q9BRV0	Q9brv0 homo sapien
34	379	21.3	416	4	Q9NPP6	Q9npp6 homo sapien
35	370	20.8	486	11	Q91Z07	Q91z07 mus musculus
36	370	20.8	487	11	Q99KA4	Q99ka4 mus musculus
37	370	20.8	584	13	Q90544	Q90544 ginglymosto
38	369	20.8	426	11	Q9DCD9	Q9dcd9 mus musculus
39	356.5	20.1	481	11	Q91WT3	Q91wt3 mus musculus
40	356.5	20.1	481	11	Q91WT1	Q91wt1 mus musculus
41	356.5	20.1	482	11	Q91X92	Q91x92 mus musculus
42	356.5	20.1	482	11	Q8K172	Q8k172 mus musculus
43	356.5	20.1	484	11	Q8VEA0	Q8vea0 mus musculus
44	356.5	20.1	488	11	Q91WR1	Q91wr1 mus musculus
45	356.5	20.1	488	11	Q8K0F2	Q8k0f2 mus musculus

ALIGNMENTS

RESULT 1

Q8TC77	PRELIMINARY;	PRT;	471 AA.
ID	Q8TC77;		
AC	01-JUN-2002 (TREMBLrel. 21, Created)		
DT	01-JUN-2002 (TREMBLrel. 21, Last sequence update)		
DT	01-MAR-2003 (TREMBLrel. 23, Last annotation update)		
DE	Hypothetical protein.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TiSSUE=Spleen;		
RA	Strausberg R.;		
RL	Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; BC024289; AAH24289.1; -		
DR	InterPro; IPR007110; IG-like.		
DR	InterPro; IPR003006; IG_MHC.		
DR	InterPro; IPR003596; IG_v.		
DR	Pfam; PF00047; IG; 4.		
DR	SMART; SM00406; IGV; 1.		
DR	PROSITE; PS0835; IG_LIKE; 4.		
DR	PROSITE; PS00290; IG_MHC; 2.		
KW	Hypothetical protein.		
SQ	SEQUENCE 471 AA; 51791 MW; 388F74CF588660E CRC64;		

Query Match 99.4%; Score 1767; DB 4; Length 471;  
Best Local Similarity 100.0%; Pred. No. 2.8e-152;  
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	3	ASTKGPSVFPLAPSSKSTSGTAAALGLVKDYEPEPVTVSWNSGALTSGVHTFPAVLQSS 62
Db	142	ASTKGPSVFPLAPSSKSTSGTAAALGLVKDYEPEPVTVSWNSGALTSGVHTFPAVLQSS 201
Qy	63	GLYSLSSVWTVPPSSLSGTQYICNVNHPKPSNTKVDKKVEPKSCDKTHTCPCPAPPELLGG 122
Db	202	GLYSLSSVWTVPPSSLSGTQYICNVNHPKPSNTKVDKKVEPKSCDKTHTCPCPAPPELLGG 261

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QY 123 PSVFLPPPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 182
Db 262 PSVFLPPPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 321
QY 183 STYRVSVLTVLHODWLNQKEVKCKVSKNALKAPAEIKTSKAKGQPREPQVYTLPPSRDE 242
Db 322 STYRVSVLTVLHODWLNQKEVKCKVSKNALKAPAEIKTSKAKGQPREPQVYTLPPSRDE 381
QY 243 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 302
Db 382 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 441
QY 303 QGQNVFSCSWMEALHNHYTQKSLSLSPGK 332
Db 442 QGQNVFSCSWMEALHNHYTQKSLSLSPGK 471

RESULT 2
Q8M4Y9 PRELIMINARY; PRT; 521 AA.
AC Q8N4Y9;
DT 01-OCT-2002 (TEMBLrel. 22, Created)
DT 01-OCT-2002 (TEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells from Tonsils;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC033178; AAH33178.1; -.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00407; Igc1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 2.
KW Hypothetical protein.
SQ SEQUENCE 521 AA; 57156 MW; 2AC7D22E72D6CAA2 CRC64;

Query Match 91.5%; Score 1626.5; DB 4; Length 521;
Best Local Similarity 81.7%; Pred. No. 28-139;
Matches 308; Conservative 11; Mismatches 11; Indels 47; Gaps 1;

QY 3 ASTKGPSVFPFAPLSSTKSTSGGTAALGCLVKDYFPEPVTWNSGALTSQTHTFPAVLQSS 62
Db 145 ASTKGPSVFPFAPLSSTKSTSGGTAALGCLVKDYFPEPVTWNSGALTSQTHTFPAVLQSS 204
QY 63 GLYSLSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKV----- 100
Db 205 GLYSLSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKV----- 100
QY 101 -----EPKSCDKHTCTCPAPPELLGGPSVFLFPPPKD 135
Db 265 DTPPPCPCEPKSCDTPPPCPCEPKSCDTPPPCPAPPELLGGPSVFLFPPPKD 135
QY 136 LMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQVNSTYRVSVLTVHL 195
Db 325 LMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQVNSTYRVSVLTVHL 384
QY 196 QDWLNQKEVKCKVSKNALKAPAEIKTSKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVK 255
Db 385 QDWLNQKEVKCKVSKNALKAPAEIKTSKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVK 444
QY 256 GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVME 315
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Db 445 GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVME 504
QY 316 ALHNHYTQKSLSLSPGK 332
Db 505 ALHNHYTQKSLSLSPGK 521

RESULT 3
Q8NF17 PRELIMINARY; PRT; 509 AA.
AC Q8NF17;
DT 01-OCT-2002 (TEMBLrel. 22, Created)
DT 01-OCT-2002 (TEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TEMBLrel. 23, Last annotation update)
DE FLJ00385 protein (Fragment).
GN FLJ00385.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Jikuya H., Takano J., Kikuno R., Nagase T., Ohata O.;
RL "The nucleotide sequence of a long cDNA clone isolated from human spleen."
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK090464; BAC03445.1; -.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00407; Igc1; 3.
DR PROSITE; PS00835; IG LIKE; 3.
DR PROSITE; PS00290; IG_MHC; 2.
FT NON TER 1
SQ SEQUENCE 509 AA; 56111 MW; 089498D8076E863C CRC64;

Query Match 90.9%; Score 1615.5; DB 4; Length 509;
Best Local Similarity 81.6%; Pred. No. 1.9e-138;
Matches 306; Conservative 11; Mismatches 11; Indels 47; Gaps 1;

QY 3 ASTKGPSVFPFAPLSSTKSTSGGTAALGCLVKDYFPEPVTWNSGALTSQTHTFPAVLQSS 62
Db 64 ASTKGPSVFPFAPLSSTKSTSGGTAALGCLVKDYFPEPVTWNSGALTSQTHTFPAVLQSS 123
QY 63 GLYSLSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKV----- 100
Db 124 GLYSLSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKV----- 100
QY 101 -----EPKSCDKHTCTCPAPPELLGGPSVFLFPPPKD 135
Db 184 DTPPPCPCEPKSCDTPPPCPCEPKSCDTPPPCPAPPELLGGPSVFLFPPPKD 243
QY 136 LMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQVNSTYRVSVLTVHL 195
Db 244 LMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQVNSTYRVSVLTVHL 303
QY 196 QDWLNQKEVKCKVSKNALKAPAEIKTSKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVK 255
Db 304 QDWLNQKEVKCKVSKNALKAPAEIKTSKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVK 363
QY 256 GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVME 315
Db 364 GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVME 423
QY 316 ALHNHYTQKSLSLSP 330
Db 424 ALHNHYTQKSLSLSP 438

RESULT 4
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Q8TC63
ID Q8TC63 PRELIMINARY; PRT; 473 AA.
AC Q8TC63;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Strauberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
EMBL; BC025985; AA25985.1; -.
DR InterPro; IPR000923; BlueCu.1.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00196; COPPER_BLUE; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 3.
KW Hypothetical protein.
SQ SEQUENCE 473 AA; 51986 MW; E29920B09BA369F5 CRC64;

Query Match 89.5%; Score 1590.5; DB 4; Length 473;
Best Local Similarity 90.9%; Pred. No. 3.2e-136;
Matches 300; Conservative 12; Mismatches 15; Indels 3; Gaps 1;

QY 3 ASTKGPSVFPPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 62
DB 147 ASTKGPSVFPPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 206

QY 63 GLYSLSVWTVPPSSSLGTQYICNVNHPKNTKVDKKVPEKSKDKHTHTCPCPAPELIGG 122
DB 207 GLYSLSVWTVPPSSSLGTQYICNVNHPKNTKVDKKVPEKSKDKHTHTCPCPAPELIGG 122

QY 123 PSVFLPFPKPKDLMISRTPEVTCVVDVSHEDPEVKFNWYDGVGVHNAKTKPREEQYN 182
DB 264 PSVFLPFPKPKDLMISRTPEVTCVVDVSHEDPEVKFNWYDGVGVHNAKTKPREEQYN 323

QY 183 STYRVSVLTVLHODWLNGLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 242
DB 324 STYRVSVLTVLHODWLNGLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 383

QY 243 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVDKSRW 302
DB 384 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVDKSRW 443

QY 303 QQGNVFSCSWMEALHNHYTQKSLSLSPGK 332
DB 444 QQGNVFSCSWMEALHNHYTQKSLSLSPGK 473

RESULT 5
Q95M34
ID Q95M34 PRELIMINARY; PRT; 337 AA.
AC Q95M34;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Immunoglobulin gamma 1 heavy chain constant region (Fragment).
GN IGHCL1.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
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RA Wagner B.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=98383416; PubMed=9717671;
RA Wagner B., Overesch G., Sheoran A., Holmes M., Richards C.,
RA Leibold W., Radbruch A.;
RT "Organization of the equine immunoglobulin heavy chain constant region
genes. III. Alignment of c-mu, c-gamma, c-epsilon and c-alpha genes.";
RL Immunobiology 199; 105-119 (1998).
EMBL; AJ300675; CAC44624.1; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_C1.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00407; IGC1; 2.
DR PROSITE; PS50835; IG_LIKE; 3.
DR PROSITE; PS00290; IG_MHC; 2.
FT NON_TER
SQ SEQUENCE 337 AA; 37438 MW; A60BF2B01DEFD1F6 CRC64;

Query Match 71.2%; Score 1266.5; DB 6; Length 337;
Best Local Similarity 69.2%; Pred. No. 6.3e-107;
Matches 234; Conservative 43; Mismatches 52; Indels 9; Gaps 3;

QY 3 ASTKGPSVFPPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 62
DB 1 ASTTGPKVFALAPCGTSDSTVALGCLVSGYFPEPVKSVNSGSLTSGVHTFPAVLQSS 60

QY 63 GLYSLSVWTVPPSSSLGTQYICNVNHPKNTKVDKKVPEKSKDKHTHTCPCPAPELIGG 116
DB 61 GFYSLSVWTVPPASTVSEIYICNVVHAASFVKVDKIEIPDNHVKVCDMS-KCPKCPA 119

QY 117 PELLGGSVFLFPKPKDLMISRTPEVTCVVDVSHEDPEVKFNWYDGVGVHNAKTKP 176
DB 120 PELLGGSVFLFPKPKDLMISRTPEVTCVVDVSHEDPEVKFNWYDGVGVHNAKTKP 179

QY 177 REQYNSTYRVSVLTVLHODWLNGLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTL 236
DB 180 KEQFNSTYRVSVLTVLHODWLNGLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTL 239

QY 237 PPSRDELTQNVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLK 294
DB 240 APHPDELKSKSVTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLK 299

QY 295 LTVDKSRNQGNVFSCSWMEALHNHYTQKSLSLSPGK 332
DB 300 LSVDRNRWQQGTTFTTCGMHEALHNHYTQKNVSKNPGK 337

RESULT 6
Q96P08
ID Q96P08 PRELIMINARY; PRT; 701 AA.
AC Q96P08;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Factor VII active site mutant immunocorjugate.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21477448; PubMed=11593034;
RA Hu Z., Garen A.;
RT "Targeting tissue factor on tumor vascular endothelial cells and tumor
cells for immunotherapy in mouse models of prostatic cancer.";
RL Proc. Natl. Acad. Sci. U.S.A. 98; 12180-12185 (2001).
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
EMBL; AF272774; AAK58686.1; -.
DR HSSP; P00761; 1AN1.
DR InterPro; IPR000152; Asx_hydroxyl.
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Best Local Similarity 62.7%; Pred. No. 1.4e-96;  
Matches 208; Conservative 55; Mismatches 59; Indels 10; Gaps 4;

QY 3 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSNWNGALTSYGHTTPAVLQSS 62  
DB 140 AKTTPSPVYPLAPGSAAGTNSMTLGLCLVKGYFPEPTVTWNSGSLSSGHTTPAVLQSD 199  
QY 63 GLYSLSVVTVPSSSLGQTQYICNNHKPNTKVKVPEKSCDKHTCTCP--CPAPELL 120  
DB 200 -LYTSSSVTVPSSTWSELTVCNVAHPASSTKVDKIVPRDCG----CKPCICTVPEV- 253  
QY 121 GGPVSFLFPFPKPKDTLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQ 180  
DB 254 --SSVFIIPPFPKPKDVLITLTPKVTCTVVVDISKDDPEVQFSWFDVDEVHTAQTQPREEQ 311  
QY 191 YNSTYRVVSVLTVLHODWLNKEKYCKVSNKALPAPIETKISKAKGQPREPOVYITLPPSR 240  
DB 312 FNSTFRSVSELPIMHQDWLNKEFKCRVNSAFAPIETKISKTKGRPKAPQVYITPPPK 371  
QY 241 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFFLYSKLTVDK 300  
DB 372 EQMAKDKVSLTCMTIDFFPEDITVEWQNGQPAENYKNTQPIMDTDSGYFVYKLVNQKS 431  
QY 301 RWQGNVPSCSVMHEALHNHYTQKSLSLSPGK 332  
DB 432 NWEAGNTFTCSVLHEGLHNHTKLSLSPGK 463

RESULT 9  
Q9R1A4 PRELIMINARY; PRT; 437 AA.  
AC Q9R1A4  
DT 01-MAY-2000 (TremBLrel. 13, Created)  
DT 01-MAY-2000 (TremBLrel. 13, Last sequence update)  
DT 01-MAR-2003 (TremBLrel. 23, Last annotation update)  
DE Gamal heavy chain of Mab7 (Fragment).  
GN IGH-4.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Wilde K.G.; Yu X.; Ekramoddoullah A.K.M.; Misra S.;  
RT "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal  
RT antibody (Mab 7, its light and heavy chains) and construction of a  
RT single chain antibody (scFv)."  
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF152372; AAD40243.1; --  
DR HSSP; F01842; 7FAB.  
DR MGD; MGI:96446; Igh-4.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig MHC.  
DR InterPro; IPR003596; Ig\_V.  
DR Pfam; PF00047; Ig; 4.  
DR SMART; SM00406; Igv; 1.  
DR PROSITE; PS50835; IG LIKE; 4.  
DR PROSITE; PS00290; IG MHC; 1.  
FT NON TER 1  
FT NON TER 437  
SQ SEQUENCE 437 AA; 48142 MW; 5C3A7B3BE7D697C CRC64;

Query Match 64.7%; Score 1151; DB 11; Length 437;  
Best Local Similarity 62.3%; Pred. No. 2.9e-96;  
Matches 207; Conservative 56; Mismatches 59; Indels 10; Gaps 4;

QY 3 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSNWNGALTSYGHTTPAVLQSS 62  
DB 114 AKTTPSPVYPLAPGSAAGTNSMTLGLVKGYFPEPTVTWNSGSLSSGHTTPAVLQSD 173  
QY 63 GLYSLSVVTVPSSSLGQTQYICNNHKPNTKVKVPEKSCDKHTCTCP--CPAPELL 120  
DB 174 -LYTSSSVTVPSSTWSELTVCNVAHPASSTKVDKIVPRDCG----CKPCICTVPEV- 227

QY 121 GGPVSFLFPFPKPKDTLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQ 180  
DB 228 --SSVFIIPPFPKPKDVLITLTPKVTCTVVVDISKDDPEVQFSWFDVDEVHTAQTQPREEQ 285  
QY 181 YNSTYRVVSVLTVLHODWLNKEKYCKVSNKALPAPIETKISKAKGQPREPOVYITLPPSR 240  
DB 286 FNSTFRSVSELPIMHQDWLNKEFKCRVNSAFAPIETKISKTKGRPKAPQVYITPPPK 345  
QY 241 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFFLYSKLTVDK 300  
DB 346 EQMAKDKVSLTCMTIDFFPEDITVEWQNGQPAENYKNTQPIMDTDSGYFVYKLVNQKS 405  
QY 301 RWQGNVPSCSVMHEALHNHYTQKSLSLSPGK 332  
DB 406 NWEAGNTFTCSVLHEGLHNHTKLSLSPGK 437

RESULT 10  
Q9D8L4 PRELIMINARY; PRT; 473 AA.  
AC Q9D8L4  
DT 01-JUN-2001 (TremBLrel. 17, Created)  
DT 01-JUN-2001 (TremBLrel. 17, Last sequence update)  
DT 01-MAR-2003 (TremBLrel. 23, Last annotation update)  
DE 1810060009rik protein.  
GN IGH-1 OR 1810060009RIK.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA STRAIN=C57BL/6J; TISSUE=Pancreas;  
RA MEDLINE=21085860; PubMed=11217851;  
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
RA Aizawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,  
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
RA Fleischmann W., Gaasterland T., Glissi C., King B., Kochiwa H.,  
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,  
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
RA Blake J., Offelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
RA Lyons P., Marchionni L., Mashima J., Mazarelli J., Mombaerts P.,  
RA Norone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
RA Suzuki H., Toyo-Oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,  
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,  
RA Hayashizaki Y.;  
RT "Functional annotation of a full-length mouse cDNA collection.";  
RL Nature 409:685-690(2001).  
DR EMBL; AK007918; BAB25349.1; --  
DR HSSP; F01842; 7FAB.  
DR MGD; MGI:96443; Igh-1.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig MHC.  
DR InterPro; IPR003596; Ig\_V.  
DR Pfam; PF00047; Igv; 4.  
DR SMART; SM00406; Igv; 1.  
DR PROSITE; PS50835; IG LIKE; 4.  
DR PROSITE; PS00290; IG MHC; 1.  
SQ SEQUENCE 473 AA; 51699 MW; 90ED57A514475FBB CRC64;

Query Match 64.0%; Score 1137.5; DB 11; Length 473;  
Best Local Similarity 61.9%; Pred. No. 5.5e-95;  
Matches 208; Conservative 53; Mismatches 66; Indels 7; Gaps 2;

QY 3 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSNWNGALTSYGHTTPAVLQSS 62  
DB 114 AKTTPSPVYPLAPGSAAGTNSMTLGLVKGYFPEPTVTWNSGSLSSGHTTPAVLQSD 173  
QY 63 GLYSLSVVTVPSSSLGQTQYICNNHKPNTKVKVPEKSCDKHTCTCP--CPAPELL 120  
DB 174 -LYTSSSVTVPSSTWSELTVCNVAHPASSTKVDKIVPRDCG----CKPCICTVPEV- 227

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Db 139 AKTAPSVPLAPVCGGTTGGSVTLGCLVKGYFPEPVTLTWNSGSLSSGVHTFPALLQ-S 197
QY 63 GLYSLSSVTVPSSSLGTTQYICNVNHKPSNTKYDKVPEPK-----SCDKTHCTPPCPA 116
Db 198 GLYTLSSSVTVTSNTWPSQITICNAVAHPASSTKVDKIEPRVPITQNPFCPLKCEPCPCAA 257
QY 117 PELLGGPSVFLFPKPKD*LMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 176
Db 258 PLLGGPSVFLFPKPKD*LMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 317
QY 177 REEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTL 236
Db 318 HREDYNTSLRVVSALPQIQDWMGSKGPKCKVNNALPSPIEKTISKGRGVPRAQVYVL 377
QY 237 PPSRDELTKNOVSLTCLVKGFPSPDIKAVENSGQPENNYKTTTPVLDSDGSFFLYSKLT 296
Db 378 PPAEEMTKKESLTCMIGFPLPAETIAVDWTSNGRTEQNYKNTAIVLSDSDGSFYMYSKLR 437
QY 297 VDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 332
Db 438 VQKSTWERSGLFACSVVHGLEHNLHTTKTSRSLGK 473

RESULT 11
Q99L31 PRELIMINARY; PRT; 468 AA.
AC Q99L31
DT 01-JUN-2001 (TEMBLrel. 17, Created)
DT 01-JUN-2001 (TEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TEMBLrel. 23, Last annotation update)
DE Similar to RIKEN CDNA 1810060009 gene.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003878; AAH03878.1; -.
DR HSSP; P01842; 7FAB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 1.
DR PROSITE; PS00290; IG_MHC; 1.
SQ SEQUENCE 468 AA; 51661 MW; 96352328B332ADB CRC64;

Query Match 63.1%; Score 1122; DB 11; Length 468;
Best Local Similarity 63.6%; Pred. No. 1.4e-93;
Matches 211; Conservative 44; Mismatches 73; Indels 4; Gaps 3;

QY 3 ASTKGSPVFLPAPSSKSTGGTAALGCLVKDYPPEPVTVWNSGALTSGVHTFPAVLQSS 62
Db 139 AKTAPSVPLAPVCGDGTGSSVTLGCLVKGYFPEPVTLTWNSGSLSSGVHTFPALLQSD 198
QY 63 GLYSLSSVTVPSSSLGTTQYICNVNHKPSNTKYDKVPEPKCDTHCTCP--CPAPELL 120
Db 199 -LYTLSSSVTVTSWPSGSIICNVVAHPASSTKVDKIEPRG-PTIKPCPPCKCPAPNLL 256
QY 121 GGPSVFLFPKPKD*LMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREQ 180
Db 257 GGPSVFLFPKPKD*LMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREQ 316
QY 181 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSR 240
Db 317 YNSTLRVVSALPQIQDWMGSKGPKCKVNNKALPAPIEKTISKPKGSRAPQVYVLPPE 376
QY 241 DELTKQVSLTCLVKGFPSPDIKAVENSGQPENNYKTTTPVLDSDGSFFLYSKLTVDKS 300
Db 377 EEMTKQVTLTQVTFMPEDIVVWNTNGKTELNYKTEPVLDSGDSFYMYSKLRVEKK 436

Query Match 63.1%; Score 1122; DB 11; Length 468;
Best Local Similarity 63.6%; Pred. No. 1.4e-93;
Matches 211; Conservative 44; Mismatches 73; Indels 4; Gaps 3;

QY 3 ASTKGSPVFLPAPSSKSTGGTAALGCLVKDYPPEPVTVWNSGALTSGVHTFPAVLQSS 62
Db 139 AKTAPSVPLAPVCGDGTGSSVTLGCLVKGYFPEPVTLTWNSGSLSSGVHTFPALLQSD 198
QY 63 GLYSLSSVTVPSSSLGTTQYICNVNHKPSNTKYDKVPEPKCDTHCTCP--CPAPELL 120
Db 199 -LYTLSSSVTVTSWPSGSIICNVVAHPASSTKVDKIEPRG-PTIKPCPPCKCPAPNLL 256
QY 121 GGPSVFLFPKPKD*LMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREQ 180
Db 257 GGPSVFLFPKPKD*LMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREQ 316
QY 181 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSR 240
Db 317 YNSTLRVVSALPQIQDWMGSKGPKCKVNNKALPAPIEKTISKPKGSRAPQVYVLPPE 376
QY 241 DELTKQVSLTCLVKGFPSPDIKAVENSGQPENNYKTTTPVLDSDGSFFLYSKLTVDKS 300
Db 377 EEMTKQVTLTQVTFMPEDIVVWNTNGKTELNYKTEPVLDSGDSFYMYSKLRVEKK 436
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QY 301 RWOQGNVFCSCVMHEALHNHYTQKSLSLSPGK 332
Db 437 NWVERNSYSCSVVHGLEHNLHTTKTSRTPGK 468

RESULT 12
Q99L25 PRELIMINARY; PRT; 473 AA.
AC Q99L25
DT 01-JUN-2001 (TEMBLrel. 17, Created)
DT 01-JUN-2001 (TEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TEMBLrel. 23, Last annotation update)
DE Similar to RIKEN CDNA 1810060009 gene.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003888; AAH03888.1; -.
DR HSSP; P01842; 7FAB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 1.
DR PROSITE; PS00290; IG_MHC; 1.
SQ SEQUENCE 473 AA; 52449 MW; BE9889B7986DA155 CRC64;

Query Match 63.1%; Score 1122; DB 11; Length 473;
Best Local Similarity 63.6%; Pred. No. 1.4e-93;
Matches 211; Conservative 44; Mismatches 73; Indels 4; Gaps 3;

QY 3 ASTKGSPVFLPAPSSKSTGGTAALGCLVKDYPPEPVTVWNSGALTSGVHTFPAVLQSS 62
Db 144 AKTAPSVPLAPVCGDGTGSSVTLGCLVKGYFPEPVTLTWNSGSLSSGVHTFPALLQSD 203
QY 63 GLYSLSSVTVPSSSLGTTQYICNVNHKPSNTKYDKVPEPKCDTHCTCP--CPAPELL 120
Db 204 -LYTLSSSVTVTSWPSGSIICNVVAHPASSTKVDKIEPRG-PTIKPCPPCKCPAPNLL 261
QY 121 GGPSVFLFPKPKD*LMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREQ 180
Db 262 GGPSVFLFPKPKD*LMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREQ 321
QY 181 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSR 240
Db 322 YNSTLRVVSALPQIQDWMGSKGPKCKVNNKALPAPIEKTISKPKGSRAPQVYVLPPE 381
QY 241 DELTKQVSLTCLVKGFPSPDIKAVENSGQPENNYKTTTPVLDSDGSFFLYSKLTVDKS 300
Db 382 EEMTKQVTLTQVTFMPEDIVVWNTNGKTELNYKTEPVLDSGDSFYMYSKLRVEKK 441
QY 301 RWOQGNVFCSCVMHEALHNHYTQKSLSLSPGK 332
Db 442 NWVERNSYSCSVVHGLEHNLHTTKTSRTPGK 473

RESULT 13
Q91Z05 PRELIMINARY; PRT; 473 AA.
AC Q91Z05
DT 01-DEC-2001 (TEMBLrel. 19, Created)
DT 01-DEC-2001 (TEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TEMBLrel. 23, Last annotation update)
DE Hypothetical 51.9 kDa protein.
GN AU044919.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

ON NCBI\_TaxID=10090;

OX [1]

RA SEQUENCE FROM N.A.

RL Strausberg R.;

RM Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC010327; AAH0327.1; -.

DR MGI; MGI:2144967; AU044919.

DR InterPro; IPR000345; CytC\_heme\_bind.

DR InterPro; IPR007110; Ig-Like.

DR InterPro; IPR003006; Ig\_MHC.

DR InterPro; IPR003596; Ig\_V.

DR Pfam; PF00047; Ig; 3.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS00190; CYTOCHROME\_C; 1.

DR PROSITE; PS00835; IG LIKE; 4.

DR PROSITE; PS00290; IG\_MHC; 1.

DR Hypothetical protein.

KW Hypothetical protein.

SQ SEQUENCE 473 AA; 51946 MW; CF625F0099332AF12 CRC64;

Query Match 61.2%; Score 1088; DB 11; Length 473;

Best Local Similarity 60.8%; Pred. No. 1.8e-90;

Matches 205; Conservative 49; Mismatches 75; Indels 8; Gaps 3;

3 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 62

138 AKTTPSVYPLAPGGDTGGSSVTLGCLVKGYFPEPVTVSWNSGALTSGVHTFPAVLQ-S 196

63 GLYSLSVVTVPSSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKT-HTCPP-----CP 115

197 GLYTMSSSVTVPSSTWPSQTVCVAHPASSTVVDKLEPSGPISTINPCPCKECHKCP 256

116 APELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 175

257 APNLEGGPSVFIFPPNPKDVLMIISLTPTKVTCCVVVDVSEDDPDVQISWFFVNNVEVHTAQ 316

176 PREQYNSTIRVVSVLTIVLHQDLNGKEYCKVSNKALPAPIETKISKAKGQPREPQVYT 235

317 THREDYNSTIRVVSALPFOHQDWMGSKFKCKVNNKDLPSPIERTISKIKGLVRAPQVYI 376

236 LPSPDELTKNQVSLTCLVKGYFPEPVTVSWNSGALTSGVHTFPAVLQSS 295

377 LPPPAQLSRKQVSLTCLVKGYFPEPVTVSWNSGALTSGVHTFPAVLQSS 436

296 TVDKSRWQGNVFCSCVMEALHNYHTOKSLSPGK 332

437 DIKTSKWEKTSFSCNVRHEGLKNVYLKKTISRSPGK 473

RESULT 14

Q8R3H6 PRELIMINARY; PRT; 474 AA.

AC Q8R3H6

DT 01-JUN-2002 (TrEMBLrel. 21, Created)

DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

DE Hypothetical 51.7 kDa protein.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OC NCBI\_TaxID=10090;

OX [1]

RA SEQUENCE FROM N.A.

RL Strausberg R.;

RM Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC025447; AAH25447.1; -.

DR InterPro; IPR000345; CytC\_heme\_bind.

DR InterPro; IPR007110; Ig-Like.

DR InterPro; IPR003006; Ig\_MHC.

DR InterPro; IPR003596; Ig\_V.

DR Pfam; PF00047; Ig; 3.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS00190; CYTOCHROME\_C; 1.

Query Match 25.0%; Score 444.5; DB 4; Length 597;

Best Local Similarity 26.5%; Pred. No. 8.8e-32;

Matches 116; Conservative 68; Mismatches 142; Indels 111; Gaps 15;

4 STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 60

146 SASAPFLFPLVSCNSPSTSSVAVGCLAQDPLDPSITTSWKYKNSDSSITGFFSVLR 205

61 SSGLYSLSSVVTVPSSSL-GTQTY-ICNVNHPKSN-----TKVDKVEPK 103

PROSITE; PS00190; CYTOCHROME\_C; 1.

DR PROSITE; PS00835; IG LIKE; 4.

DR PROSITE; PS00290; IG\_MHC; 1.

KW Hypothetical protein.

SQ SEQUENCE 474 AA; 51748 MW; 8608B57C6CD2874A CRC64;

Query Match 61.2%; Score 1088; DB 11; Length 474;

Best Local Similarity 60.8%; Pred. No. 1.8e-90;

Matches 205; Conservative 49; Mismatches 75; Indels 8; Gaps 3;

3 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 62

139 AKTTPSVYPLAPGGDTGGSSVTLGCLVKGYFPEPVTVSWNSGALTSGVHTFPAVLQ-S 197

63 GLYSLSVVTVPSSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKT-HTCPP-----CP 115

198 GLYTMSSSVTVPSSTWPSQTVCVAHPASSTVVDKLEPSGPISTINPCPCKECHKCP 257

116 APELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 175

258 APNLEGGPSVFIFPPNPKDVLMIISLTPTKVTCCVVVDVSEDDPDVQISWFFVNNVEVHTAQ 317

176 PREQYNSTIRVVSVLTIVLHQDLNGKEYCKVSNKALPAPIETKISKAKGQPREPQVYT 235

318 THREDYNSTIRVVSALPFOHQDWMGSKFKCKVNNKDLPSPIERTISKIKGLVRAPQVYI 377

236 LPSPDELTKNQVSLTCLVKGYFPEPVTVSWNSGALTSGVHTFPAVLQSS 295

378 LPPPAQLSRKQVSLTCLVKGYFPEPVTVSWNSGALTSGVHTFPAVLQSS 437

296 TVDKSRWQGNVFCSCVMEALHNYHTOKSLSPGK 332

438 DIKTSKWEKTSFSCNVRHEGLKNVYLKKTISRSPGK 474

RESULT 15

Q9BU10 PRELIMINARY; PRT; 597 AA.

AC Q9BU10

DT 01-JUN-2001 (TrEMBLrel. 17, Created)

DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

DE Hypothetical protein.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OC NCBI\_TaxID=9606;

OX [1]

RA SEQUENCE FROM N.A.

RC Tissue=Lymph;

RA Strausberg R.;

RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC002963; AAH02963.1; -.

DR HSP; P01825; 7FAB.

DR InterPro; IPR007110; Ig-Like.

DR InterPro; IPR003006; Ig\_MHC.

DR InterPro; IPR003596; Ig\_V.

DR Pfam; PF00047; Ig; 5.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS00835; IG LIKE; 5.

DR PROSITE; PS00290; IG\_MHC; 3.

DR Hypothetical protein.

KW Hypothetical protein.

SQ SEQUENCE 597 AA; 65274 MW; 2DAFA8FB7B055851 CRC64;

Query Match 25.0%; Score 444.5; DB 4; Length 597;

Best Local Similarity 26.5%; Pred. No. 8.8e-32;

Matches 116; Conservative 68; Mismatches 142; Indels 111; Gaps 15;

4 STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 60

146 SASAPFLFPLVSCNSPSTSSVAVGCLAQDPLDPSITTSWKYKNSDSSITGFFSVLR 205

61 SSGLYSLSSVVTVPSSSL-GTQTY-ICNVNHPKSN-----TKVDKVEPK 103

PROSITE; PS00190; CYTOCHROME\_C; 1.

```
Db 206 -GKXYAATSQVLLPSKDVMOGTDHVVCKVQHPNGNKKKNWLPVIAELPKVSVFVPPR 264
QY 104 S-----CDKHTCP-----PCPAPELLGOPS----- 124
Db 265 DGFFGNPRKSLICQATGSPRQIOVSWMLREGKQVSGVTTDQVQAEAKESGPTTYKVT 324
QY 125 -----VPLFPKPKDTILMISRT 141
Db 325 TITIKESDWLSQSMFTCRVDHGLTFQQNASSMCPVDQDTAIRVFAIPPS-FASIFLTKS 383
QY 142 PEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVWSVLTVLHQQDWLNG 201
Db 384 TKLTCILVTLDTTYD-SVTISWTRQNGEAVKTHNISESHPNATPSAVGEASICEDDWSG 442
QY 202 KEYKCKVSNKALPAPIEKTISKAKGQ-REPOVYTLPPSRDELT-KNOVSLTCLVKGPYP 259
Db 443 ERFTCTVHTDLPSPKQTIISRPKGVALLHRPDVYLLPPAREQNLRESATITCLVTCFSP 502
QY 260 SDIAYEWESNGQF--ENNYKTTPPVLD--SDGSFELYSKLTVDKSRMOQGNVFCVVMHE 315
Db 503 ADVFVQWMOQGQPLSPKQVTSAPNPEPQAPGRYFAHSILITVSEENKNTGETITCVVAHE 562
QY 316 ALHNHYTQKSLSLSPGK 332
Db 563 ALPNRVTERTVDKSTGK 579
```

Search completed: January 13, 2004, 12:43:09  
Job time : 60.441 secs



KW 08-FEB-1991; 91US-0654205.  
 XX (PROG-) PROGENICS PHARM INC.  
 XX PA Beaudry GA, Maddon RJ;  
 XX PI WPI; 1992-299758/36.  
 XX DR N-PSDB; AA027831.  
 XX  
 XX CD4-gamma 1 chimeric heavy chain homo-dimer and its expression  
 PT vector - for preventing and treating HIV infection useful as a  
 PT diagnostic agent  
 XX  
 XX Example; Fig 4; 88pp; English.  
 XX  
 CC The human CD4 cDNA is excised from the plasmid pSP6T4 and cloned  
 CC into M13mp18. In order to excise a fragment containing the CH1  
 CC exon of the human gamma 1 heavy chain gene, the plasmid pBR  
 CC gamma 1 is digested with SacII and the SacII sites are then  
 CC made flush using T4 DNA polymerase. The fragment containing  
 CC the CH1 exon is then purified and ligated to the M13mp18(CD4)  
 CC vector. Oligonucleotide-mediated site-directed mutagenesis is then  
 CC performed to juxtapose the CD4 and CH1 sequences in frame. The  
 CC CD4-CH1 chimeric gene is then linearized and ligated to the  
 CC Pet1-Pst1 DNA fragment of the plasmid pBR gamma 1 containing the  
 CC hinge, CH2, and CH3 exons of the human gamma 1 chain gene  
 CC designated CD4-IgG1HC-pRCMV (ATCC 75192).  
 CC (Updated on 25-MAR-2003 to correct PN field.)  
 CC  
 XX Sequence 534 AA;  
 XX  
 XX Query Match 99.7%; Score 1773; DB 13; Length 534;  
 XX Best Local Similarity 100.0%; Pred. No. 2.4e-125;  
 XX Matches 331; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 FASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 61  
 DB 204 FASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 61  
 QY 62 SGLYSLSVVTVPPSSSLGTQYICNVNHPKNTKVDKVEPKSCDKTHCTCPAPPELLG 121  
 DB 264 SGLYSLSVVTVPPSSSLGTQYICNVNHPKNTKVDKVEPKSCDKTHCTCPAPPELLG 323  
 QY 122 GSVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNKYVDGVEVHNKATKPREEQ 181  
 DB 324 GSVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNKYVDGVEVHNKATKPREEQ 383  
 QY 182 NSTYRVSVLTVLHODWLNKGEYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRD 241  
 DB 384 NSTYRVSVLTVLHODWLNKGEYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRD 443  
 QY 242 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSR 301  
 DB 444 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSR 503  
 QY 302 WQGGNVFSCSVNHEALHNHYTQKSLSLSPGK 332  
 DB 504 WQGGNVFSCSVNHEALHNHYTQKSLSLSPGK 534  
 RESULT 2  
 AAB04071  
 ID AAB04071 standard; Protein; 330 AA.  
 XX AAB04071;  
 AC AAB04071;  
 XX  
 DT 11-APR-2001 (first entry)  
 XX Zcytor 10::IgG gamma fusion peptide.  
 DE zcytor 10 cytokine receptor; cytokine; receptor; antibody; ligand;  
 KW binding; detection; modulation; recombinant cell;  
 KW

KW haematopoietic cell; lymphoid cell; myeloid cell; lymph;  
 KW immune system; blood; bone; inflammatory response; inflammation;  
 KW spleen; human.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 XX WO2000068381-A1.  
 XX  
 XX 16-NOV-2000.  
 XX  
 XX 11-MAY-2000; 2000WO-US12924.  
 XX  
 XX 11-MAY-1999; 99US-0309861.  
 XX  
 XX (ZYMO ) ZYMOGENETICS INC.  
 XX  
 XX Presnell SR, Foster DC, Hammond AK, Lok S;  
 XX  
 XX WPI; 2001-016096/02.  
 XX  
 XX N-PSDB; AAA54473.  
 XX  
 XX New cytokine receptor mouse zcytor 10, useful for detecting ligands  
 PT that stimulate proliferation or development of haematopoietic,  
 PT lymphoid and myeloid cells  
 XX  
 XX Example 17; Page 120-121; 134pp; English.  
 XX  
 CC Isolating a nucleotide which encodes the zcytor 10 cytokine  
 CC receptor enables the production of recombinant cells expressing the  
 CC receptor. Those cells can then be used to detect the presence of a  
 CC modulator of zcytor10 protein by culturing the cells in the presence  
 CC of a test ligand and comparing levels of activity of mouse zcytor10  
 CC in the presence and absence of the test sample. Similarly, detection  
 CC of zcytor10 receptor ligand within a test sample can be achieved.  
 CC The method comprising contacting a test sample containing an amino  
 CC acid sequence from Cys15 or Gly25 to Pro230 of the zcytor 10  
 CC cytokine receptor and detecting the binding of the polypeptide to a  
 CC ligand in the sample. Specified peptide fragments of the zcytor 10  
 CC cytokine receptor and the methods described are used to identify  
 CC ligands that stimulate the proliferation and/or development of  
 CC haematopoietic, lymphoid and myeloid cells. Peptide fragments of  
 CC the cytokine receptor are useful for treating lymphoid, immune,  
 CC inflammatory, splenic, blood or bone disorders and for generating  
 CC antibodies directed against the receptor. A vector expressing a  
 CC secreted human zcytor 10 heterodimer is constructed. In this  
 CC construct the extracellular cytokine binding domain of zcytor 10  
 CC is fused to the heavy chain of IgG gamma and the extracellular  
 CC portion of the heteromeric cytokine receptor subunit (an  
 CC interleukin receptor subunit) is fused to human kappa light  
 CC chain (See GENESEQ record AAA54474). The two sequences are fused  
 CC together using two primers (AAA54475, AAA54476).  
 CC  
 XX Sequence 330 AA;  
 XX  
 XX Query Match 99.4%; Score 1767; DB 22; Length 330;  
 XX Best Local Similarity 100.0%; Pred. No. 3.7e-125;  
 XX Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 62  
 DB 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 60  
 QY 63 GLYSLSVVTVPPSSSLGTQYICNVNHPKNTKVDKVEPKSCDKTHCTCPAPPELLG 122  
 DB 61 GLYSLSVVTVPPSSSLGTQYICNVNHPKNTKVDKVEPKSCDKTHCTCPAPPELLG 120  
 QY 123 PSVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNKYVDGVEVHNKATKPREEQ 182  
 DB 121 PSVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNKYVDGVEVHNKATKPREEQ 180  
 QY 183 STYRVSVLTVLHODWLNKGEYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRD 242



Db 181 STYRWVSVLTVLHQMGLNGKEYKCVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240  
 QY 243 LTKNQVSLTCLVKGFPYSDIAVWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 302  
 Db 241 LTKNQVSLTCLVKGFPYSDIAVWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 300  
 QY 303 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 332  
 Db 301 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 330

RESULT 3  
 ABB81641  
 ID ABB81641 standard; Protein: 330 AA.  
 XX  
 AC ABB81641;  
 XX  
 DT 25-SEP-2002 (first entry)  
 XX  
 DE Human IgG gamma 1 heavy chain SEQ ID NO:15.  
 XX  
 KW Human; zcytor19; cytokine receptor; immunosuppressive; cytostatic;  
 KW antihemetic; antiarthritic; neuroprotective; antiinflammatory;  
 KW antidiabetic; nephrotropic; dermatological; anti-HIV; haemostatic;  
 KW vaccine; immune system; T-cell specific leukaemia; lymphoma; lupus;  
 KW autoimmune disease; rheumatoid arthritis; multiple sclerosis; HIV;  
 KW diabetes mellitus; inflammatory bowel disease; Crohn's disease; asthma;  
 KW immunologic renal disease; glomerulonephritis; vasculitis; polyarteritis;  
 KW mesangio proliferative disease; chronic lymphocytic leukaemia; bronchitis;  
 KW secondary glomerulonephritis; scleroderma; amyloidosis; multiple myeloma;  
 KW haemolytic uraemic syndrome; renal neoplasm; urological neoplasms;  
 KW emphysema; chronic airway disease.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200244209-A2.  
 XX  
 XX 06-JUN-2002.  
 XX  
 XX 28-NOV-2001; 2001WO-US44808.  
 XX  
 XX 28-NOV-2000; 2000US-253561P.  
 XX  
 XX 07-FEB-2001; 2001US-267211P.  
 XX  
 XX (ZYMO) ZYMOGENETICS INC.  
 XX  
 XX Presnell SR, Xu W, Novak JE, Whitmore TE, Grant FU;  
 PI  
 XX  
 XX WPI; 2002-527700/56.  
 XX  
 XX N-PSDB; ABQ73076.  
 XX  
 XX Novel Zcytor19 polypeptides and polynucleotides useful for stimulating  
 PT immune responses in animals for producing antibodies, and for treating  
 PT autoimmune diseases, leukemia and asthma -  
 XX  
 XX Example 7; Page 171-172; 200pp; English.  
 PS  
 XX  
 CC The present invention describes an isolated human zcytor19 protein (I),  
 CC and truncated zcytor19 proteins. (I) has immunosuppressive, cytostatic,  
 CC antitumetic, antiarthritic, neuroprotective, antiinflammatory,  
 CC antidiabetic, nephrotropic, dermatological, anti-HIV and haemostatic  
 CC activities, and can be used in vaccines. (I) or an antibody binding (I)  
 CC can be used for suppressing the immune system for reducing rejection of  
 CC tissue or organ transplants and grafts and for treating T-cell specific  
 CC leukaemias or lymphomas and autoimmune diseases including rheumatoid  
 CC arthritis, multiple sclerosis, diabetes mellitus, inflammatory bowel  
 CC disease and Crohn's disease. The antibodies can also be used for treating  
 CC immunologic renal diseases, glomerulonephritis, mesangio proliferative  
 CC disease, chronic lymphocytic leukaemia, secondary glomerulonephritis or  
 CC vasculitis associated with lupus, polyarteritis, scleroderma, HIV-related  
 CC diseases, amyloidosis and haemolytic uraemic syndrome. (I) and the  
 CC antibodies can also be used for renal or urological neoplasms and  
 CC multiple myelomas, asthma, bronchitis, emphysema and other chronic

CC airway diseases. Human zcytor19 is located to chromosome 1, more  
 CC specifically to chromosome 1p36.11. The present sequence represents  
 CC a human IgG gamma 1 heavy chain protein, which is used in an example  
 CC from the present invention.  
 XX  
 SQ Sequence 330 AA;  
 Query Match 99.4%; Score 1767; DB 23; Length 330;  
 Best Local Similarity 100.0%; Pred. No. 3.7e-125;  
 Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 ASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 62  
 Db 1 ASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60  
 QY 63 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKHTCTCPPELGG 122  
 Db 61 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKHTCTCPPELGG 120  
 QY 123 PSVELFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDQVGEVHNAKTTPREQYN 182  
 Db 121 PSVELFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDQVGEVHNAKTTPREQYN 180  
 QY 183 STYRWVSVLTVLHQMGLNGKEYKCVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 242  
 Db 181 STYRWVSVLTVLHQMGLNGKEYKCVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240  
 QY 243 LTKNQVSLTCLVKGFPYSDIAVWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 302  
 Db 241 LTKNQVSLTCLVKGFPYSDIAVWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 300  
 QY 303 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 332  
 Db 301 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 330

RESULT 4  
 AAE21960  
 ID AAE21960 standard; Protein: 330 AA.  
 XX  
 AC AAE21960;  
 XX  
 DT 25-JUL-2002 (first entry)  
 XX  
 DE Human death domain containing receptor (DR6) protein-related protein.  
 XX  
 KW Human; therapy; death domain containing receptor; DR6; receptor; anaemia;  
 KW apoptosis; rheumatoid arthritis; eczema; asthma; psoriasis; pancreatitis;  
 KW diabetes; cancer; multiple sclerosis; Graves disease; glomerulonephritis;  
 KW transplant rejection; systemic lupus erythematosus; hepatitis; cirrhosis;  
 KW autoimmune; gastritis; dermatosis; cardiopathy; infertility; haemostatic;  
 KW H. pylori-associated ulceration; antiinflammatory; vasotropic; virucide;  
 KW acquired immunodeficiency syndrome; AIDS; human immunodeficiency virus;  
 KW HIV; haemolytic uraemic syndrome; HUS; immunodeficiency; neuroprotective;  
 KW adult respiratory distress syndrome; ARDS; cytostatic; thyromimetic;  
 KW dermatological; hepatotropic; antibacterial.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200185209-A2.  
 XX  
 XX 15-NOV-2001.  
 XX  
 XX 30-APR-2001; 2001WO-US11735.  
 XX  
 XX 10-MAY-2000; 2000US-203015P.  
 XX  
 XX (ELIL) LILLY & CO ELI.  
 XX  
 XX Heuer JG, Liu J, Na S, Song HY, Yang D;  
 XX WPI; 2002-351283/38.  
 XX



QY 183 STYRVSVLTIVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKQPREPOVYTLPPSRDE 242  
 DB 181 STYRVSVLTIVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKQPREPOVYTLPPSRDE 240  
 QY 243 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 302  
 DB 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 300  
 QY 303 QOQNVFSCSVWHEALHNHYTQKSLSLSPGK 332  
 DB 301 QOQNVFSCSVWHEALHNHYTQKSLSLSPGK 330

## RESULT 6

AAM47856

ID AAM47856 standard; Protein; 330 AA.

XX AC AAM47856;

XX DT 22-FEB-2002 (first entry)

XX DE Human Ig-gammal heavy chain constant region amino acid sequence.  
 XX KW Human; immunoadhesin; intercellular adhesion molecule; ICAM-1;  
 KW human rhinovirus; immunoglobulin heavy chain; J chain; HRV; common cold;  
 KW transgenic plant.

XX OS Homo sapiens.

XX PN WO2001183529-A2.  
 XX PD 08-NOV-2001.

XX PF 28-APR-2001; 2001WO-US13932.  
 XX PR 28-APR-2000; 2000US-200298P.

XX PA (PLAN-) PLANET BIOTECHNOLOGY INC.  
 XX PI Larrick JW, Wycoff KL;

XX DR N-PSDB; ABA05265.  
 XX PT Immunoadhesin for treating human rhinovirus infection comprises  
 PT chimeric intercellular adhesion molecule-1, and optionally a J chain  
 PT and secretory component in association

XX PS Disclosure; Fig 7; 138pp; English.

CC The invention relates to an immunoadhesin comprising:  
 CC (a) a chimeric intercellular adhesion molecule (ICAM)-1 comprising a  
 CC rhinovirus receptor protein linked to at least a portion of an  
 CC immunoglobulin heavy chain; and  
 CC (b) optionally a J chain and secretory component associated with the  
 CC chimeric ICAM-1 molecule. The immunoadhesin has plant-specific  
 CC glycosylation and virucide activity. The immunoadhesin is useful for  
 CC reducing infection by human rhinovirus (HRV) and hence the initiation or  
 CC spread of the common cold by HRV. The immunoadhesin binds to HRV and  
 CC reduces its infectivity, competing with cell surface ICAM-1 for binding  
 CC sites, interfering with virus entry or uncoating and directing premature  
 CC release of viral RNA and formation of empty capsids. Expression of the  
 CC immunoadhesin in plants would be tetrameric, rather than dimeric.  
 CC Immunoadhesin having multiple binding sites have a higher effective  
 CC affinity for the virus, thereby increasing the effectiveness of the  
 CC immunoadhesin. Association of secretory component and immunoglobulin J  
 CC chain increases the stability of the immunoadhesin in the mucosal  
 CC environment. Production is significantly less expensive in plants than in  
 CC animal cell culture and production in plants is safer for human use,  
 CC since plants are not known to harbor any animal viruses. The present  
 CC sequence is that of a human immunoglobulin protein sequence, useful to  
 CC the invention.

XX SQ Sequence 330 AA;  
 Query Match 99.4%; Score 1767; DB 23; Length 330;  
 Best Local Similarity 100.0%; Pred. No. 3.7e-125; Indels 0; Gaps 0;  
 Matches 330; Conservative 0; Mismatches 0;  
 QY 3 ASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 62  
 DB 1 ASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60  
 QY 63 GLYSLSVVTVTPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHSTCPCPAPELGG 122  
 DB 61 GLYSLSVVTVTPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHSTCPCPAPELGG 120  
 QY 123 PSVFLFPPPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEOYN 182  
 DB 121 PSVFLFPPPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEOYN 180  
 QY 183 STYRVSVLTIVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKQPREPOVYTLPPSRDE 242  
 DB 181 STYRVSVLTIVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKQPREPOVYTLPPSRDE 240  
 QY 243 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 302  
 DB 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 300  
 QY 303 QOQNVFSCSVWHEALHNHYTQKSLSLSPGK 332  
 DB 301 QOQNVFSCSVWHEALHNHYTQKSLSLSPGK 330

## RESULT 7

ABP71856

ID ABP71856 standard; protein; 330 AA.

XX AC ABP71856;  
 XX DT 17-APR-2003 (first entry)

XX DE Human IgG1 Fc gamma region.  
 XX KW Human; fusion protein; IgE Fc epsilon; IgG Fc gamma; Fc epsilonRI; allergy;  
 KW Fc epsilonRII; Fc gammaRIIb; protein therapy; IgE; IgG; asthma; hay fever;  
 KW allergic asthma; allergic rhinitis; hay fever; food allergy;  
 KW atopic dermatitis; drug allergy; peanut allergen.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers  
 FT Region 1..98 /label= CH1 region  
 FT Region 99..113 /label= Hinge\_region  
 FT Region 114..223 /label= CH2\_region  
 FT Region 224..330 /label= CH3\_region

XX WO2002102320-A2.

XX PN 27-DEC-2002.  
 XX PD 14-JUN-2002; 2002WO-US19448.

XX PR 15-JUN-2001; 2001US-298710P.  
 XX PA (TANO-) TANOX INC.

XX PI An L, Wu H, Fung MSC;  
 XX DR WPI; 2003-167440/16.

PT New fusion protein which binds to FcεpsilonRI or RII receptor and  
 PT FcγmαRIIb receptor, useful for treating or preventing allergies and  
 PT asthma, comprises an IGE FcεpsilonI fragment and an IGE Fcγmα fragment  
 XX

PS Disclosure; Fig 5; 32pp; English.

XX The invention relates to a novel fusion protein comprising an IGE  
 CC FcεpsilonI fragment and an IGE Fcγmα fragment, which binds to an  
 CC FcεpsilonRI and/or FcεpsilonRII receptor and an FcγmαRIIb receptor. The  
 CC fusion protein of the invention may have a use in protein therapy. The  
 CC fusion protein is useful in treating or preventing IGE-mediated allergies  
 CC and asthma, such as allergic asthma, allergic rhinitis, hay fever, food  
 CC allergy, atopic dermatitis and drug allergy. The allergic response is  
 CC particularly caused by peanut allergen. The present sequence represents  
 XX the human IGE1 Fcγmα fragment.

XX Sequence 330 AA;

Query Match 99.4%; Score 1767; DB 24; Length 330;  
 Best Local Similarity 100.0%; Pred. No. 3.7e-125; Indels 0; Gaps 0;  
 Matches 330; Conservative 0; Mismatches 0;

QY 3 ASTKGSVPFLAPSSKSTSGGTAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVLQSS 62  
 DB 1 ASTKGSVPFLAPSSKSTSGGTAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVLQSS 60  
 QY 63 GLYSLSVVTVFSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKHTHTCPPCPAPPELLGG 122  
 DB 61 GLYSLSVVTVFSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKHTHTCPPCPAPPELLGG 120  
 QY 123 PSVFLPPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 182  
 DB 121 PSVFLPPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180  
 QY 183 STYRVSVLVLTVLHODWLNKGEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 242  
 DB 181 STYRVSVLVLTVLHODWLNKGEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240  
 QY 243 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFPLYSKLTVDKSRW 302  
 DB 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFPLYSKLTVDKSRW 300  
 QY 303 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 332  
 DB 301 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 330

RESULT 8

AAE32627  
 ID AAE32627 standard; Protein; 330 AA.

XX AAE32627;

DT 24-MAR-2003 (first entry)

DE Human immunoglobulin G1 (IgG1) heavy chain Fc region.

DE Human; immunogenic; therapy; immunoglobulin G1; IgG1.

XX Homo sapiens.

XX WO200279415-A2.

XX 10-OCT-2002.

XX 29-MAR-2002; 2002WO-US09650.

XX 30-MAR-2001; 2001US-280625P.

XX (LEXI-) LEXIGEN PHARM CORP.

XX Gillies SD;

XX WPI; 2003-111794/10.

XX Reducing the immunogenicity of a fusion protein by changing an amino  
 PT acid within the junction region spanning a fusion junction of a fusion  
 PT protein to reduce the ability of the candidate T-cell epitope to  
 PT interact with a T-cell receptor -

PS Disclosure; Page 49-50; 67pp; English.

XX The present invention relates to a method of reducing the immunogenicity  
 CC of a fusion protein. The method involves identifying a candidate T-cell  
 CC epitope within a junction region spanning a fusion junction of a fusion  
 CC protein and changing an amino acid within the junction region to reduce  
 CC the ability of the candidate T-cell epitope to interact with a T-cell  
 CC receptor. The method is useful for reducing the immunogenicity of fusion  
 CC proteins for use in therapy. The present sequence is human immunoglobulin  
 CC G1 (IgG1) heavy chain Fc region. This sequence is used to illustrate the  
 CC method of the invention.

XX Sequence 330 AA;

Query Match 99.4%; Score 1767; DB 24; Length 330;  
 Best Local Similarity 100.0%; Pred. No. 3.7e-125; Indels 0; Gaps 0;  
 Matches 330; Conservative 0; Mismatches 0;

QY 3 ASTKGSVPFLAPSSKSTSGGTAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVLQSS 62  
 DB 1 ASTKGSVPFLAPSSKSTSGGTAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVLQSS 60  
 QY 63 GLYSLSVVTVFSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKHTHTCPPCPAPPELLGG 122  
 DB 61 GLYSLSVVTVFSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKHTHTCPPCPAPPELLGG 120  
 QY 123 PSVFLPPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 182  
 DB 121 PSVFLPPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180  
 QY 183 STYRVSVLVLTVLHODWLNKGEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 242  
 DB 181 STYRVSVLVLTVLHODWLNKGEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240  
 QY 243 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFPLYSKLTVDKSRW 302  
 DB 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFPLYSKLTVDKSRW 300  
 QY 303 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 332  
 DB 301 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 330

RESULT 9

AAE32915  
 ID AAE32915 standard; Protein; 330 AA.

XX AAE32915;

DT 24-MAR-2003 (first entry)

DE Human immunoglobulin G1 (IgG1) heavy chain Fc region.

DE T-cell; immunogenic; therapy; human; immunoglobulin G1; IgG1.

XX Homo sapiens.

XX WO200279232-A2.

XX 10-OCT-2002.

XX 30-MAR-2002; 2002WO-US09815.

XX 30-MAR-2001; 2001US-280625P.

XX

PA (LEXI-) LEXIGEN PHARM CORP.  
 XX Gillies SD;  
 XX WPI; 2003-103259/09.  
 XX Reducing the immunogenicity of a fusion protein comprises changing an  
 PT amino acid within the junction region to reduce the ability of the  
 PT candidate T-cell epitope identified within the junction spanning to  
 PT interact with T-cell receptor  
 XX  
 PS Disclosure; Page 49-50; 68pp; English.  
 XX  
 CC The invention relates to a method for reducing the immunogenicity of a  
 CC fusion protein which involves identifying a candidate T-cell epitope  
 CC within a junction spanning a fusion junction of a fusion protein, and  
 CC changing an amino acid within the junction region to reduce the ability  
 CC of the candidate T-cell epitope to interact with a T-cell receptor. The  
 CC method is useful for reducing the immunogenicity of a fusion protein.  
 CC It is useful for analysing, changing or modifying one or more amino  
 CC acids in the junction region of a fusion protein to identify a T-cell  
 CC epitope and reduce its ability to interact with a T-cell receptor. The  
 CC less immunogenic fusion proteins are useful in providing therapeutic  
 CC treatment. The present sequence is human immunoglobulin G1 (IgG1) heavy  
 CC chain Fc region used to illustrate the method of the invention.  
 XX  
 SQ Sequence 330 AA;  
 Query Match 99.4%; Score 1767; DB 24; Length 330;  
 Best Local Similarity 100.0%; Pred. No. 3,7e-125;  
 Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 ASTKGPSVFLAPSSKSTSGTAAALGCLVKDYPPPTVTSWNSGALTSVHTFPVAVLQSS 62  
 Db 1 ASTKGPSVFLAPSSKSTSGTAAALGCLVKDYPPPTVTSWNSGALTSVHTFPVAVLQSS 60  
 QY 63 GLYSLSWVTVPPSSSLGTQYICNVNHPKSNKTKVDKKVEPKSCDKTHTCPPCPAPPELLGG 122  
 Db 61 GLYSLSWVTVPPSSSLGTQYICNVNHPKSNKTKVDKKVEPKSCDKTHTCPPCPAPPELLGG 120  
 QY 123 PSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 182  
 Db 121 PSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180  
 QY 183 STYRVSVLTIVLQDMLNGKEYCKVSNKALPAPIEKTTISKAGQPREPQVYTLPPSRDE 242  
 Db 181 STYRVSVLTIVLQDMLNGKEYCKVSNKALPAPIEKTTISKAGQPREPQVYTLPPSRDE 240  
 QY 243 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 302  
 Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 300  
 QY 303 QGQNVFSCSVMEALHNYTKQSLSPGK 332  
 Db 301 QGQNVFSCSVMEALHNYTKQSLSPGK 330

## RESULT 10

AAR43685

ID AAR43685 standard; Protein; 351 AA.

XX AAR43685;

AC AAR43685;

XX 25-MAR-2003 (updated)

DT 25-MAY-1994 (first entry)

XX

DE Human kappa immunoglobulin light chain constant domain.

XX

KW Human; immunoglobulin; constant; region; humanised; P-selectin; light;

KW blocking; antibody; heavy; chain; variable; murine; thrombotic disease;

KW monoclonal; PBI.3; CDR; complementarity determining region; leukocyte;

KW expression vector; coexpression; pHCMV-1748RHA-gamma1ci-dhfr; epitope;

KW pHCMV-1748RHA-KR-neo; PBI.3/Humanised version A; vascular endothelium;

KW pHCMV-1747CH-gamma1ci-neo; pHCMV-1747-CL-KR-neo; PBI.3 chimera;  
 XX acute lung injury; ischaemia reperfusion injury; inflammation.  
 XX Homo sapiens.

OS

XX

PH Key

FT Domain

FT Region

FT Region

FT Domain

FT Domain

FT Domain

FT Domain

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QY 183 STYRVSVLTVLHODWLNKKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 242  
 Db 202 STYRVSVLTVLHODWLNKKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 261  
 QY 243 LTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 302  
 Db 262 LTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 321  
 QY 303 QQGNVFSCSVNHEALHNHYTQKSLSLSPGK 332  
 Db 322 QQGNVFSCSVNHEALHNHYTQKSLSLSPGK 351

RESULT 11  
 AAP91918  
 ID AAP91918 standard; protein; 371 AA.  
 XX AC AAP91918;  
 XX DT 25-MAR-2003 (updated)  
 DT 31-OCT-2002 (updated)  
 DT 14-MAY-1990 (first entry)  
 XX DE Sequence of the linked immunoglobulin gamma chain fragment.  
 XX KW Immunoglobulin gamma chain; IgG1 heavy chain constant region.  
 XX OS Homo sapiens.  
 XX PH Key Location/Qualifiers  
 FT Misc-difference 42..43 /note= "Insert site"  
 FT Misc-difference 144..145 /note= "Insert site"  
 FT EP314317-A.  
 XX PN 03-MAY-1989.  
 XX PD 03-OCT-1988; 88EP-0309194.  
 XX PR 02-OCT-1987; 87US-0104329.  
 XX PR 28-SEP-1988; 88US-0250785.  
 XX PA (GETH ) GENENTECH INC.  
 XX PI Capon DJ, Gregory TJ;  
 XX WPI; 1989-131855/18.  
 XX N-PSDB; AAN90779.  
 XX Compans. contg. adhesion variants  
 PT - useful in therapy and diagnostics, eg CD4 variants  
 PT which are therapeutically useful for treating human  
 PT immuno-deficiency virus  
 XX Disclosure; Fig 4a-4b; 36pp; English.  
 XX It may be fused to the first 180 N-terminal  
 CC residues of CD4 at the C-terminus. The fusion protein may be used for  
 CC antiviral of immunomodulatory therapy particularly in treatment of HIV  
 CC infection.  
 CC (Updated on 31-OCT-2002 to add missing OS field.)  
 CC (Updated on 25-MAR-2003 to correct PR field.)  
 CC (Updated on 25-MAR-2003 to correct PI field.)  
 XX Sequence 371 AA;  
 Query Match 99.4%; Score 1767; DB 10; Length 371;  
 Best Local Similarity 100.0%; Pred. No. 4.2e-125;  
 Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 62

Db 42 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 101  
 QY 63 GLYSLSVWTVTPSSSLGTQYICNVNHPKSTNTKVDKVEPKSCDKHTCTCPCPAPPELLGG 122  
 Db 102 GLYSLSVWTVTPSSSLGTQYICNVNHPKSTNTKVDKVEPKSCDKHTCTCPCPAPPELLGG 161  
 QY 123 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 182  
 Db 162 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 221  
 QY 183 STYRVSVLTVLHODWLNKKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 242  
 Db 222 STYRVSVLTVLHODWLNKKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 281  
 QY 243 LTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 302  
 Db 282 LTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 341  
 QY 303 QQGNVFSCSVNHEALHNHYTQKSLSLSPGK 332  
 Db 342 QQGNVFSCSVNHEALHNHYTQKSLSLSPGK 371

RESULT 12  
 ABB80109  
 ID ABB80109 standard; Protein; 442 AA.  
 XX AC ABB80109;  
 XX DT 13-JUN-2003 (first entry)  
 XX DE Heavy chain.  
 XX KW Complementarity determining region; CDR; humanised; mouse;  
 KW 286; light; heavy; variable; domain; antibody; preclinical; clinical;  
 KW Alzheimer's disease; epitope; amyloid beta peptide; Abeta;  
 KW central nervous system; plasma.  
 XX OS Homo sapiens.  
 XX OS Mus musculus.  
 XX PN WO2003015617-A2.  
 XX PD 27-FEB-2003.  
 XX PF 16-AUG-2002; 2002WO-US26321.  
 XX PR 17-AUG-2001; 2001US-313221P.  
 XX PR 17-AUG-2001; 2001US-313224P.  
 XX PR 23-OCT-2001; 2001US-334987P.  
 XX PA (UNIW ) UNIV WASHINGTON.  
 XX PA (ELIL ) LILLY & CO ELI.  
 XX PI Holtzman DM, Demattos R, Bales KR, Cummins DJ, Paul SM;  
 XX WFI; 2003-278505/27.  
 XX Diagnosing preclinical or clinical Alzheimer's disease in a subject by  
 PT administering an antibody which specifically binds an epitope -  
 XX Disclosure; Page 15-16; 64pp; English.  
 XX The sequences given in AAG80104-09 represent preferred antibodies  
 CC of the invention. This sequence represents the preferred heavy  
 CC chain. The humanised antibody of the invention may be used for  
 CC diagnosing preclinical or clinical Alzheimer's disease. The antibody  
 CC specifically binds an epitope, preferably the amyloid beta peptide  
 CC (Abeta). The antibodies sequester Abeta from its bound, circulating  
 CC form in blood and alter clearance of soluble and bound forms of Abeta  
 CC in central nervous system and plasma. The antibodies specifically bind  
 CC an epitope representing amino acids 13-28 of the Abeta molecule.



XX 27-FEB-2003.  
 XX 14-AUG-2002; 2002WO-US21324.  
 XX 17-AUG-2001; 2001US-313576P.  
 XX 28-MAY-2002; 2002US-383851P.  
 XX (ELIL ) LILLY & CO ELI.  
 XX Bales KR., Paul SM;  
 XX WPI; 2003-289975/28.  
 XX  
 PT Treating or reducing the progression of diseases associated with  
 PT amyloid-beta peptide, e.g. Alzheimer's disease, vascular dementia or  
 PT mild cognitive impairment, comprises administering an anti-amyloid-beta  
 PT peptide antibody -  
 XX  
 XX Disclosure; Page 20-22; 84pp; English.  
 XX  
 CC The invention relates to treating cognitive symptoms or reducing disease  
 CC progression in a subject having a condition or disease associated with  
 CC amyloid-beta peptide (Abeta). The method involves administering an amount  
 CC of an anti-Abeta antibody that has greater affinity for soluble Abeta  
 CC than 10<sup>-9</sup> M, that has affinity (KD) for soluble Abeta1-40 or Abeta1-42  
 CC higher than 10<sup>-9</sup> M, or that has greater affinity for soluble Abeta  
 CC than antibody 266 has. The method or the anti-Abeta antibody is useful in  
 CC preparing a medicament for treating cognitive symptoms or reducing  
 CC disease progression in a subject having a condition or disease associated  
 CC with Abeta. The condition or disease is Alzheimer's disease, Down's  
 CC syndrome, cerebral amyloid angiopathy, vascular dementia, or mild  
 CC cognitive impairment. The present sequence represents a humanised  
 CC anti-Abeta antibody 266 heavy chain.  
 XX  
 SQ Sequence 442 AA;  
 Query Match 99.4%; Score 1767; DB 24; Length 442;  
 Best Local Similarity 100.0%; Pred. No. 5.3e-125;  
 Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 62  
 Db 113 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 172  
 QY 63 GLYSLSVVTPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKTHTCPPCPAPELLGG 122  
 Db 173 GLYSLSVVTPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKTHTCPPCPAPELLGG 232  
 QY 123 PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREQYN 182  
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 QY 183 STYRVSVLTIVLQDWLNGKEYCKVSKNALPAPIEKTISKAKQPREPQVYTLPPSRDE 242  
 Db 293 STYRVSVLTIVLQDWLNGKEYCKVSKNALPAPIEKTISKAKQPREPQVYTLPPSRDE 352  
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 Db 353 LTKNQVSLTCLVKGPYSDIAVEVESNGQPENNYKTTTPVLDSDGSPFLYSKLTVDKSRW 412  
 QY 303 QGNVFSCVMHEALHNYTKQSLSPGK 332  
 Db 413 QGNVFSCVMHEALHNYTKQSLSPGK 442  
 RESULT 15  
 ABR39474  
 ID ABR39474 standard; protein; 442 AA.  
 XX  
 AC ABR39474;  
 XX  
 DT 12-JUN-2003 (first entry)

XX Humanised anti-Abeta antibody 266 analogue heavy chain.  
 DE Amyloid-beta; Abeta; antibody 266; nootropic; neuroprotective; CDR;  
 XX immunostimulant.  
 KW Synthetic.  
 XX OS  
 XX Key Location/Qualifiers  
 FH Misc-difference 56  
 FT /note= "Xaa is any amino acid, provided that if Xaa at  
 FT position 57 is neither Asp nor Pro and Xaa at position  
 FT 59 is Ser or Thr, then Xaa at position 56 is not Asn"  
 FT  
 FT Misc-difference 57  
 FT /note= "Xaa is any amino acid, provided that if Xaa at  
 FT position 56 is Asn and Xaa at position 58 is Ser or Thr,  
 FT then Xaa at position 57 is Asp or Pro"  
 FT  
 FT Misc-difference 58  
 FT /note= "Xaa is any amino acid, provided that if Xaa at  
 FT position 56 is Asn and Xaa at position 57 is neither Asp  
 FT nor Pro, then Xaa at position 58 is neither Ser nor Thr"  
 FT  
 XX WO2003016467-A2.  
 XX 27-FEB-2003.  
 XX 14-AUG-2002; 2002WO-US21324.  
 XX 17-AUG-2001; 2001US-313576P.  
 XX 28-MAY-2002; 2002US-383851P.  
 XX (ELIL ) LILLY & CO ELI.  
 XX Bales KR, Paul SM;  
 XX WPI; 2003-289975/28.  
 XX  
 PT Treating or reducing the progression of diseases associated with  
 PT amyloid-beta peptide, e.g. Alzheimer's disease, vascular dementia or  
 PT mild cognitive impairment, comprises administering an anti-amyloid-beta  
 PT peptide antibody -  
 XX  
 PS Disclosure; Page 29-31; 84pp; English.  
 XX  
 CC The invention relates to treating cognitive symptoms or reducing disease  
 CC progression in a subject having a condition or disease associated with  
 CC amyloid-beta peptide (Abeta). The method involves administering an amount  
 CC of an anti-Abeta antibody that has greater affinity for soluble Abeta  
 CC than 10<sup>-9</sup> M, that has affinity (KD) for soluble Abeta1-40 or Abeta1-42  
 CC higher than 10<sup>-9</sup> M, or that has greater affinity for soluble Abeta  
 CC than antibody 266 has. The method or the anti-Abeta antibody is useful in  
 CC preparing a medicament for treating cognitive symptoms or reducing  
 CC disease progression in a subject having a condition or disease associated  
 CC with Abeta. The condition or disease is Alzheimer's disease, Down's  
 CC syndrome, cerebral amyloid angiopathy, vascular dementia, or mild  
 CC cognitive impairment. The present sequence represents a preferred heavy  
 CC chain of a humanised anti-Abeta antibody 266 analogue that has a high  
 CC affinity for Abeta.  
 XX  
 SQ Sequence 442 AA;  
 Query Match 99.4%; Score 1767; DB 24; Length 442;  
 Best Local Similarity 100.0%; Pred. No. 5.3e-125;  
 Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 62  
 Db 113 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 172  
 QY 63 GLYSLSVVTPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKTHTCPPCPAPELLGG 122  
 Db 173 GLYSLSVVTPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKTHTCPPCPAPELLGG 232



Qy	123	PSVFLFPKPKDXTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN	182
Db	233	PSVFLFPKPKDXTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN	292
Qy	183	STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE	242
Db	293	STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE	352
Qy	243	LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW	302
Db	353	LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW	412
Qy	303	QCGNVFSCSVMEALHNNHYTKSLSPGK	332
Db	413	QCGNVFSCSVMEALHNNHYTKSLSPGK	442

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 Job time : 79.4183 secs

GenCore version 5.1.6  
 Copyright (c) 1993 - 2004 Compugen Ltd.  
 OM protein - protein search, using sw model  
 Run on: January 13, 2004, 12:43:20 ; Search time 53.062 Seconds  
 (without alignments)  
 1360.812 Million cell updates/sec

Title: US-09-990-586-98  
 Perfect score: 1778  
 Sequence: 1 EFASKGPSVFLAPSSKST.....MHEALHNYTKSLSLSPGK 332

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 747907 seqs, 201509753 residues

Total number of hits satisfying chosen parameters: 747907

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : Published Applications AA.\*

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 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pdp.\*  
 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pdp.\*  
 4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pdp.\*  
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 14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pdp.\*  
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 16: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pdp.\*  
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 18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pdp.\*

Pred. No. is the number of results predicted by chance to have a  
 score greater than or equal to the score of the result being printed,  
 and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1778	100.0	332	11	US-09-990-586-98
2	1778	100.0	332	12	US-10-310-113-167
3	1778	100.0	332	12	US-10-230-680-98
4	1767	99.4	330	11	US-09-995-898A-15
5	1767	99.4	330	11	US-09-892-949-38
6	1767	99.4	330	12	US-10-112-582-1
7	1767	99.4	330	12	US-10-110-719-8
8	1767	99.4	330	12	US-10-320-231A-81
9	1767	99.4	330	14	US-10-047-542-20
10	1767	99.4	330	15	US-10-269-805-68
11	1767	99.4	371	12	US-10-097-044A-7
12	1767	99.4	444	15	US-10-150-475A-6
13	1767	99.4	445	12	US-10-320-231A-79
14	1767	99.4	447	11	US-09-256-156-1
15	1767	99.4	451	10	US-09-822-698A-26
					Sequence 98, Appl
					Sequence 167, Appl
					Sequence 98, Appl
					Sequence 15, Appl
					Sequence 38, Appl
					Sequence 1, Appl
					Sequence 8, Appl
					Sequence 81, Appl
					Sequence 20, Appl
					Sequence 68, Appl
					Sequence 7, Appl
					Sequence 6, Appl
					Sequence 79, Appl
					Sequence 1, Appl
					Sequence 26, Appl

16 1767 99.4 470 12 US-10-104-047-3730  
 17 1767 99.4 476 10 US-09-747-669-3  
 18 1767 99.4 476 12 US-10-409-938-15  
 19 1767 99.4 476 15 US-10-290-703-3  
 20 1767 99.4 547 9 US-09-746-359A-54  
 21 1767 99.4 567 10 US-09-825-561A-16  
 22 1767 99.4 571 9 US-09-746-359A-53  
 23 1767 99.4 731 10 US-09-825-012-46  
 24 1767 99.4 741 10 US-09-825-012-55  
 25 1767 99.4 951 10 US-09-935-868-9  
 26 1767 99.4 951 12 US-10-282-182-9  
 27 1767 99.4 951 15 US-10-287-035-9  
 28 1763 99.2 475 9 US-09-740-002-27  
 29 1763 99.2 476 10 US-09-948-429B-4  
 30 1763 99.2 476 10 US-09-948-429B-12  
 31 1763 99.2 476 12 US-10-124-807-12  
 32 1763 99.2 476 12 US-10-124-807-12  
 33 1763 99.2 476 12 US-10-291-532-4  
 34 1763 99.2 476 12 US-10-291-532-12  
 35 1763 99.2 476 14 US-10-124-905-4  
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 37 1763 99.2 478 10 US-09-948-429B-8  
 38 1763 99.2 478 12 US-10-124-807-8  
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 40 1763 99.2 478 14 US-10-124-905-8  
 41 1762 99.1 729 10 US-09-825-012-61  
 42 1762 99.1 739 10 US-09-825-012-61  
 43 1761 99.0 330 12 US-10-159-006-22  
 44 1761 99.0 330 15 US-10-121-464-20  
 45 1761 99.0 451 9 US-09-920-171-14

## ALIGNMENTS

RESULT 1  
 US-09-990-586-98  
 ; Sequence 98, Application US/09990586  
 ; Publication No. US20030109680A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: JIAO, JIN-AN  
 ; APPLICANT: WONG, HING C.  
 ; TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD COAGULATION AND METHODS  
 ; TITLE OF INVENTION: OF USE THEREOF  
 ; FILE REFERENCE: 71758/46943-CIP2  
 ; CURRENT APPLICATION NUMBER: US/09/990.586  
 ; CURRENT FILING DATE: 2001-11-21  
 ; PRIOR APPLICATION NUMBER: 09/293,854  
 ; PRIOR FILING DATE: 1999-04-16  
 ; NUMBER OF SEQ ID NOS: 102  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 98  
 ; LENGTH: 332  
 ; TYPE: PPT  
 ; ORGANISM: Homo sapiens  
 ; US-09-990-586-98

Query Match 100.0%; Score 1778; DB 11; Length 332;  
 Best Local Similarity 100.0%; Pred. No. 6.6e-138;  
 Matches 332; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 EFASKGPSVFLAPSSKSTSGGTAALGCLVKGYFPEPVTVSWNSGALTSGVHTFPAVLQ 60  
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 QY 121 GGPSVFLPPKPKDGLMISTPEVTCVVDVSHDEPEVFNVTVDGVVEVHNATKPREEQ 180  
 DB 121 GGPSVFLPPKPKDGLMISTPEVTCVVDVSHDEPEVFNVTVDGVVEVHNATKPREEQ 180

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Db 241 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSGFFLYSKLTVDKS 300  
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## RESULT 2

US-10-310-113-167  
; Sequence 167, Application US/10310113  
; Publication No. US20030176664A1  
; GENERAL INFORMATION:  
; APPLICANT: JIAO, JIN-AN  
; APPLICANT: WONG, HING C.  
; APPLICANT: NIEVES, ESPERANZA LILIANA  
; APPLICANT: MOSQUERA, LUIS A.  
; TITLE OF INVENTION: USE OF ANTI-TISSUE FACTOR ANTIBODIES FOR TREATING  
; TITLE OF INVENTION: THROMBOSES  
; FILE REFERENCE: 58122(71758)  
; CURRENT APPLICATION NUMBER: US/10/310,113  
; CURRENT FILING DATE: 2002-12-04  
; PRIOR APPLICATION NUMBER: 09/990,586  
; PRIOR FILING DATE: 2001-11-21  
; PRIOR APPLICATION NUMBER: 60/343,306  
; PRIOR FILING DATE: 2001-10-29  
; PRIOR APPLICATION NUMBER: 09/293,854  
; PRIOR FILING DATE: 1999-04-16  
; PRIOR APPLICATION NUMBER: 08/814,806  
; PRIOR FILING DATE: 1997-03-10  
; NUMBER OF SEQ ID NOS: 169  
; SOFTWARE: Patent in Ver. 2.1  
; SEQ ID NO 167  
; LENGTH: 332  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-310-113-167

Query Match 100.0%; Score 1778; DB 12; Length 332;  
Best Local Similarity 100.0%; Pred. No. 6.6e-138;  
Matches 332; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 301 RMOQGNVFCSCVMHEALHNHYTKSLSLSPGK 332

## RESULT 3

US-10-230-880-98  
; Sequence 98, Application US/10230880  
; Publication No. US20030190705A1  
; GENERAL INFORMATION:  
; APPLICANT: WONG, HING C.  
; APPLICANT: STINSON, JEFFREY L.  
; APPLICANT: MOSQUERA, LUIS A.  
; TITLE OF INVENTION: METHOD OF HUMANIZING IMMUNE SYSTEM MOLECULES  
; FILE REFERENCE: 71758/58066  
; CURRENT APPLICATION NUMBER: US/10/230,880  
; CURRENT FILING DATE: 2002-12-23  
; PRIOR APPLICATION NUMBER: 09/990,586  
; PRIOR FILING DATE: 2001-11-21  
; PRIOR APPLICATION NUMBER: 60/343,306  
; PRIOR FILING DATE: 2001-10-29  
; PRIOR APPLICATION NUMBER: 09/293,854  
; PRIOR FILING DATE: 1999-04-16  
; NUMBER OF SEQ ID NOS: 174  
; SOFTWARE: Patent in Ver. 2.1  
; SEQ ID NO 98  
; LENGTH: 332  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-230-880-98

Query Match 100.0%; Score 1778; DB 12; Length 332;  
Best Local Similarity 100.0%; Pred. No. 6.6e-138;  
Matches 332; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 EFASKGSPVFPPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQ 60  
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QY 61 SSGLYSLSVWTVPPSSSLGTQTYICNVNHPKSNKVDKVPKSCDKHTCCPCPAPELL 120  
Db 61 SSGLYSLSVWTVPPSSSLGTQTYICNVNHPKSNKVDKVPKSCDKHTCCPCPAPELL 120  
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Db 301 RMOQGNVFCSCVMHEALHNHYTKSLSLSPGK 332

## RESULT 4

US-09-995-898A-15  
; Sequence 15, Application US/09995898A  
; Publication No. US20030027253A1  
; GENERAL INFORMATION:  
; APPLICANT: Presnell, Scott R.  
; APPLICANT: Xu, Wenfeng  
; APPLICANT: No. US20030027253A1ak, Julia E.  
; APPLICANT: Whitmore, Theodore E.  
; APPLICANT: Grant, Francis J.  
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR19  
; FILE REFERENCE: 00-108  
; CURRENT APPLICATION NUMBER: US/09/995,898A  
; CURRENT FILING DATE: 2001-11-28  
; PRIOR APPLICATION NUMBER: US 60/253,561  
; PRIOR FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: US 60/267,211  
; PRIOR FILING DATE: 2001-02-07  
; NUMBER OF SEQ ID NOS: 50

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/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 15
/ LENGTH: 330
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-995-898A-15

Query Match
Best Local Similarity 99.4%; Score 1767; DB 11; Length 330;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ASTKGPSVFLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 62
Db 1 ASTKGPSVFLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
QY 63 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHTCPCPAPELLGG 122
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Db 121 PSVFLFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
QY 183 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYTLPPSRDE 242
Db 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYTLPPSRDE 240
QY 243 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 302
Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 300
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Db 301 QGQNVFSCSVMEALHNHYTQKSLSLSPGK 330

RESULT 6
US-10-112-582-1
/ Sequence 1, Application US/10112582
/ Publication No. US20030166877A1
/ GENERAL INFORMATION:
/ APPLICANT: Gillies, Stephen
/ TITLE OF INVENTION: Reducing the Immunogenicity of Fusion Proteins
/ FILE REFERENCE: LEX-017
/ CURRENT APPLICATION NUMBER: US/10/112,582
/ CURRENT FILING DATE: 2002-03-29
/ PRIOR APPLICATION NUMBER: US 60/280,625
/ PRIOR FILING DATE: 2001-03-30
/ NUMBER OF SEQ ID NOS: 59
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 1
/ LENGTH: 330
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc feature
/ OTHER INFORMATION: human Ig gamma heavy chain C region
US-10-112-582-1

Query Match 99.4%; Score 1767; DB 12; Length 330;
Best Local Similarity 100.0%; Pred. No. 5.3e-137;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ASTKGPSVFLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 62
Db 1 ASTKGPSVFLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
QY 63 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHTCPCPAPELLGG 122
Db 61 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHTCPCPAPELLGG 120
QY 123 PSVFLFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 182
Db 121 PSVFLFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
QY 183 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYTLPPSRDE 242
Db 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYTLPPSRDE 240
QY 243 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 302
Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 300
QY 303 QGQNVFSCSVMEALHNHYTQKSLSLSPGK 332
Db 301 QGQNVFSCSVMEALHNHYTQKSLSLSPGK 330

Query Match 99.4%; Score 1767; DB 11; Length 330;
Best Local Similarity 100.0%; Pred. No. 5.3e-137;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ASTKGPSVFLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 62
Db 1 ASTKGPSVFLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
QY 63 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHTCPCPAPELLGG 122
Db 61 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHTCPCPAPELLGG 120
QY 123 PSVFLFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 182
Db 121 PSVFLFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
QY 183 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYTLPPSRDE 242
Db 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYTLPPSRDE 240
QY 243 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 302
Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 300
QY 303 QGQNVFSCSVMEALHNHYTQKSLSLSPGK 332
Db 301 QGQNVFSCSVMEALHNHYTQKSLSLSPGK 330

Query Match 99.4%; Score 1767; DB 11; Length 330;
Best Local Similarity 100.0%; Pred. No. 5.3e-137;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ASTKGPSVFLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 62
Db 1 ASTKGPSVFLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
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RESULT 7
US-10-310-719-8
; Sequence 8, Application US/10310719
; Publication No. US20030166163A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; TITLE OF INVENTION: Immunocytokines With Modulated Selectivity
; FILE REFERENCE: LEX-020
; CURRENT APPLICATION NUMBER: US/10/310,719
; CURRENT FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: 60/337,113
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/371,966
; PRIOR FILING DATE: 2002-04-12
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc
; LOCATION: (1)..(330)
; OTHER INFORMATION: IgG1 constant region
US-10-310-719-8

Query Match          99.4%; Score 1767; DB 12; Length 330;
Best Local Similarity 100.0%; Pred. No. 5.3e-137;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ASYKGPSVFFPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 62
DB 1 ASYKGPSVFFPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60
QY 63 GLYSLSVVTVPSSSLGTQTYICNVNHPKSNKVDKKVEPKSCDKTHHTCPCPAPPELLGG 122
DB 61 GLYSLSVVTVPSSSLGTQTYICNVNHPKSNKVDKKVEPKSCDKTHHTCPCPAPPELLGG 120
QY 123 PSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 182
DB 121 PSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
QY 183 STYRVSVLTVLQDMLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 242
DB 181 STYRVSVLTVLQDMLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
QY 243 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 302
DB 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 300
QY 303 QQGNVFCSCVMHEALHNYTKQSLSPGK 332
DB 301 QQGNVFCSCVMHEALHNYTKQSLSPGK 330

RESULT 8
US-10-320-231A-81
; Sequence 81, Application US/10320231A
; Publication No. US20030194405A1
; GENERAL INFORMATION:
; APPLICANT: Neben, Steven
; APPLICANT: Takeuchi, Toshihiko
; APPLICANT: Tomkinson, Adrian
; TITLE OF INVENTION: Antibody Inhibiting Stem Cell Factor Activity And Use For
; FILE REFERENCE: 7430*163
; CURRENT APPLICATION NUMBER: US/10/320,231A
; CURRENT FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: US 60/342,174
; PRIOR FILING DATE: 2001-12-17
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 81

QY 3 ASYKGPSVFFPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 62
DB 1 ASYKGPSVFFPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60
QY 63 GLYSLSVVTVPSSSLGTQTYICNVNHPKSNKVDKKVEPKSCDKTHHTCPCPAPPELLGG 122
DB 61 GLYSLSVVTVPSSSLGTQTYICNVNHPKSNKVDKKVEPKSCDKTHHTCPCPAPPELLGG 120
QY 123 PSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 182
DB 121 PSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
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; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-320-231A-81

Query Match          99.4%; Score 1767; DB 12; Length 330;
Best Local Similarity 100.0%; Pred. No. 5.3e-137;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ASYKGPSVFFPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 62
DB 1 ASYKGPSVFFPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60
QY 63 GLYSLSVVTVPSSSLGTQTYICNVNHPKSNKVDKKVEPKSCDKTHHTCPCPAPPELLGG 122
DB 61 GLYSLSVVTVPSSSLGTQTYICNVNHPKSNKVDKKVEPKSCDKTHHTCPCPAPPELLGG 120
QY 123 PSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 182
DB 121 PSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
QY 183 STYRVSVLTVLQDMLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 242
DB 181 STYRVSVLTVLQDMLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
QY 243 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 302
DB 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 300
QY 303 QQGNVFCSCVMHEALHNYTKQSLSPGK 332
DB 301 QQGNVFCSCVMHEALHNYTKQSLSPGK 330

RESULT 9
US-10-047-542-20
; Sequence 20, Application US/10047542
; Publication No. US20020168367A1
; GENERAL INFORMATION:
; APPLICANT: LARRICK, JAMES W.
; APPLICANT: WYCOFF, KEITH L.
; TITLE OF INVENTION: NOVEL IMMUNOADHESINS FOR TREATING AND PREVENTING VIRAL
; TITLE OF INVENTION: AND BACTERIAL DISEASES
; FILE REFERENCE: 030905.0004.CIP1
; CURRENT APPLICATION NUMBER: US/10/047,542
; CURRENT FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: PCT/US01/13932
; PRIOR FILING DATE: 2001-04-28
; PRIOR APPLICATION NUMBER: 60/200,298
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-047-542-20

Query Match          99.4%; Score 1767; DB 14; Length 330;
Best Local Similarity 100.0%; Pred. No. 5.3e-137;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ASYKGPSVFFPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 62
DB 1 ASYKGPSVFFPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60
QY 63 GLYSLSVVTVPSSSLGTQTYICNVNHPKSNKVDKKVEPKSCDKTHHTCPCPAPPELLGG 122
DB 61 GLYSLSVVTVPSSSLGTQTYICNVNHPKSNKVDKKVEPKSCDKTHHTCPCPAPPELLGG 120
QY 123 PSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 182
DB 121 PSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
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QY 183 STYRVSVLTVLHODWLNKGYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 242  
 DB 191 STYRVSVLTVLHODWLNKGYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240  
 QY 243 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 302  
 DB 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 300  
 QY 303 QCGNVFSCSVMEALHNHYTQKSLSLSPGK 332  
 DB 301 QCGNVFSCSVMEALHNHYTQKSLSLSPGK 330

RESULT 10  
 US-10-097-044A-7  
 ; Sequence 68, Application US/10269805  
 ; Publication No. US20030124129A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: OLINER, JONATHAN D.  
 ; TITLE OF INVENTION: ANGIOPOIETIN-2 SPECIFIC BINDING AGENTS  
 ; FILE REFERENCE: A-722  
 ; CURRENT APPLICATION NUMBER: US/10/269,805  
 ; PRIOR FILING DATE: 2002-10-10  
 ; PRIOR APPLICATION NUMBER: US 60/328,604  
 ; NUMBER OF SEQ ID NOS: 76  
 ; SOFTWARE: Patent in version 3.1  
 ; SEQ ID NO 68  
 ; LENGTH: 330  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-269-805-68

Query Match 99.4%; Score 1767; DB 15; Length 330;  
 Best Local Similarity 100.0%; Pred. No. 5.3e-137;  
 Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 62  
 DB 1 ASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60  
 QY 63 GLYSLSVWTVPPSSLSGTQYICNVNHPKSTNTKVDKVEPKSCDKTHCTCPCPAPELGG 122  
 DB 61 GLYSLSVWTVPPSSLSGTQYICNVNHPKSTNTKVDKVEPKSCDKTHCTCPCPAPELGG 120  
 QY 123 PSVFLPPPKPOTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 182  
 DB 121 PSVFLPPPKPOTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180  
 QY 183 STYRVSVLTVLHODWLNKGYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 242  
 DB 181 STYRVSVLTVLHODWLNKGYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240  
 QY 243 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 302  
 DB 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 300  
 QY 303 QCGNVFSCSVMEALHNHYTQKSLSLSPGK 332  
 DB 301 QCGNVFSCSVMEALHNHYTQKSLSLSPGK 330

RESULT 11  
 US-10-097-044A-7  
 ; Sequence 7, Application US/10097044A  
 ; Publication No. US20030143220A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Capon, Daniel J.  
 ; Gregory, Timothy J.  
 ; TITLE OF INVENTION: Adhesion Variants  
 ; NUMBER OF SEQUENCES: 25  
 ; CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.  
 STREET: 460 Point San Bruno Blvd  
 CITY: South San Francisco  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94080

COMPUTER READABLE FORM:  
 MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patin (Genentech)  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/10/097,044A  
 FILING DATE: 28-May-2002  
 CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/08/457,918  
 FILING DATE: 1-JUN-1995  
 APPLICATION NUMBER: 08/236311  
 FILING DATE: 02-MAY-1994  
 APPLICATION NUMBER: 07/936190  
 FILING DATE: 26-AUG-1992  
 APPLICATION NUMBER: 07/842777  
 FILING DATE: 18-FEB-1992  
 APPLICATION NUMBER: 07/250785  
 FILING DATE: 28-SEP-1988  
 APPLICATION NUMBER: 07/104329  
 FILING DATE: 02-OCT-1987

ATTORNEY/AGENT INFORMATION:  
 NAME: Kubinec, Jeffrey S.  
 REGISTRATION NUMBER: 36,575  
 REFERENCE/DOCKET NUMBER: P0444P1C3

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 415/225-8228  
 TELEFAX: 415/952-9881  
 TELE: 910/371-7168

INFORMATION FOR SEQ ID NO: 7:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 371 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear

US-10-097-044A-7

Query Match 99.4%; Score 1767; DB 12; Length 371;  
 Best Local Similarity 100.0%; Pred. No. 6.2e-137;  
 Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 62  
 DB 42 ASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 101  
 QY 63 GLYSLSVWTVPPSSLSGTQYICNVNHPKSTNTKVDKVEPKSCDKTHCTCPCPAPELGG 122  
 DB 102 GLYSLSVWTVPPSSLSGTQYICNVNHPKSTNTKVDKVEPKSCDKTHCTCPCPAPELGG 161  
 QY 123 PSVFLPPPKPOTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 182  
 DB 162 PSVFLPPPKPOTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 221  
 QY 183 STYRVSVLTVLHODWLNKGYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 242  
 DB 222 STYRVSVLTVLHODWLNKGYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 281  
 QY 243 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 302  
 DB 282 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 341  
 QY 303 QCGNVFSCSVMEALHNHYTQKSLSLSPGK 332  
 DB 342 QCGNVFSCSVMEALHNHYTQKSLSLSPGK 371

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RESULT 12
US-10-150-475A-6
; Sequence 6, Application US/10150475A
; Publication No. US20030103985A1
; GENERAL INFORMATION:
; APPLICANT: Adolfs, G. et al.
; TITLE OF INVENTION: Cytotoxic CD44 Antibody Immunoconjugates
; FILE REFERENCE: 1/1211
; CURRENT APPLICATION NUMBER: US/10/150,475A
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: US 60/307,451
; PRIOR FILING DATE: 2001-07-24
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence: Humanised
; OTHER INFORMATION: Murine Antibody B1M4 4 Heavy Chain SEQ ID NO: 6
US-10-150-475A-6
Query Match          99.4%; Score 1767; DB 15; Length 444;
Best Local Similarity 100.0%; Pred. No. 7.9e-137;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 62
Db 115 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 174
QY 63 GLYSLSVVTVPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHTCPCPAPPELLGG 122
Db 175 GLYSLSVVTVPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHTCPCPAPPELLGG 234
QY 123 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREQYN 182
Db 235 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREQYN 294
QY 183 STYRVVSVLTVQLHODWLNKGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 242
Db 295 STYRVVSVLTVQLHODWLNKGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 354
QY 243 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRW 302
Db 355 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRW 414
QY 303 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 332
Db 415 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 444

RESULT 13
US-10-320-231A-79
; Sequence 79, Application US/10320231A
; Publication No. US20030194405A1
; GENERAL INFORMATION:
; APPLICANT: Neben, Steven
; APPLICANT: Takeuchi, Toshihiko
; APPLICANT: Tomkinson, Adrian
; TITLE OF INVENTION: Antibody Inhibiting Stem Cell Factor Activity And Use For
; TITLE OF INVENTION: Treatment Of Asthma
; FILE REFERENCE: 7430*163
; CURRENT APPLICATION NUMBER: US/10/320,231A
; CURRENT FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: US 60/342,174
; PRIOR FILING DATE: 2001-12-17
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 79
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Artificial
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; FEATURE:
; OTHER INFORMATION: synthetic sequence
US-10-320-231A-79
Query Match          99.4%; Score 1767; DB 12; Length 445;
Best Local Similarity 100.0%; Pred. No. 7.9e-137;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 62
Db 116 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 175
QY 63 GLYSLSVVTVPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHTCPCPAPPELLGG 122
Db 176 GLYSLSVVTVPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHTCPCPAPPELLGG 235
QY 123 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREQYN 182
Db 236 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREQYN 295
QY 183 STYRVVSVLTVQLHODWLNKGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 242
Db 296 STYRVVSVLTVQLHODWLNKGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 355
QY 243 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRW 302
Db 356 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRW 415
QY 303 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 332
Db 416 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 445

RESULT 14
US-09-256-156-1
; Sequence 1, Application US/09256156A
; Publication No. US20030105294A1
; GENERAL INFORMATION:
; APPLICANT: GULLIES, Stephen D
; APPLICANT: LO, Kin-Ming
; APPLICANT: WESOLOWSKI, John
; TITLE OF INVENTION: Enhancing the Circulating Half-life of Antibody-based
; TITLE OF INVENTION: Fusion Proteins
; FILE REFERENCE: LEX-003
; CURRENT APPLICATION NUMBER: US/09/256,156A
; CURRENT FILING DATE: 1999-02-24
; EARLIER APPLICATION NUMBER: US 60/075,887
; EARLIER FILING DATE: 1998-02-25
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 447
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: IGG-1 CHAIN C REGION
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(117)
; OTHER INFORMATION: The Xaa at positions 1 to 117 are non-conserved
; OTHER INFORMATION: amino acids
US-09-256-156-1
Query Match          99.4%; Score 1767; DB 11; Length 447;
Best Local Similarity 100.0%; Pred. No. 7.9e-137;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 62
Db 118 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 177
QY 63 GLYSLSVVTVPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHTCPCPAPPELLGG 122
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Job time : 54.062 secs

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Db 178 GLYSLSVVTVFSSSLGTQYICNVNHPSTKVDKVEPKSCDKTHTCPPCPAPELLGG 237
QY 123 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN 182
Db 238 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN 297
QY 183 STYRVVSVLTVLHODWLNKGEYKCKVSNKALPAPIETISKAKGQPREPQVYTLPPSRDE 242
Db 298 STYRVVSVLTVLHODWLNKGEYKCKVSNKALPAPIETISKAKGQPREPQVYTLPPSRDE 357
QY 243 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 302
Db 358 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 417
QY 303 QQGNVFCSVMHEALHNHYTQKSLSLSPGK 332
Db 418 QQGNVFCSVMHEALHNHYTQKSLSLSPGK 447
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RESULT 15  
US-09-822-698A-26  
; Sequence 26, Application US/09822698A  
; Patent No. US20020146750A1  
; GENERAL INFORMATION:  
; APPLICANT: Hoogenboom, Hendricus R.J.M.  
; APPLICANT: Henderikx, Maria P.G.  
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof  
; FILE REFERENCE: DYX-015.1 US  
; CURRENT APPLICATION NUMBER: US/09/822,698A  
; CURRENT FILING DATE: 2001-03-30  
; PRIOR APPLICATION NUMBER: US 09/538,913  
; PRIOR FILING DATE: 2000-03-30  
; NUMBER OF SEQ ID NOS: 112  
; SOFTWARE: Microsoft Word  
; SEQ ID NO 26  
; LENGTH: 451  
; TYPE: PRT  
; ORGANISM: artificial sequence  
; FEATURE:  
; OTHER INFORMATION: immunoglobulin heavy chain of MUC1-specific PHI-IgG1  
US-09-822-698A-26

Query Match 99.4%; Score 1767; DB 10; Length 451;  
Best Local Similarity 100.0%; Pred. No. 8e-137;  
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 62  
Db 122 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 181  
QY 63 GLYSLSVVTVFSSSLGTQYICNVNHPSTKVDKVEPKSCDKTHTCPPCPAPELLGG 122  
Db 182 GLYSLSVVTVFSSSLGTQYICNVNHPSTKVDKVEPKSCDKTHTCPPCPAPELLGG 241  
QY 123 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN 182  
Db 242 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN 301  
QY 183 STYRVVSVLTVLHODWLNKGEYKCKVSNKALPAPIETISKAKGQPREPQVYTLPPSRDE 242  
Db 302 STYRVVSVLTVLHODWLNKGEYKCKVSNKALPAPIETISKAKGQPREPQVYTLPPSRDE 361  
QY 243 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 302  
Db 362 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 421  
QY 303 QQGNVFCSVMHEALHNHYTQKSLSLSPGK 332  
Db 422 QQGNVFCSVMHEALHNHYTQKSLSLSPGK 451

Search completed: January 13, 2004, 13:13:45



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 13, 2004, 12:33:50 ; Search time 28.7057 Seconds  
(without alignments)  
489.353 Million cell updates/sec

Title: US-09-990-586-98

Perfect score: 1778

Sequence: 1 EFASKGPSVFLAPSSKST.....MHEALHNHYTKSLSPGK 332

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA.\*

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2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*

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4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*

5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep.\*

6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1767	99.4	371	1	US-08-236-311-7
2	1767	99.4	371	3	US-08-457-918-7
3	1767	99.4	446	3	US-08-397-411-7
4	1767	99.4	449	1	US-08-458-516-13
5	1767	99.4	476	2	US-08-378-939-10
6	1767	99.4	951	4	US-09-313-342-9
7	1763	99.2	462	4	US-09-289-942A-7
8	1763	99.2	475	4	US-09-740-002-27
9	1763	99.2	476	3	US-08-487-550-4
10	1763	99.2	476	4	US-08-487-550-12
11	1763	99.2	476	4	US-09-526-098-4
12	1763	99.2	476	3	US-09-526-098-12
13	1763	99.2	478	3	US-08-487-550-8
14	1763	99.2	478	4	US-09-526-098-8
15	1762	99.1	459	1	US-08-157-101A-7
16	1761	99.0	330	4	US-09-301-593-22
17	1761	99.0	451	2	US-08-887-352B-14
18	1761	99.0	451	2	US-08-887-352B-16
19	1761	99.0	451	2	US-08-887-352B-18
20	1761	99.0	451	3	US-08-466-151-65
21	1761	99.0	451	3	US-09-109-207C-14
22	1761	99.0	451	3	US-09-109-207C-16
23	1761	99.0	451	3	US-09-109-207C-18
24	1761	99.0	451	3	US-09-282-505-2
25	1761	99.0	451	3	US-09-054-255-2
26	1761	99.0	451	3	US-09-296-005-14
27	1761	99.0	451	3	US-09-296-005-16

28 1761 99.0 451 3 US-09-296-005-18 Sequence 18, Appl  
29 1761 99.0 451 4 US-09-282-846-2 Sequence 2, Appl  
30 1761 99.0 451 4 US-09-680-145-2 Sequence 2, Appl  
31 1761 99.0 452 3 US-09-027-449-71 Sequence 71, Appl  
32 1761 99.0 452 3 US-09-026-985-71 Sequence 71, Appl  
33 1761 99.0 452 4 US-09-121-952A-71 Sequence 71, Appl  
34 1761 99.0 452 4 US-09-234-340A-71 Sequence 18, Appl  
35 1761 99.0 453 4 US-09-301-593-18 Sequence 22, Appl  
36 1761 99.0 454 3 US-07-934-373C-22 Sequence 22, Appl  
37 1761 99.0 454 3 US-08-437-642B-22 Sequence 22, Appl  
38 1761 99.0 454 4 US-08-146-206C-22 Sequence 22, Appl  
39 1761 99.0 454 5 PCT-US93-07832-22 Sequence 22, Appl  
40 1761 99.0 467 3 US-09-049-672A-8 Sequence 8, Appl  
41 1759 98.9 475 4 US-09-740-002-25 Sequence 25, Appl  
42 1758 98.9 472 4 US-09-301-593-30 Sequence 30, Appl  
43 1758 98.9 472 4 US-09-301-593-43 Sequence 43, Appl  
44 1758 98.9 473 3 US-09-049-672A-4 Sequence 4, Appl  
45 1756 98.8 449 4 US-09-679-397-2 Sequence 2, Appl

#### ALIGNMENTS

RESULT 1  
US-08-236-311-7  
; Sequence 7, Application US/08236311  
; Patent No. 5585335  
; GENERAL INFORMATION:  
; APPLICANT: Capon, Daniel J.  
; APPLICANT: Gregory, Timothy J.  
; TITLE OF INVENTION: Adhesion Variants  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: patin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/236,311  
; FILING DATE: 02-MAY-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/936190  
; FILING DATE: 26-AUG-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/842777  
; FILING DATE: 18-FEB-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/250785  
; FILING DATE: 28-SEP-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/104329  
; FILING DATE: 02-OCT-1987  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hasak, Janet E.  
; REGISTRATION NUMBER: 28,616  
; REFERENCE/DOCKET NUMBER: 444PIC2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415/225-1896  
; TELEFAX: 415/952-9881  
; TELEX: 910/371-7168  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 371 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear

US-08-236-311-7

Query Match 99.4%; Score 1767; DB 1; Length 371;  
Best Local Similarity 100.0%; Pred. No. 2e-160;  
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ASTKGPSVFPPLAPSKSTSGTAAALGCLVXDYFPEPVTVSWNSGALTSGVHTTFAVLQSS 62  
DB 42 ASTKGPSVFPPLAPSKSTSGTAAALGCLVXDYFPEPVTVSWNSGALTSGVHTTFAVLQSS 101  
QY 63 GLYSLSSVVTVPSSSLGTQTYICNVNHPKNTKVDKVEPKSCDKTHTCCPCAPPELLGG 122  
DB 102 GLYSLSSVVTVPSSSLGTQTYICNVNHPKNTKVDKVEPKSCDKTHTCCPCAPPELLGG 161  
QY 123 PSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 182  
DB 162 PSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 221  
QY 183 STYRVSVLTVLHODWLNKGEYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDE 242  
DB 222 STYRVSVLTVLHODWLNKGEYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDE 281  
QY 243 LTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVDKSRW 302  
DB 282 LTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVDKSRW 341  
QY 303 QQGNVFSCSVNHEALHNHYTQKSLSLSPGK 332  
DB 342 QQGNVFSCSVNHEALHNHYTQKSLSLSPGK 371

## RESULT 2

US-08-457-918-7  
; Sequence 7, Application US/08457918  
; Patent No. 6117655  
; GENERAL INFORMATION:  
; APPLICANT: Capon, Daniel J.  
; APPLICANT: Gregory, Timothy J.  
; TITLE OF INVENTION: Adhesion Variants  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: patin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/457,918  
; FILING DATE: 1-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/236311  
; FILING DATE: 02-MAY-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/936190  
; FILING DATE: 26-AUG-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/842777  
; FILING DATE: 18-FEB-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/250785  
; FILING DATE: 28-SEP-1988  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/104329  
; FILING DATE: 02-OCT-1987  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kubinec, Jeffrey S.

REGISTRATION NUMBER: 36,575  
REFERENCE/DOCKET NUMBER: P0444P1C3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-8228  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 371 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-457-918-7

Query Match 99.4%; Score 1767; DB 3; Length 371;  
Best Local Similarity 100.0%; Pred. No. 2e-160;  
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ASTKGPSVFPPLAPSKSTSGTAAALGCLVXDYFPEPVTVSWNSGALTSGVHTTFAVLQSS 62  
DB 42 ASTKGPSVFPPLAPSKSTSGTAAALGCLVXDYFPEPVTVSWNSGALTSGVHTTFAVLQSS 101  
QY 63 GLYSLSSVVTVPSSSLGTQTYICNVNHPKNTKVDKVEPKSCDKTHTCCPCAPPELLGG 122  
DB 102 GLYSLSSVVTVPSSSLGTQTYICNVNHPKNTKVDKVEPKSCDKTHTCCPCAPPELLGG 161  
QY 123 PSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 182  
DB 162 PSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 221  
QY 183 STYRVSVLTVLHODWLNKGEYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDE 242  
DB 222 STYRVSVLTVLHODWLNKGEYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDE 281  
QY 243 LTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVDKSRW 302  
DB 282 LTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVDKSRW 341  
QY 303 QQGNVFSCSVNHEALHNHYTQKSLSLSPGK 332  
DB 342 QQGNVFSCSVNHEALHNHYTQKSLSLSPGK 371

## RESULT 3

US-08-397-411-7  
; Sequence 7, Application US/08397411  
; Patent No. 6129914  
; GENERAL INFORMATION:  
; APPLICANT: Weiner, George  
; APPLICANT: Gingrich, Roger  
; APPLICANT: Link, Brian  
; APPLICANT: Tso, J. Yun  
; TITLE OF INVENTION: Bispecific Antibody Effective to Treat  
; TITLE OF INVENTION: B-Cell Lymphoma and Cell Line  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew  
; STREET: One Market Plaza, Steuart Tower, Suite 2000  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94105  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/397,411  
; FILING DATE: 01-MAR-1995  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/859,583  
; FILING DATE: 27-MAR-1992

ATTORNEY/AGENT INFORMATION:  
 NAME: Smith, William M.  
 REGISTRATION NUMBER: 30,223  
 REFERENCE/DOCKET NUMBER: 011823-004901  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 415-326-2400  
 TELEFAX: 415-326-2422  
 INFORMATION FOR SEQ ID NO: 7:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 446 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-08-397-411-7

Query Match 99.4%; Score 1767; DB 3; Length 446;  
 Best Local Similarity 100.0%; Pred. No. 2.6e-160;  
 Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 62  
 DB 117 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 176  
 QY 63 GLYSLSVVTVPPSSSLGTQTYICNVNHPKNTKVDKXVEPKSCDKHTCCPPCPAPPELLGG 122  
 DB 177 GLYSLSVVTVPPSSSLGTQTYICNVNHPKNTKVDKXVEPKSCDKHTCCPPCPAPPELLGG 236  
 QY 123 PSVFLFPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYDGVGVHNAKTKPREEQYN 182  
 DB 237 PSVFLFPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYDGVGVHNAKTKPREEQYN 296  
 QY 183 STYRVSVLTVLHODWLNKKEYCKVSNKALPAPIEKTISKAKQPREPOVYTLPPSRDE 242  
 DB 297 STYRVSVLTVLHODWLNKKEYCKVSNKALPAPIEKTISKAKQPREPOVYTLPPSRDE 356  
 QY 243 LTKQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSEFFLYSKLTVDKSRW 302  
 DB 357 LTKQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSEFFLYSKLTVDKSRW 416  
 QY 303 QQGNVFCSCVMHEALHNHYTKSLSLSPGK 332  
 DB 417 QQGNVFCSCVMHEALHNHYTKSLSLSPGK 446

RESULT 4  
 US-08-458-516-13  
 ; Sequence 13, Application US/08458516  
 ; Patent No. 5777085  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Co, Man Sung  
 ; APPLICANT: Tso, J. Yun  
 ; TITLE OF INVENTION: Humanized Antibodies Reactive with  
 ; TITLE OF INVENTION: GP1IB/IIIA  
 ; NUMBER OF SEQUENCES: 23  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: William M. Smith  
 ; STREET: One Market Plaza, Steuart Tower, Suite 2000  
 ; CITY: San Francisco  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 94105  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/458,516  
 ; FILING DATE:  
 ; CLASSIFICATION: 424  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/059,159

FILING DATE: 03-MAY-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Smith, William M.  
 REGISTRATION NUMBER: 30,223  
 REFERENCE/DOCKET NUMBER: 11823-37-3  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 415-326-2400  
 TELEFAX: 415-326-2422  
 INFORMATION FOR SEQ ID NO: 13:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 449 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-458-516-13

Query Match 99.4%; Score 1767; DB 1; Length 449;  
 Best Local Similarity 100.0%; Pred. No. 2.6e-160;  
 Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 62  
 DB 120 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 179  
 QY 63 GLYSLSVVTVPPSSSLGTQTYICNVNHPKNTKVDKXVEPKSCDKHTCCPPCPAPPELLGG 122  
 DB 180 GLYSLSVVTVPPSSSLGTQTYICNVNHPKNTKVDKXVEPKSCDKHTCCPPCPAPPELLGG 239  
 QY 123 PSVFLFPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYDGVGVHNAKTKPREEQYN 182  
 DB 240 PSVFLFPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYDGVGVHNAKTKPREEQYN 299  
 QY 183 STYRVSVLTVLHODWLNKKEYCKVSNKALPAPIEKTISKAKQPREPOVYTLPPSRDE 242  
 DB 300 STYRVSVLTVLHODWLNKKEYCKVSNKALPAPIEKTISKAKQPREPOVYTLPPSRDE 359  
 QY 243 LTKQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSEFFLYSKLTVDKSRW 302  
 DB 360 LTKQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSEFFLYSKLTVDKSRW 419  
 QY 303 QQGNVFCSCVMHEALHNHYTKSLSLSPGK 332  
 DB 420 QQGNVFCSCVMHEALHNHYTKSLSLSPGK 449

RESULT 5  
 US-08-378-939-10  
 ; Sequence 10, Application US/08378939  
 ; Patent No. 5876961  
 ; GENERAL INFORMATION:  
 ; APPLICANT: CROME, JAMES SCOTT  
 ; APPLICANT: LEWIS, ALAN PETER  
 ; TITLE OF INVENTION: PRODUCTION OF ANTIBODIES  
 ; NUMBER OF SEQUENCES: 46  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: ROTHWELL, FIGG, ERNST & KURZ  
 ; STREET: 555 THIRTEENTH ST. N.W.  
 ; CITY: WASHINGTON  
 ; STATE: D. C.  
 ; COUNTRY: U.S.  
 ; ZIP: 20004  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/378,939  
 ; FILING DATE:  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/952640

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; FILING DATE: 01-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: ERNST, BARBARA G
; REGISTRATION NUMBER: 30,377
; REFERENCE/DOCKET NUMBER: 1808-118
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 783-6040
; TELEFAX: (202) 783-6031
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 476 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: Protein
; US-08-378-939-10

Query Match          99.4%; Score 1767; DB 2; Length 476;
Best Local Similarity 100.0%; Pred. No. 2,9e-160;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 147 ASTKGPSVFFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 206
QY 63 GLYSLSVVTVPSSSLGTQYICNVNHPKSTNTKVDKKVEPKSCDKTHCTCPCPAPPELLGG 122
DB 207 GLYSLSVVTVPSSSLGTQYICNVNHPKSTNTKVDKKVEPKSCDKTHCTCPCPAPPELLGG 266
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DB 267 PSVFLPPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 326
QY 183 STYRVSVLTIVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPSRDE 242
DB 327 STYRVSVLTIVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPSRDE 386
QY 243 LTRNQVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 302
DB 387 LTRNQVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 446
QY 303 QQGNVFSCSVWHEALHNHYTQKSLSLSPGK 332
DB 447 QQGNVFSCSVWHEALHNHYTQKSLSLSPGK 476

RESULT 6
US-09-313-942-9
; Sequence 9, Application US/09313942
; Patent No. 6472179
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: REG 203-A
; CURRENT APPLICATION NUMBER: US/09/313,942
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 09/313,942
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 60/101,858
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 951
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-313-942-9

Query Match          99.4%; Score 1767; DB 4; Length 951;
Best Local Similarity 100.0%; Pred. No. 8,2e-160;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ASTKGPSVFFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 62
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DB 622 ASTKGPSVFFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 681
QY 63 GLYSLSVVTVPSSSLGTQYICNVNHPKSTNTKVDKKVEPKSCDKTHCTCPCPAPPELLGG 122
DB 682 GLYSLSVVTVPSSSLGTQYICNVNHPKSTNTKVDKKVEPKSCDKTHCTCPCPAPPELLGG 741
QY 123 PSVFLPPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 182
DB 742 PSVFLPPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 801
QY 183 STYRVSVLTIVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPSRDE 242
DB 802 STYRVSVLTIVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPSRDE 861
QY 243 LTRNQVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 302
DB 862 LTRNQVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 921
QY 303 QQGNVFSCSVWHEALHNHYTQKSLSLSPGK 332
DB 922 QQGNVFSCSVWHEALHNHYTQKSLSLSPGK 951

RESULT 7
US-09-289-942A-7
; Sequence 7, Application US/09289942A
; Patent No. 6482928
; GENERAL INFORMATION:
; APPLICANT: Pai, Emil F.
; APPLICANT: Klein, Michel H.
; APPLICANT: Chong, Pele
; APPLICANT: Pedyczak, Arthur
; TITLE OF INVENTION: Fab'-EPI TOPE COMPLEX FROM THE HIV-1 CROSS-NEUTRALIZING
; FILE REFERENCE: MONOCLONAL ANTIBODY 2F5
; CURRENT APPLICATION NUMBER: US/09/289,942A
; CURRENT FILING DATE: 1999-04-13
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
; US-09-289-942A-7

Query Match          99.2%; Score 1763; DB 4; Length 462;
Best Local Similarity 99.7%; Pred. No. 6,7e-160;
Matches 329; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 ASTKGPSVFFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 62
DB 133 ASTKGPSVFFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 192
QY 63 GLYSLSVVTVPSSSLGTQYICNVNHPKSTNTKVDKKVEPKSCDKTHCTCPCPAPPELLGG 122
DB 193 GLYSLSVVTVPSSSLGTQYICNVNHPKSTNTKVDKKVEPKSCDKTHCTCPCPAPPELLGG 252
QY 123 PSVFLPPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 182
DB 253 PSVFLPPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 312
QY 183 STYRVSVLTIVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPSRDE 242
DB 313 STYRVSVLTIVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPSRDE 372
QY 243 LTRNQVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 302
DB 373 LTRNQVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 432
QY 303 QQGNVFSCSVWHEALHNHYTQKSLSLSPGK 332
DB 433 QQGNVFSCSVWHEALHNHYTQKSLSLSPGK 462
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RESULT 8  
US-09-740-002-27  
; Sequence 27, Application US/09740002  
; Patent No. 6537809  
; GENERAL INFORMATION:  
; APPLICANT: BRAMS, PETER  
; TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN MONOCLONAL ANTIBODIES  
; TITLE OF INVENTION: SPECIFIC TO RSV F-PROTEIN AND METHODS FOR THEIR  
; FILE REFERENCE: 037003-0275759  
; CURRENT APPLICATION NUMBER: US/09/740,002  
; PRIOR FILING DATE: 2000-12-20  
; PRIOR FILING DATE: 1999-06-18  
; PRIOR APPLICATION NUMBER: 09/335,697  
; PRIOR FILING DATE: 1995-06-07  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 27  
; LENGTH: 475  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-740-002-27

Query Match 99.2%; Score 1763; DB 4; Length 475;  
Best Local Similarity 99.7%; Pred. No. 6.9e-160;  
Matches 329; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVDFPEPVTVSNWNGALTSVHTFPVAVLQSS 62  
DB 146 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVDFPEPVTVSNWNGALTSVHTFPVAVLQSS 205  
QY 63 GLYSLSVVTVFSSSLGTQTYICNVNHPKSNKVDKVPKSCDKTHTCPCPAPELGG 122  
DB 206 GLYSLSVVTVFSSSLGTQTYICNVNHPKSNKVDKVPKSCDKTHTCPCPAPELGG 265  
QY 123 PSVFLFPKPKDMLISRTPEVTCVVDVSHEDPEVKFNWYDGVVHNNAKTKPREQYN 182  
DB 266 PSVFLFPKPKDMLISRTPEVTCVVDVSHEDPEVKFNWYDGVVHNNAKTKPREQYN 325  
QY 183 STYRVSVLTVLHODWLNKGYKCKVSNKALPAPIEKTISKAKQPREPQVYTLPPSRDE 242  
DB 326 STYRVSVLTVLHODWLNKGYKCKVSNKALPAPIEKTISKAKQPREPQVYTLPPSRDE 385  
QY 243 LTKQVSLTCLVKGFPYSDIAVEWESNGQPNYKTPPVLDSDGSEFLYSLKLTVDKSRW 302  
DB 386 LTKQVSLTCLVKGFPYSDIAVEWESNGQPNYKTPPVLDSDGSEFLYSLKLTVDKSRW 445  
QY 303 QQGNVFCSCVMHEALHNYTKSLSPGK 332  
DB 446 QQGNVFCSCVMHEALHNYTKSLSPGK 475

RESULT 9  
US-08-487-550-4  
; Sequence 4, Application US/08487550  
; Patent No. 6113898  
; GENERAL INFORMATION:  
; APPLICANT: Anderson, Darrell R.  
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC  
; TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,  
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS  
; TITLE OF INVENTION: IMMUNOSUPPRESSANTS"  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
; STREET: 699 Prince Street  
; CITY: Alexandria  
; STATE: VA  
; COUNTRY: USA

ZIP: 22314  
COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/487,550  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Teskin, Robin L.  
; REGISTRATION NUMBER: 35,030  
; REFERENCE/DOCKET NUMBER: 012712-131  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-836-6620  
; TELEFAX: 703-836-2021  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 476 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-487-550-4

Query Match 99.2%; Score 1763; DB 3; Length 476;  
Best Local Similarity 99.7%; Pred. No. 7e-160;  
Matches 329; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVDFPEPVTVSNWNGALTSVHTFPVAVLQSS 62  
DB 147 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVDFPEPVTVSNWNGALTSVHTFPVAVLQSS 206  
QY 63 GLYSLSVVTVFSSSLGTQTYICNVNHPKSNKVDKVPKSCDKTHTCPCPAPELGG 122  
DB 207 GLYSLSVVTVFSSSLGTQTYICNVNHPKSNKVDKVPKSCDKTHTCPCPAPELGG 266  
QY 123 PSVFLFPKPKDMLISRTPEVTCVVDVSHEDPEVKFNWYDGVVHNNAKTKPREQYN 182  
DB 267 PSVFLFPKPKDMLISRTPEVTCVVDVSHEDPEVKFNWYDGVVHNNAKTKPREQYN 326  
QY 183 STYRVSVLTVLHODWLNKGYKCKVSNKALPAPIEKTISKAKQPREPQVYTLPPSRDE 242  
DB 327 STYRVSVLTVLHODWLNKGYKCKVSNKALPAPIEKTISKAKQPREPQVYTLPPSRDE 386  
QY 243 LTKQVSLTCLVKGFPYSDIAVEWESNGQPNYKTPPVLDSDGSEFLYSLKLTVDKSRW 302  
DB 387 LTKQVSLTCLVKGFPYSDIAVEWESNGQPNYKTPPVLDSDGSEFLYSLKLTVDKSRW 446  
QY 303 QQGNVFCSCVMHEALHNYTKSLSPGK 332  
DB 447 QQGNVFCSCVMHEALHNYTKSLSPGK 476

RESULT 10  
US-08-487-550-12  
; Sequence 12, Application US/08487550  
; Patent No. 6113898  
; GENERAL INFORMATION:  
; APPLICANT: Anderson, Darrell R.  
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC  
; TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,  
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS  
; TITLE OF INVENTION: IMMUNOSUPPRESSANTS"  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
; STREET: 699 Prince Street  
; CITY: Alexandria  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22314  
; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA: US/08/487,550  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Teskin, Robin L.  
REGISTRATION NUMBER: 35,030  
TELEPHONE: 703-836-6620  
TELEFAX: 703-836-2021  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 476 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-487-550-12

Query Match 99.2%; Score 1763; DB 3; Length 476;  
Best Local Similarity 99.7%; Pred. No. 7e-160;  
Matches 329; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 3 ASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 62  
DB 147 ASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 206  
QY 63 GLYSLSSVTVTPSSSLGTQYICNVNHPKNTKVDKVEPKSCDKTHCTCPPELGG 122  
DB 207 GLYSLSSVTVTPSSSLGTQYICNVNHPKNTKVDKVEPKSCDKTHCTCPPELGG 266  
QY 123 PSVELFPPKDTLMISRTPEVTCVVVDVSHEDPEVKFNKYVDGVEVHNAKTKPREEQYN 182  
DB 267 PSVELFPPKDTLMISRTPEVTCVVVDVSHEDPEVKFNKYVDGVEVHNAKTKPREEQYN 326  
QY 183 STYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIETISKAKGQPREPQVYTLPPSRDE 242  
DB 327 STYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIETISKAKGQPREPQVYTLPPSRDE 386  
QY 243 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVDKSRW 302  
DB 387 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVDKSRW 446  
QY 303 QQGNVFCSCVMHEALHNYTKQSLSPGK 332  
DB 447 QQGNVFCSCVMHEALHNYTKQSLSPGK 476

RESULT 11  
US-09-526-098-4  
Sequence 4, Application US/09526098  
Patent No. 6492134

GENERAL INFORMATION:  
APPLICANT: Anderson, Darrell R.  
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF."  
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS  
TITLE OF INVENTION: IMMUNOSUPPRESSANTS"  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
STREET: 699 Prince Street  
CITY: Alexandria  
STATE: VA  
COUNTRY: USA  
ZIP: 22314  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA: US/09/526,098  
FILING DATE: 07-JUN-1995  
CLASSIFICATION:  
PRIOR APPLICATION NUMBER: 09/383,916  
FILING DATE:  
APPLICATION NUMBER: US 08/487,550  
FILING DATE: 07-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Teskin, Robin L.  
REGISTRATION NUMBER: 35,030  
REFERENCE/DOCKET NUMBER: 012712-131  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-836-6620  
TELEFAX: 703-836-2021  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 476 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-526-098-4

Query Match 99.2%; Score 1763; DB 4; Length 476;  
Best Local Similarity 99.7%; Pred. No. 7e-160;  
Matches 329; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 3 ASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 62  
DB 147 ASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 206  
QY 63 GLYSLSSVTVTPSSSLGTQYICNVNHPKNTKVDKVEPKSCDKTHCTCPPELGG 122  
DB 207 GLYSLSSVTVTPSSSLGTQYICNVNHPKNTKVDKVEPKSCDKTHCTCPPELGG 266  
QY 123 PSVELFPPKDTLMISRTPEVTCVVVDVSHEDPEVKFNKYVDGVEVHNAKTKPREEQYN 182  
DB 267 PSVELFPPKDTLMISRTPEVTCVVVDVSHEDPEVKFNKYVDGVEVHNAKTKPREEQYN 326  
QY 183 STYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIETISKAKGQPREPQVYTLPPSRDE 242  
DB 327 STYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIETISKAKGQPREPQVYTLPPSRDE 386  
QY 243 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVDKSRW 302  
DB 387 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVDKSRW 446  
QY 303 QQGNVFCSCVMHEALHNYTKQSLSPGK 332  
DB 447 QQGNVFCSCVMHEALHNYTKQSLSPGK 476

RESULT 12  
US-09-526-098-12  
Sequence 12, Application US/09526098  
Patent No. 6492134

GENERAL INFORMATION:  
APPLICANT: Anderson, Darrell R.  
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF."  
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS  
TITLE OF INVENTION: IMMUNOSUPPRESSANTS"  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
STREET: 699 Prince Street  
CITY: Alexandria  
STATE: VA  
COUNTRY: USA  
ZIP: 22314

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent in Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/526,098  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 09/383,916  
 FILING DATE:  
 APPLICATION NUMBER: US 08/487,550  
 FILING DATE: 07-JUN-1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Teskin, Robin L.  
 REGISTRATION NUMBER: 35,030  
 REFERENCE/DOCKET NUMBER: 012712-131  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 703-836-6620  
 TELEFAX: 703-836-2021  
 INFORMATION FOR SEQ ID NO: 12:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 476 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-09-526-098-12

Query Match 99.2%; Score 1763; DB 4; Length 476;  
 Best Local Similarity 99.7%; Pred. No. 7e-160;  
 Matches 329; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 3 ASTKGPSVFPLAPSSKSTSGTAAALGLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 62  
 Db 147 ASTKGPSVFPLAPSSKSTSGTAAALGLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 206  
 QY 63 GLYSLSVVTVFPSSSLGTQYICNVNHPKNTKVDKVEPKSCDKTHTCPCPAPPELLGG 122  
 Db 207 GLYSLSVVTVFPSSSLGTQYICNVNHPKNTKVDKKAEPKSCDKTHTCPCPAPPELLGG 266  
 QY 123 PSVFLFPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNATKPREQYN 182  
 Db 267 PSVFLFPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNATKPREQYN 326  
 QY 183 STYRWVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 242  
 Db 327 STYRWVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 386  
 QY 243 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 302  
 Db 387 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 446  
 QY 303 QQGNVFCVSNVMEALHNHYTQKSLSLSPGK 332  
 Db 447 QQGNVFCVSNVMEALHNHYTQKSLSLSPGK 476

RESULT 13  
 US-08-487-550-8  
 Sequence 8, Application US/08487550  
 Patent No. 6113898  
 GENERAL INFORMATION:  
 APPLICANT: Anderson, Darrell R.  
 TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC  
 TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,  
 TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS  
 TITLE OF INVENTION: IMMUNOSUPPRESSANTS"  
 NUMBER OF SEQUENCES: 12  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
 STREET: 699 Prince Street  
 CITY: Alexandria

STATE: VA  
 COUNTRY: USA  
 ZIP: 22314  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent in Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/487,550  
 FILING DATE: 07-JUN-1995  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Teskin, Robin L.  
 REGISTRATION NUMBER: 35,030  
 REFERENCE/DOCKET NUMBER: 012712-131  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 703-836-6620  
 TELEFAX: 703-836-2021  
 INFORMATION FOR SEQ ID NO: 8:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 478 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-487-550-8  
 Query Match 99.2%; Score 1763; DB 3; Length 478;  
 Best Local Similarity 99.7%; Pred. No. 7e-160;  
 Matches 329; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 3 ASTKGPSVFPLAPSSKSTSGTAAALGLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 62  
 Db 149 ASTKGPSVFPLAPSSKSTSGTAAALGLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 208  
 QY 63 GLYSLSVVTVFPSSSLGTQYICNVNHPKNTKVDKVEPKSCDKTHTCPCPAPPELLGG 122  
 Db 209 GLYSLSVVTVFPSSSLGTQYICNVNHPKNTKVDKKAEPKSCDKTHTCPCPAPPELLGG 268  
 QY 123 PSVFLFPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNATKPREQYN 182  
 Db 269 PSVFLFPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNATKPREQYN 328  
 QY 183 STYRWVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 242  
 Db 329 STYRWVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 388  
 QY 243 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 302  
 Db 389 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 448  
 QY 303 QQGNVFCVSNVMEALHNHYTQKSLSLSPGK 332  
 Db 449 QQGNVFCVSNVMEALHNHYTQKSLSLSPGK 478

RESULT 14  
 US-09-526-098-8  
 Sequence 8, Application US/09526098  
 Patent No. 6492134  
 GENERAL INFORMATION:  
 APPLICANT: Anderson, Darrell R.  
 TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC  
 TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,  
 TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS  
 TITLE OF INVENTION: IMMUNOSUPPRESSANTS"  
 NUMBER OF SEQUENCES: 12  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
 STREET: 699 Prince Street  
 CITY: Alexandria  
 STATE: VA  
 COUNTRY: USA

ZIP: 22314  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/526,098  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/383,916  
FILING DATE:  
APPLICATION NUMBER: US 08/487,550  
FILING DATE: 07-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Teskin, Robin L.  
REGISTRATION NUMBER: 35,030  
REFERENCE/DOCKET NUMBER: 012712-131  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-836-6620  
TELEFAX: 703-836-2021  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 478 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-526-098-8

Query Match 99.2%; Score 1763; DB 4; Length 478;  
Best Local Similarity 99.7%; Pred. No. 7e-160;  
Matches 329; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	3	ASTKGPSVFPPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSVHTFPAVLQSS	62
Db	149	ASTKGPSVFPPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSVHTFPAVLQSS	208
QY	63	GLYSLSVVTVPSSSLGTQYICNVNHPKSNPKVDKVPKSCDKHTCCPPCPAPPELLGG	122
Db	209	GLYSLSVVTVPSSSLGTQYICNVNHPKSNPKVDKVPKSCDKHTCCPPCPAPPELLGG	268
QY	123	PSVFLPPPKPDLMISRTPEVTCVVDVSHEDPEVKFNWYDGVGVHNAKTKPREEQYN	182
Db	269	PSVFLPPPKPDLMISRTPEVTCVVDVSHEDPEVKFNWYDGVGVHNAKTKPREEQYN	328
QY	183	STYRVSVLTVLHQQDLNGKEYCKVSNKALPAPIEKTISKAKGQPRFPQVYTLPPSRDE	242
Db	329	STYRVSVLTVLHQQDLNGKEYCKVSNKALPAPIEKTISKAKGQPRFPQVYTLPPSRDE	388
QY	243	LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW	302
Db	389	LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW	448
QY	303	QQGNVFSCSVMHEALHNHYTQKSLSLSPGK	332
Db	449	QQGNVFSCSVMHEALHNHYTQKSLSLSPGK	478

## RESULT 15

US-08-157-101A-7  
Sequence 7, Application US/08157101A  
Patent No. 5808032  
GENERAL INFORMATION:  
APPLICANT: KURIHARA, TATSUYA  
APPLICANT: MATSUKURA, SHIGEKAZU  
APPLICANT: TSURUOKA, NOBUO  
APPLICANT: ARIMA, KENJI  
APPLICANT: NISHIHARA, TATSURO  
TITLE OF INVENTION: ANTI-HBs ANTIBODY GENES AND EXPRESSION  
TITLE OF INVENTION: PLASMIDS THEREFOR  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:

ADDRESSEE: PILLSBURY, MADISON & SUTRO  
STREET: 1100 NEW YORK AVENUE, N.W.  
CITY: WASHINGTON  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/157,101A  
FILING DATE: 05-APR-1994  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: TITUS, MARLANA K  
REGISTRATION NUMBER: 35843  
REFERENCE/DOCKET NUMBER: 9437/204199  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-861-3711  
TELEFAX: 202-822-0944  
TELEX: 6714627 CUCH  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 459 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-157-101A-7

Query Match 99.1%; Score 1762; DB 1; Length 459;  
Best Local Similarity 99.7%; Pred. No. 8.2e-160;  
Matches 329; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	3	ASTKGPSVFPPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSVHTFPAVLQSS	62
Db	130	ASTKGPSVFPPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSVHTFPAVLQSS	189
QY	63	GLYSLSVVTVPSSSLGTQYICNVNHPKSNPKVDKVPKSCDKHTCCPPCPAPPELLGG	122
Db	190	GLYSLSVVTVPSSSLGTQYICNVNHPKSNPKVDKVPKSCDKHTCCPPCPAPPELLGG	249
QY	123	PSVFLPPPKPDLMISRTPEVTCVVDVSHEDPEVKFNWYDGVGVHNAKTKPREEQYN	182
Db	250	PSVFLPPPKPDLMISRTPEVTCVVDVSHEDPEVKFNWYDGVGVHNAKTKPREEQYN	309
QY	183	STYRVSVLTVLHQQDLNGKEYCKVSNKALPAPIEKTISKAKGQPRFPQVYTLPPSRDE	242
Db	310	STYRVSVLTVLHQQDLNGKEYCKVSNKALPAPIEKTISKAKGQPRFPQVYTLPPSRDE	369
QY	243	LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW	302
Db	370	LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW	429
QY	303	QQGNVFSCSVMHEALHNHYTQKSLSLSPGK	332
Db	430	QQGNVFSCSVMHEALHNHYTQKSLSLSPGK	459

Search completed: January 13, 2004, 12:46:35  
Job time : 30.7057 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 13, 2004, 12:22:35 ; Search time 7.75633 Seconds  
(without alignments)  
1326.664 Million cell updates/sec

Title: US-09-990-586-99

Perfect score: 553

Sequence: 1 RTVAAPSVFIIPPSPDEQLKS.....EVTHQGLSPVTKSFNRGEC 107

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 76:\*

1: Pir1.\*

2: Pir2.\*

3: Pir3.\*

4: Pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	553	100.0	215	2 JE0244	Ig kappa chain NIG
2	553	100.0	215	2 JE0242	Ig kappa chain NIG
3	553	100.0	215	2 JE0243	Ig kappa chain NIG
4	550	99.5	135	2 S52059	JC-kappa protein -
5	548	99.1	106	1 K3HU	Ig kappa chain C r
6	537	97.1	216	2 JE0241	Ig kappa chain Am3
7	520	94.0	215	2 A23746	Ig kappa chain V-I
8	513	92.8	99	2 A37927	Ig kappa chain C r
9	507	91.7	99	2 S26653	Ig kappa chain C r
10	372	67.3	240	2 S06084	Ig kappa chain pre
11	367	66.4	106	1 KIRB	Ig kappa chain C r
12	366	66.2	178	2 PT0219	Ig kappa chain C r
13	359	64.9	106	1 KIRTA	Ig kappa chain C r
14	358	64.7	217	2 S42772	Ig kappa chain - m
15	358	64.7	218	2 S68241	Ig kappa chain V r
16	358	64.7	219	2 S38865	Ig kappa chain - m
17	352	63.7	218	2 JC5810	nonoclonal antibody
18	352	63.7	219	2 PC4203	Ig kappa chain (mo
19	352	63.7	219	2 S16112	Ig kappa chain V r
20	352	63.7	219	2 S52028	Ig kappa chain - m
21	352	63.7	220	2 A31790	Ig kappa chain V r
22	352	63.7	225	2 S37484	Ig kappa chain - m
23	352	63.7	234	2 S14237	Ig kappa chain pre
24	352	63.7	234	2 S01320	Ig kappa chain pre
25	352	63.7	235	2 S25058	Ig kappa chain - m
26	350	63.3	106	1 KIMS	Ig kappa chain C r
27	350	63.3	126	2 I54782	Gene Pvt-1a/Ig-Ck
28	348	62.9	225	2 JL0029	Ig kappa chain pre
29	345	62.4	230	2 S33161	Ig kappa chain - s

30	321	58.0	214	2 S68212	Ig kappa chain (Wa
31	312	56.4	210	2 A56169	Ig kappa chain V r
32	308.5	55.8	106	2 G30907	Ig kappa-B4 chain
33	306.5	55.4	106	1 K4RBBS	Ig kappa-2 chain C
34	277.5	50.2	229	2 A20969	Ig kappa chain pre
35	257.5	46.6	103	1 K4RB	Ig kappa-B4 chain
36	256	46.3	104	2 F53275	Ig kappa-1 chain C
37	246.5	44.6	104	1 K9RB	Ig kappa-B9 chain
38	245	44.3	238	2 A49633	Ig lambda-like cha
39	241	43.6	104	1 K5RBV	Ig kappa chain C r
40	237	42.9	118	2 A46518	Ig L1 chain J-C re
41	231	41.8	103	2 B36167	Ig lambda chain C
42	231	41.8	213	2 A21177	Ig light chain pre
43	225	40.7	108	1 K3PG	Ig light chain C r
44	223.5	40.4	103	1 K5RB	Ig kappa-B5 chain
45	222	40.1	197	2 S29593	Ig kappa chain (W)

ALIGNMENTS

RESULT 1

JE0244

Ig kappa chain NIG2 precursor - human

C:Species: Homo sapiens (man)

C:Date: 05-Dec-1998 #sequence\_revision 05-Dec-1998 #text\_change 21-Jan-2000

C:Accession: JE0244

R:Alim, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Kazi, H.; T

submitted to JIPID, November 1998

A:Description: A new subgroup of k type light chains (VKV) identified in cases of AL amy

A:Reference number: JE0243

A:Accession: JE0244

A:Molecule type: protein

A:Residues: 1-215 <Ali>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 553; DB 2; Length 215;

Best Local Similarity 100.0%; Pred. No. 2.6e-47;

Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIIPPSPDEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQSVTEQD 60

Db 109 RTVAAPSVFIIPPSPDEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQSVTEQD 168

QY 61 SKDSTYSLSSTLTLSKADYKHKVACEVTHQGLSSPVTKSFNRGEC 107

Db 169 SKDSTYSLSSTLTLSKADYKHKVACEVTHQGLSSPVTKSFNRGEC 215

RESULT 2

JE0242

Ig kappa chain NIG26 precursor - human

C:Species: Homo sapiens (man)

C:Date: 05-Dec-1998 #sequence\_revision 05-Dec-1998 #text\_change 21-Jan-2000

C:Accession: JE0242

R:Alim, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda, T

submitted to JIPID, November 1998

A:Description: Structure relationship of kappa type light chains with AL amyloidosis: Mul

A:Reference number: JE0241

A:Accession: JE0242

A:Molecule type: protein

A:Residues: 1-215 <Ali>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

F:16-91/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 553; DB 2; Length 215;

Best Local Similarity 100.0%; Pred. No. 2.6e-47;

Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIIPPSPDEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQSVTEQD 60

Db 109 RTVAAPSVFIIPPSPDEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQSVTEQD 168

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QY 61 SKDSTYSLSTLTKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107
|||
Db 169 SKDSTYSLSTLTKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 215

RESULT 3
JE0243
Ig kappa chain NIG93 precursor - human
C:Species: Homo sapiens (man)
C>Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C:Accession: JE0243
R:Alim, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, H.; T
submitted to JIPID, November 1998
A:Description: A new subgroup of k type light chains (Vk) identified in cases of AL amy
A:Reference number: JE0243
A:Accession: JE0243
A:Molecule type: protein
A:Residues: 1-215 <ALI>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:16-90/Domain: immunoglobulin homology <IMV>

Query Match 100.0%; Score 553; DB 2; Length 215;
Best Local Similarity 100.0%; Pred. No. 2.6e-47;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIFPPSDEQLKSGTASVVLNNFPYRKAVQWKVDNALQSGNSQESVTEQD 60
|||
Db 109 RTVAAPSVFIFPPSDEQLKSGTASVVLNNFPYRKAVQWKVDNALQSGNSQESVTEQD 168

QY 61 SKDSTYSLSTLTKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107
|||
Db 169 SKDSTYSLSTLTKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 215

RESULT 4
S52059
JC-kappa protein - human
C:Species: Homo sapiens (man)
C>Date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 08-Sep-2000
C:Accession: S52059
R:Frances, V.; Pandrau-Garcia, D.; Guret, C.; Ho, S.; Wang, Z.; Duvert, V.; Saeland, S.;
EMBO J. 13, 5937-5943, 1994
A:Title: A surrogate 15 kDa JC-kappa protein is expressed in combination with mu heavy c
A:Reference number: S52059; MUID:95112804; PMID:7813432
A:Accession: S52059
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-135 <FRA>
C:Superfamily: pre-B cell omega light chain; immunoglobulin homology

Query Match 99.5%; Score 550; DB 2; Length 135;
Best Local Similarity 99.1%; Pred. No. 2.9e-47;
Matches 106; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIFPPSDEQLKSGTASVVLNNFPYRKAVQWKVDNALQSGNSQESVTEQD 60
|||
Db 29 RTVAAPSVFIFPPSDEQLKSGTASVVLNNFPYRKAVQWKVDNALQSGNSQESVTEQD 88

QY 61 SKDSTYSLSTLTKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107
|||
Db 89 SKDSTYSLSTLTKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 135

RESULT 5
K3HU
Ig kappa chain C region - human
C:Species: Homo sapiens (man)
C>Date: 31-Dec-1980 #sequence_revision 02-Jul-1998 #text_change 21-Jul-2000
C:Accession: B90562; A91651; A90806; A94417; A91639; A92047; A94242; B37927; A02116; S02
R:Gottlieb, P.D.; Cunningham, B.A.; Rutishauser, U.; Edelman, G.M.
Biochemistry 9, 3155-3161, 1970
A:Title: The covalent structure of a human gammaG-immunoglobulin. VI. Amino acid sequenc
```

```
A:Reference number: A90562; MUID:71064023; PMID:5489770
A:Contents: myeloma protein Eu
A:Accession: B90562
A:Molecule type: protein
A:Residues: 1-106 <GOT>
A>Note: this sequence has the Inv (3) allotypic marker, 45-Ala and 83-Val
R:Gall, W.E.; Edelman, G.M.
Biochemistry 9, 3188-3196, 1970
A:Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfic
A:Reference number: A90565; MUID:71064027; PMID:4923144
A:Contents: annotation; Eu, disulfide bonds
R:Buter, L.; Barnikol, H.U.; Watanabe, S.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 353, 189-208, 1972
A:Title: Die Primärstruktur einer monoklonalen Immunglobulin-L-Kette vom kappa-Typ, Sul
A:Reference number: A91651; MUID:72188439; PMID:5027703
A:Contents: Bence Jones protein Ti
A:Accession: A91651
A:Molecule type: protein
A:Residues: 1-106 <SUT>
R:Hieter, P.A.; Max, E.E.; Seidman, J.G.; Maizel Jr., J.V.; Leder, P.
Cell 22, 197-207, 1980
A:Title: Cloned human and mouse kappa immunoglobulin constant and J region genes conserv
A:Reference number: A90806; MUID:81042304; PMID:6775818
A:Accession: A90806
A:Molecule type: DNA
A:Residues: 1-106 <HIE>
A:Cross-references: GB:J00241; NID:933140; PIDN:CAA23823.1; PID:gl335148
A>Note: the sequence was determined from the germline gene
R:Hilschmann, N.; Barnikol, H.U.; Hess, M.; Langer, B.; Ponstingl, H.; Steinmetz-Kayne,
in Gamma Globulins: Structure and Function, Franek, F., and Shugar, D., eds., pp.57-74,
A:Reference number: A94417
A:Contents: Bence Jones protein Roy
A:Accession: A94417
A:Molecule type: protein
A:Residues: 1-44, A', 46-56, Q', 58-82, L', 84-106 <HIL>
A>Note: this sequence has the Inv (1,2) allotypic marker, 45-Ala and 83-Leu
R:Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 348, 1718-1722, 1967
A:Title: Die vollständige Aminosäuresequenz des Bence-Jones-Proteins Cum. (kappa-Typ).
A:Reference number: A91639; MUID:68242259; PMID:5586923
A:Contents: Bence Jones protein Cum
A:Accession: A91639
A:Molecule type: protein
A:Residues: 1-56, Q', 58-106 <H12>
R:Titani, K.; Shinoda, T.; Putnam, F.W.
J. Biol. Chem. 244, 3550-3560, 1969
A:Title: The amino acid sequence of a kappa type Bence-Jones protein. III. The complete
A:Reference number: A92047; MUID:69234734; PMID:4893882
A:Contents: Bence Jones protein Ag
A:Accession: A92047
A:Molecule type: protein
A:Residues: 1-13, N', 15-106 <TIT>
R:Köhler, H.; Shimizu, A.; Paul, C.; Putnam, F.W.
Science 169, 56-59, 1970
A:Title: Macroglobulin structure: variable sequence of light and heavy chains.
A:Reference number: A94242; MUID:70201507; PMID:5447531
A:Contents: Waldenström's macroglobulin Ou
A:Accession: A94242
A:Molecule type: protein
A:Residues: 1-13, N', 15-106 <KOH>
R:Kurtz, J.H.; Bowcock, A.M.; Erlich, H.A.; Nevo, S.; Cavalli-Sforza, L.L.
Am. J. Hum. Genet. 48, 613-620, 1991
A:Title: Km typing with PCR: application to population screening.
A:Reference number: A37927; MUID:91150772; PMID:1900145
A:Accession: B37927
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 8-106 <KUR>
A>Note: allotype Inv(3)
R:Steiner, V.; Chang, J.Y.
FEBS Lett. 222, 6-10, 1987
A:Title: Chemical modification of the carboxyl groups of protein substrates enhances the
A:Reference number: S02572; MUID:88005152; PMID:3115831
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A:Contents: annotation  
 C:Genetics:  
 A:Gene: GDB:IGKC  
 A:Cross-references: GDB:120088; OMIM:147200  
 A:Map position: 2p12-2p12  
 C:Complex: an immunoglobulin heterotetramer subunit consists of two identical light (kap) chain disulfide bonds; in some cases, such as IGA and IGM, the subunits associate into 1a  
 C:Superfamily: immunoglobulin C region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:19-88/Domain: immunoglobulin homology <IMM>  
 F:26-86/Disulfide bonds: #status experimental  
 F:106/Disulfide bonds: interchain (to heavy chain) #status experimental

Query Match 99.1%; Score 548; DB 1; Length 106;  
 Best Local Similarity 100.0%; Pred. No. 3.4e-47;  
 Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TVAAPSVFIFPPSDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS 61  
 Db 1 TVAAPSVFIFPPSDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS 60

QY 62 KDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107  
 Db 61 KDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 106

RESULT 6  
 J02041  
 IG kappa chain Am37 precursor - human  
 C:Species: Homo sapiens (man)  
 C:Date: 05-Dec-1998 #sequence\_revision 05-Dec-1998 #text\_change 21-Jan-2000  
 C:Accession: J02041  
 R:Alim, M.A.; Yamaki, S.; Hoesain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda, T.  
 Submitted to JIPID, November 1998  
 A:Description: Structure relationship of kappa type light chains with AL amyloidosis: Mul  
 A:Reference number: J02041  
 A:Accession: J02041  
 A:Molecule type: protein  
 A:Residues: 1-216 <ALI>  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 F:16-92/Domain: immunoglobulin homology <IMM>

Query Match 97.1%; Score 537; DB 2; Length 216;  
 Best Local Similarity 97.2%; Pred. No. 9.9e-46;  
 Matches 104; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIFPPSDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60  
 Db 110 RTVAAPSVFIFPPSDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 169

QY 61 SKDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107  
 Db 170 SKDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 216

RESULT 7  
 A23746  
 IG kappa chain V-III (KAU cold agglutinin) - human  
 C:Species: Homo sapiens (man)  
 C:Date: 30-Dec-1991 #sequence\_revision 30-Dec-1991 #text\_change 21-Jan-2000  
 C:Accession: A23746  
 R:Leoni, J.; Ghiso, J.; Goni, F.; Frangione, B.  
 J. Biol. Chem. 266, 2836-2842, 1991  
 A:Title: The primary structure of the Fab fragment of protein KAU, a monoclonal immunogl  
 A:Reference number: A23746; MUID:91131575; PMID:1993660  
 A:Accession: A23746  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-215 <LEO>  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:16-91/Domain: immunoglobulin homology <IMM>

Query Match 94.0%; Score 520; DB 2; Length 215;  
 Best Local Similarity 98.1%; Pred. No. 4.7e-44;  
 Matches 104; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIFPPSDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60  
 Db 109 RTVAAPSVFIFPPSDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 168

QY 61 SKDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 106  
 Db 169 SKDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 214

RESULT 8  
 A37927  
 IG kappa chain C region (allotype Inv(1,2)) - human (fragment)  
 C:Species: Homo sapiens (man)  
 C:Date: 28-Feb-1992 #sequence\_revision 28-Feb-1992 #text\_change 21-Jan-2000  
 C:Accession: A37927  
 R:Kurth, J.H.; Bowcock, A.M.; Erlich, H.A.; Nevo, S.; Cavalli-Sforza, L.L.  
 Am. J. Hum. Genet. 48, 613-620, 1991  
 A:Title: Km typing with PCR: application to population screening.  
 A:Reference number: A37927; MUID:91150772; PMID:1900145  
 A:Accession: A37927  
 A:Status: preliminary; not compared with conceptual translation  
 A:Molecule type: DNA  
 A:Residues: 1-99 <KUR>  
 C:Superfamily: immunoglobulin C region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:12-81/Domain: immunoglobulin homology <IMM>

Query Match 92.8%; Score 513; DB 2; Length 99;  
 Best Local Similarity 99.0%; Pred. No. 9e-44;  
 Matches 98; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 9 FIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKSTYSL 68  
 Db 1 FIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKSTYSL 60

QY 69 SSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107  
 Db 61 SSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 99

RESULT 9  
 S26653  
 IG kappa chain C region - chimpanzee (fragment)  
 C:Species: Pan troglodytes (chimpanzee)  
 C:Date: 19-Mar-1997 #sequence\_revision 18-Jul-1997 #text\_change 21-Jan-2000  
 C:Accession: S26653  
 R:Erlich, P.H.; Moustafa, Z.A.; Harfeldt, K.B.; Isaacson, C.; Oestberg, L.  
 Hum. Antibodies Hybridomas 1, 23-26, 1990  
 A:Title: Potential of primate monoclonal antibodies to substitute for human antibodies:  
 A:Reference number: S26652; MUID:91355693; PMID:2129418  
 A:Accession: S26653  
 A:Status: translation not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-99 <EHR>  
 A:Cross-references: EMBL:X65287  
 C:Superfamily: immunoglobulin C region; immunoglobulin homology  
 C:Keywords: immunoglobulin  
 F:19-88/Domain: immunoglobulin homology <IMM>

Query Match 91.7%; Score 507; DB 2; Length 99;  
 Best Local Similarity 100.0%; Pred. No. 3.5e-43;  
 Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TVAAPSVFIFPPSDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS 61  
 Db 1 TVAAPSVFIFPPSDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS 60

QY 62 KDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 100

```
Db 61 KDSTYSLSTLTLSKADYKHKYVACEVTHQGLSSPVTK 99
RESULT 10
IG kappa chain precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 21-Jan-2000
C:Accession: S06084
R:Crowe, J.S.; Smith, M.A.; Cooper, H.J.
Nucleic Acids Res. 17, 7992, 1989
A:Title: Nucleotide sequence of Y3-Ag 1.2.3. rat myeloma immunoglobulin kappa chain cDNA
A:Reference number: S06084; MUID:90016888; PMID:2508067
A:Accession: S06084
A:Molecule type: mRNA
A:Residues: 1-240 <CRG>
A:Cross-references: EMBL:X16129; NID:G56457; PIDN:CAA34256.1; PID:G56458
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-240/Product: IG kappa chain #status predicted <MAR>
F:153-222/Domain: immunoglobulin homology <IMM>
Query Match 67.3%; Score 372; DB 2; Length 240;
Best Local Similarity 65.4%; Pred. No. 2.3e-29;
Matches 70; Conservative 13; Mismatches 24; Indels 0; Gaps 0;
QY 1 RTVAAPSVFIPPPDEQLKSGTASVCLNNFYPRKAVQWKVDNALQSGNSQESVTEQD 60
Db 134 RADAAPTVSIIPPPTEQLATGASVCLMNNFYPRDISVKKIKDGTERRDGVLDSTVDQD 193
QY 61 SKDSTYSLSTLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 107
Db 194 SKDSTYSNSTLSLSKADYSHNLYTCVHVHTKSSSPVVKSFNRNEC 240
RESULT 11
KIRTB
IG kappa chain C region (allele b) - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 18-Aug-1982 #sequence_revision 18-Aug-1982 #text_change 28-May-1999
C:Accession: A93901; A92807; A02117
R:Sheppard, H.W.; Gutman, G.A.
Proc.Natl. Acad. Sci. U.S.A. 78, 7064-7068, 1981
A:Title: Allelic forms of rat kappa chain genes: evidence for strong selection at the le
A:Reference number: A93901; MUID:82082587; PMID:6273908
A:Accession: A93901
A:Molecule type: DNA
A:Residues: 1-106 <SHE>
A:Cross-references: GB:V01241; GB:J00745; GB:J02574; GB:J02575; NID:G57849; PIDN:CAA2455
A:Experimental source: strain LOU
R:Starace, V.; Querinjean, P.
J. Immunol. 115, 59-62, 1975
A:Title: The primary structure of a rat kappa Bence Jones protein: phylogenetic relation
A:Reference number: A92807; MUID:75212238; PMID:807630
A:Contents: Bence Jones protein S211
A:Accession: A92807
A:Molecule type: Protein
A:Residues: 1, 'N', '3-29, 'K', '31-47, 49-78, 'Q', '80-86, 'Q', '88-98, 'W', '99, 'N', '101-106 <STA>
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light
chain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into 1a
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: heterotetramer
F:19-88/Domain: immunoglobulin homology <IMM>
F:26-86/Disulfide bonds: #status predicted
F:106/Disulfide bonds: interchain (to heavy chain) #status predicted
Query Match 66.4%; Score 367; DB 1; Length 106;
Best Local Similarity 65.4%; Pred. No. 2.6e-29;
Matches 68; Conservative 14; Mismatches 22; Indels 0; Gaps 0;
QY 4 AAPSVPFIPPPDEQLKSGTASVCLNNFYPRKAVQWKVDNALQSGNSQESVTEQD 63
Db 61 KDSTYSLSTLTLSKADYKHKYVACEVTHQGLSSPVTK 99
RESULT 12
PT0219
IG kappa chain V-C region (PLC18) - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 11-Jan-2000
C:Accession: PT0219
R:Lammers, B.M.; Beaman, K.D.; Kim, Y.B.
Mol. Immunol. 28, 877-880, 1991
A:Title: Sequence analysis of porcine immunoglobulin light chain cDNAs.
A:Reference number: PT0219; MUID:91342694; PMID:1715030
A:Accession: PT0219
A:Molecule type: mRNA
A:Residues: 1-178 <LAM>
A:Cross-references: GB:M59321; NID:G164508; PIDN:AAA03520.1; PID:G164509
A:Experimental source: spleen, strain Minnesota Miniature
A:Note: the authors translated the codon CTC for residue 141 as Ser
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-70/Domain: V region (fragment) <VRG>
F:12-18/Region: complementarity-determining 1
F:19-51/Region: framework 1
F:52-60/Region: complementarity-determining 2
F:61-70/Region: framework 2
F:71-178/Domain: C region <CRG>
F:96-156/Disulfide bonds: #status predicted
F:176/Disulfide bonds: interchain #status predicted
Query Match 66.2%; Score 366; DB 2; Length 178;
Best Local Similarity 64.5%; Pred. No. 6.1e-29;
Matches 69; Conservative 13; Mismatches 25; Indels 0; Gaps 0;
QY 1 RTVAAPSVFIPPPDEQLKSGTASVCLNNFYPRKAVQWKVDNALQSGNSQESVTEQD 60
Db 70 RADAXPSVFIIPPPKEQLATPTVSVCLINNFPFRESVKWKVDGVQSSGHPDSVTEQD 129
QY 61 SKDSTYSLSTLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 107
Db 130 SKDSTYSLSTLTSLPTSOYLSHNLVCEVTHKTLASPLVTSFNRNEC 176
RESULT 13
KIRTA
IG kappa chain C region (allele a) - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 18-Aug-1982 #sequence_revision 10-Sep-1982 #text_change 22-Jun-1999
C:Accession: A02118
R:Sheppard, H.W.; Gutman, G.A.
Proc. Natl. Acad. Sci. U.S.A. 78, 7064-7068, 1981
A:Title: Allelic forms of rat kappa chain genes: evidence for strong selection at the l
A:Reference number: A93901; MUID:82082587; PMID:6273908
A:Accession: A02118
A:Molecule type: DNA
A:Residues: 1-106 <SHE>
A:Cross-references: GB:J02574; GB:J00745; NID:G204820; PIDN:AAA4141.1; PID:G204821
A:Experimental source: strain DA
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (ka
chain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into 1
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: heterotetramer
F:19-88/Domain: immunoglobulin homology <IMM>
F:26-86/Disulfide bonds: #status predicted
F:106/Disulfide bonds: interchain (to heavy chain) #status predicted
Query Match 64.9%; Score 359; DB 1; Length 106;
Best Local Similarity 63.5%; Pred. No. 1.6e-28;
Matches 66; Conservative 16; Mismatches 22; Indels 0; Gaps 0;
```

QY 4 RAPSVEIIPPDEQLKSGTASVCLLNFPYKQVQKVDNALQSGNSQESVTEQDSKD 63  
Db 3 AAPTQVSIIPPSMQEQLTSGATVCFVNNFYPRDISVKWKIDGSRQGVLDSDVTDQSKD 62  
QY 64 STYLSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107  
Db 63 STYSMSSTLSLTKEVYERHNLTCVVHKTSSTSSPVTKSFNRGEC 106

## RESULT 14

S42772  
Ig kappa chain - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 21-Jan-2000  
C:Accession: S42772  
R:Schellekens, G.A.  
submitted to the EMBL Data Library, November 1993  
A:Reference number: S42771  
A:Accession: S42772  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-217 <SCH>  
A:Cross-references: EMBL:X75536; NID:9414143; PIDN:CAA53226.1; PID:9414144  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:14-93/Domain: immunoglobulin homology <IMM>

Query Match 64.7%; Score 358; DB 2; Length 217;  
Best Local Similarity 61.7%; Pred. No. 4.8e-28;  
Matches 66; Conservative 15; Mismatches 26; Indels 0; Gaps 0;  
QY 1 RTVAAPSVFIIPPSDEQLKSGTASVCLLNFPYKQVQKVDNALQSGNSQESVTEQD 60  
Db 111 RADAAPTQVSIIPPSMQEQLTSGATVCFVNNFYPRDISVKWKIDGSRQGVLDSDVTDQD 170  
QY 61 SKDSTYLSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107  
Db 171 SKDSTYMSSTLTLTQKDEYERHNSYTCATHKTSPIVKSFNRGEC 217

## RESULT 15

Ig kappa chain V region (Mab13-1) - mouse (fragment)  
N:Alternate names: immunoglobulin light chain  
C:Species: Mus musculus (house mouse)  
C:Date: 24-Aug-1996 #sequence\_revision 13-Mar-1997 #text\_change 20-Jun-2000  
C:Accession: S68241; S68214  
R: Takagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.; Imanaka, T.  
submitted to the EMBL Data Library, March 1994  
A:Description: Specific peroxidase activity by formation of an antibody L-chain-porphyrin  
A:Reference number: S68241  
A:Accession: S68241  
A:Molecule type: mRNA  
A:Residues: 1-218 <TAK>  
A:Cross-references: EMBL:D29670; NID:9473962; PIDN:BAAO6141.1; PID:9473963  
R: Takagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.; Imanaka, T.  
FEBS Lett. 375, 273-276, 1995  
A:Title: Thermostable peroxidase activity with a recombinant antibody L chain-porphyrin  
A:Reference number: S68211; MUID:96085223; PMID:7498516  
A:Accession: S68214  
A:Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 'NI', 3-212 <TAW>  
A:Cross-references: EMBL:D29670  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: immunoglobulin

Query Match 64.7%; Score 358; DB 2; Length 218;  
Best Local Similarity 61.7%; Pred. No. 4.9e-28;  
Matches 66; Conservative 15; Mismatches 26; Indels 0; Gaps 0;  
QY 1 RTVAAPSVFIIPPSDEQLKSGTASVCLLNFPYKQVQKVDNALQSGNSQESVTEQD 60

Db 112 RADAAPTQVSIIPPSMQEQLTSGATVCFVNNFYPRDISVKWKIDGSRQGVLDSDVTDQD 171  
QY 61 SKDSTYLSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107  
Db 172 SKDSTYMSSTLTLTQKDEYERHNSYTCATHKTSPIVKSFNRGEC 218  
Search completed: January 13, 2004, 12:44:42  
Job time : 7.75633 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 13, 2004, 12:19:34 ; Search time 4.67249 Seconds  
(without alignments)  
1076.912 Million cell updates/sec

Title: US-09-990-586-99

Perfect score: 553

Sequence: 1 RTVAAPSVFIFPPSDEQLK.....EVTHQGLSSPVTKSFNRGEC 107

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	548	99.1	106	1 KAC HUMAN	P01834 homo sapien
2	367	66.4	106	1 KAC RAT	P01835 rattus norv
3	359	64.9	106	1 KAC RAT	P01836 rattus norv
4	350	63.3	106	1 KAC MOUSE	P01837 mus musculu
5	306.5	55.4	106	1 KAC RABIT	P01839 oryctolagus
6	257.5	46.6	103	1 KAC9 RABIT	P01840 oryctolagus
7	246.5	44.6	104	1 KAC6 RABIT	P01838 oryctolagus
8	241	43.6	104	1 KAC6 RABIT	P01840 oryctolagus
9	231	41.8	103	1 LAC CHICK	P03984 oryctolagus
10	225	40.7	108	1 KAC RANCA	P20763 gallus gall
11	223.5	40.4	103	1 KAC5 RABIT	P11272 rana catesb
12	210.5	38.1	103	1 LAC1 MOUSE	P01841 oryctolagus
13	208.5	37.7	105	1 LAC HUMAN	P01843 mus musculu
14	203.5	36.8	105	1 LAC RABIT	P01842 homo sapien
15	190	34.4	104	1 LAC1 RAT	P01847 oryctolagus
16	187.5	33.9	213	1 ILLI HUMAN	P20766 rattus norv
17	183	33.1	104	1 LAC2 RAT	P15814 homo sapien
18	180.5	32.6	105	1 LAC3 RAT	P20767 rattus norv
19	178	32.2	104	1 LAC3 MOUSE	P01846 sus scrofa
20	174	31.5	104	1 LAC2 MOUSE	P01845 mus musculu
21	164.5	29.7	329	1 GC2 CAVEO	P01844 mus musculu
22	161.5	29.2	105	1 LAC5 MUSSP	P01862 cavia porce
23	157.5	28.5	421	1 EPC MOUSE	P20765 mus musculu
24	153.5	27.8	330	1 GCAC MOUSE	P01863 mus musculu
25	153.5	27.8	339	1 GCAC MOUSE	P01863 mus musculu
26	151	27.3	326	1 GC2 HUMAN	P01865 mus musculu
27	151	27.3	327	1 GC4 HUMAN	P01859 homo sapien
28	150.5	27.2	335	1 GCAB MOUSE	P01861 homo sapien
29	149	26.9	290	1 GC3 HUMAN	P01864 mus musculu
30	148	26.8	330	1 GC1 HUMAN	P01860 homo sapien
31	146.5	26.5	105	1 LAC5 MOUSE	P01857 homo sapien
32	145	26.2	336	1 GCB MOUSE	P20764 mus musculu
33	145	26.2	405	1 GCEN_MOUSE	P01866 mus musculu
					P01867 mus musculu

34	143.5	25.9	323	1 GC RABIT	P01870 oryctolagus
35	143	25.9	454	1 MUC MESAU	P06337 mesocricetu
36	142.5	25.8	457	1 MUC SUNMU	P20768 suncus muri
37	141.5	25.6	429	1 EPC RAT	P01855 rattus norv
38	137.5	24.9	329	1 GC RAT	P20762 rattus norv
39	137	24.8	324	1 GC1 MOUSE	P01868 mus musculu
40	137	24.8	393	1 GC1M_MOUSE	P01869 mus musculu
41	136	24.6	455	1 MUC MOUSE	P01872 mus musculu
42	136	24.6	476	1 MUCM_MOUSE	P01873 mus musculu
43	135	24.4	322	1 GCA RAT	P20760 rattus norv
44	135	24.4	329	1 GC3 MOUSE	P22436 mus musculu
45	135	24.4	398	1 GC3M_MOUSE	P03987 mus musculu

#### ALIGNMENTS

RESULT 1  
KAC HUMAN  
ID\_ KAC HUMAN STANDARD; PRT; 106 AA.  
AC P01834;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Ig kappa chain C region.  
GN IGKC.  
OS Homo sapiens (Human)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE (MYELOMA PROTEIN EU).  
RX MEDLINE=71064023; PubMed=5489770;  
RA Gottlieb P.D., Cunningham B.A., Rutishauser U., Edelman G.M.;  
RT "The covalent structure of a human gamma G-immunoglobulin. VI. Amino acid sequence of the light chain.";  
RL Biochemistry 9:3155-3161(1970).  
RN [2]  
RP DISULFIDE BONDS.  
RX MEDLINE=71064027; PubMed=4923144;  
RA Gall W.E., Edelman G.M.;  
RT "The covalent structure of a human gamma G-immunoglobulin. X. Intrachain disulfide bonds.";  
RL Biochemistry 9:3188-3196(1970).  
RN [3]  
RP SEQUENCE (BENCE-JONES PROTEIN TI).  
RX MEDLINE=72188439; PubMed=5027703;  
RA Suter L., Barnikol H.U., Watanabe S., Hilschmann N.;  
RT "Rule of antibody structure. The primary structure of a monoclonal immunoglobulin L-chain of kappa-type, subgroup 3 (Bence-Jones protein TI). IV. The complete amino acid sequence and its significance for the mechanism of antibody production.";  
RL Hoppe-Seyler's Z. Physiol. Chem. 353:189-208(1972).  
RN [4]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=81042304; PubMed=6775818;  
RA Hieber P.A., Max E.E., Seidman J.G., Maizel J.V. Jr., Leder P.;  
RT "Cloned human and mouse kappa immunoglobulin constant and J region genes conserve homology in functional segments.";  
RL Cell 22:197-207(1980).  
RN [5]  
RP SEQUENCE (BENCE-JONES PROTEIN ROY).  
RX Hilschmann N., Barnikol H.U., Hess M., Langer B., Ponstingl H., Steinmetz-Kayne M., Suter L., Watanabe S.;  
RT (In) Franek F., Shugar D. (eds.);  
RL Gamma globulins: structure and function, pp.57-74, Academic Press, New York (1969).  
RN [6]  
RP SEQUENCE (BENCE-JONES PROTEIN CUM).  
RX MEDLINE=68242259; PubMed=5586923;  
RA Hilschmann N.;  
RT "The complete amino acid sequence of Bence Jones protein Cum (kappa-type).";

RL Hoppe-Seyler's Z. Physiol. Chem. 348:1718-1722(1967).  
RN [7]  
RP SEQUENCE (BENCE-JONES PROTEIN AG).  
RX MEDLINE=69234734; PubMed=4893682;  
RA Titani K., Shinoda T., Putnam F.W.;  
RT "The amino acid sequence of a kappa type Bence-Jones protein. 3. The  
RT complete sequence and the location of the disulfide bridges.";  
RL J. Biol. Chem. 244:3550-3560(1969).  
RN [8]  
RP SEQUENCE (WALDENSTROM'S MACROGLOBULIN OU).  
RX MEDLINE=7021507; PubMed=5447531;  
RA Kohler H., Shimizu A., Paul C., Putnam F.W.;  
RT "Macroglobulin structure: variable sequence of light and heavy  
RT chains.";  
RL Science 169:56-59(1970).  
RN [9]  
RP SEQUENCE OF 1-33; 38-41 AND 62-80.  
RX TISSUE=Abdominal adipose tissue;  
RA Olsen K.E., Sletten K., Westermarck P.;  
RT subcutaneous fat biopsy; kappa IV immunoglobulin light chain.";  
RL Biochem. Biophys. Res. Commun. 245:713-716(1998).  
CC -1- MISCELLANEOUS: THE EU SEQUENCE HAS THE INV (3) ALLOTYPIC MARKER,  
CC 45-ALA & 83-VAL. THE ROY SEQUENCE HAS THE INV (1,2) ALLOTYPIC  
CC MARKER, 45-ALA AND 83-LEU.  
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
CC  
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CC  
DR ENBL; J00241; AAA58989.1; -;  
DR ENBL; V00557; CAA23823.1; -;  
DR PIR; B90562; K3HU.  
DR PDB; 1D53; 09-FEB-00.  
DR PDB; 1D51; 09-FEB-00.  
DR PDB; 1D6V; 04-OCT-00.  
DR PDB; 1HEZ; 10-AUG-01.  
DR PDB; 1LKL; 12-MAR-97.  
DR PDB; 1I72; 08-AUG-01.  
DR PDB; 1M1M; 15-MAY-97.  
DR Genew; HGNC:5716; IGKC.  
DR MIM; 147200; -;  
DR GO; GO:0003823; Fiantigen binding activity; NAS.  
DR GO; GO:0006955; P-immune response; NAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig-cl.  
DR Pfam; PF00047; Ig\_1.  
DR SMART; SM00407; IGcl; 1.  
DR PROSITE; PS00835; IG\_LIKE; 1.  
DR PROSITE; PS00230; IG\_MHC; 1.  
KW Immunoglobulin domain; Immunoglobulin C region; 3D-structure.  
FT NON\_TER 1 1  
FT DOMAIN 5 102 IG-LIKE.  
FT DISULFID 26 86 INTERCHAIN (WITH A HEAVY CHAIN).  
FT CONFLICT 106 106 V -> L (IN INV(1,2) MARKER).  
FT VARIANT 83 83 /FTID=VAR\_003897.  
FT CONFLICT 14 14 D -> N (IN REF. 7 AND 8).  
FT CONFLICT 57 57 E -> Q (IN REF. 5 AND 6).  
FT SEQUENCE 106 AA; 11609 MW; 51984D1FDD372CE8 CRC64;  
Query Match 99.1%; Score 548; DB 1; Length 106;  
Best Local Similarity 100.0%; Pred. No. 4.5e-48;  
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 TVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS 61

Db 1 TVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS 60  
QY 62 KDSYSLSSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 107  
Db 61 KDSYSLSSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 106  
RESULT 2  
KACB RAT  
ID KACB RAT STANDARD; PRT; 106 AA.  
AC P01835;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE IG kappa chain C region, B allele.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Louvain;  
RX MEDLINE=82082587; PubMed=6273908;  
RA Sheppard H.W., Gutman G.A.;  
RT "Allelic forms of rat kappa chain genes: evidence for strong  
RT selection at the level of nucleotide sequence.";  
RL Proc. Natl. Acad. Sci. U.S.A. 78:7064-7068(1981).  
RN [2]  
RP SEQUENCE (BENCE-JONES PROTEIN S211).  
RX MEDLINE=75212238; PubMed=807630;  
RA Starace V., Querinjean P.;  
RT "The primary structure of a rat kappa Bence Jones protein:  
RT phylogenetic relationships of V- and C-region genes.";  
J. Immunol. 115:59-62(1975).  
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
DR PIR; A93901; KIRTB.  
DR HSP; P01842; 2MCG.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig-cl.  
DR InterPro; IPR003006; IG\_MHC.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00407; IGcl; 1.  
DR PROSITE; PS00835; IG\_LIKE; 1.  
DR PROSITE; PS00230; IG\_MHC; 1.  
KW Immunoglobulin domain; Immunoglobulin C region.  
FT NON\_TER 1 1  
FT DOMAIN 5 102 IG-LIKE.  
FT DISULFID 26 86 INTERCHAIN (WITH A HEAVY CHAIN).  
FT CONFLICT 106 106 D -> N (IN REF. 2).  
FT CONFLICT 30 30 N -> K (IN REF. 2).  
FT CONFLICT 48 48 MISSING (IN REF. 2).  
FT CONFLICT 79 79 E -> Q (IN REF. 2).  
FT CONFLICT 87 87 E -> Q (IN REF. 2).  
FT CONFLICT 98 98 V -> W (IN REF. 2).  
FT CONFLICT 100 100 S -> N (IN REF. 2).  
SQ SEQUENCE 106 AA; 11601 MW; 4CFA7CA820D1CA36 CRC64;  
Query Match 66.4%; Score 367; DB 1; Length 106;  
Best Local Similarity 65.4%; Pred. No. 5.3e-30;  
Matches 68; Conservative 14; Mismatches 22; Indels 0; Gaps 0;  
QY 4 AAPSVEIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK 63  
Db 3 AAPTVEIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK 62  
QY 64 STYSLSSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 107  
Db 63 STYSLSSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 106  
RESULT 3

[3] SEQUENCE FROM N.A., AND REVISIONS TO 53-59.  
RX MEDLINE=79084137; PubMed=103625;  
RA Hanly P.H., Brownlee G.G., Cheng C.-C., Gait M.J., Milstein C.;  
RT "Complete sequence of constant and 3' noncoding regions of an  
RT immunoglobulin mRNA using the dideoxynucleotide method of RNA  
RT sequencing."; Cell 15:1067-1075(1978).  
RL [4]  
RN  
RP SEQUENCE FROM N.A.  
RX MEDLINE=82059477; PubMed=6170937;  
RA Hanly P.H., Gait M.J., Milstein C.;  
RT "Complete sequence of an immunoglobulin mRNA using specific priming  
RT and the dideoxynucleotide method of RNA sequencing."; Nucleic  
RL Acids Res. 9:4485-4494(1981).  
RN [5]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=811915; PubMed=6262318;  
RA Max E.E., Maizel J.V. Jr., Leder P.;  
RT "The nucleotide sequence of a 5.5-kilobase DNA segment containing the  
RT mouse kappa immunoglobulin J and C region genes."; J. Biol.  
RN Chem. 256:5116-5120(1981).  
RP [6]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=81198949; PubMed=6785724;  
RA Altenburger W., Neumaier P.S., Steinmetz M., Zachau H.G.;  
RT "DNA sequence of the constant gene region of the mouse immunoglobulin  
RT kappa chain."; Nucleic Acids Res. 9:971-981(1981).  
RN [7]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=88329081; PubMed=3138116;  
RA de Waele P., Feys V., van de Voorde A., Molemans F., Piers W.;  
RT "Expression in non-lymphoid cells of mouse recombinant immunoglobulin  
RT directed against the tumour marker human placental alkaline  
RT phosphatase."; Eur. J. Biochem. 176:287-295(1988).  
RN  
RP  
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
CC  
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CC or send an email to license@isb-sib.ch).  
CC  
CC EMBL: V00807; CAA24189.1; -  
DR PIR: B90262; KIMS.  
DR PDB: 1AIF; 01-FEB-97.  
DR PDB: 1FGK; 02-OCT-00.  
DR PDB: 1IGC; 03-JUN-95.  
DR PDB: 1K85; 08-APR-98.  
DR PDB: 1KCR; 11-MAY-02.  
DR PDB: 1KCS; 11-MAY-02.  
DR PDB: 1KCU; 11-MAY-02.  
DR PDB: 1KCV; 11-MAY-02.  
DR PDB: 25C8; 09-JUL-99.  
DR MGD: MGI:96495; Iqk-C.  
DR InterPro: IPR007110; Iq-like.  
DR InterPro: IPR003597; Iq-cl.  
DR InterPro: IPR003006; Iq\_MHC.  
DR Pfam: PF00047; Iq; 1.  
DR SMART: SM00407; Iqcl; 1.  
DR SMART: PS00835; Iq LIKE; 1.  
DR PROSITE: PS00290; Iq\_MHC; 1.  
DR Immunoglobulin domain; Immunoglobulin C region; 3D-structure.  
KW NON TER 1 102 IG-LIKE.  
FT DOMAIN 5 102  
FT DISULFID 26 86  
FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).  
SQ SEQUENCE 106 AA; 11778 MW; 4B51F5EF49AEB5 CRC64;



Query Match 63.3%; Score 350; DB 1; Length 106;  
 Best Local Similarity 61.5%; Pred. No. 2.6e-28;  
 Matches 64; Conservative 15; Mismatches 25; Indels 0; Gaps 0;

QY 4 AAPSVPFPPSDEQLKSGTASVWCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKD 63  
 DB 3 AAPTVSIFPPSDEQLKSGTASVWCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKD 62

QY 64 STYLSSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 107  
 DB 63 STYMSSTLTLTQDEYERHNSYTCEATKSTSPVKSFRNEC 106

RESULT 5  
 KACB\_RABIT  
 ID KACB\_RABIT STANDARD; PRT; 106 AA.  
 AC P01839;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE IG kappa-B4 chain C region.  
 GN K-BAS  
 OS Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 OX NCBI\_TaxID=9986;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=83300036; PubMed=6412231;  
 RA Heidmann O., Auffray C., Cazenave P.-A., Rougeon F.;  
 RT "Multiplicity of constant kappa light chain genes in the rabbit  
 genome: a B4b4 homozygous rabbit contains a kappa-bas gene.";  
 RL EMBO J. 2:437-441(1983).  
 CC -1- MISCELLANEOUS: IN BASILEA RABBITS, THE MAJOR TYPE OF LIGHT CHAIN  
 IS LAMBDA. THE KAPPA CHAIN SHOWN IS A MINOR COMPONENT. ALL OTHER  
 RABBIT B ALLOTYPES HAVE 64-CYS.  
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
 CC  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL; V01241; CAA24558.1; -  
 DR EMBL; V00885; -; NOT\_ANNOTATED\_CDS.  
 DR PIR; A02121; K4RBBS.  
 DR HSP; P01842; 7FAB.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig\_c1.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00407; IGc1; 1.  
 DR PROSITE; PS00835; IG\_LIKE; 1.  
 DR PROSITE; PS00290; IG\_MHC; FALSE NEG.  
 KW Immunoglobulin domain; Immunoglobulin C region.  
 FT NON TER 1 99 IG-LIKE.  
 FT DOMAIN 6 99  
 FT DISULFID 27 87  
 FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).  
 SQ SEQUENCE 106 AA; 11279 MW; AF9B928DDA853849 CRC64;

Query Match 55.4%; Score 306.5; DB 1; Length 106;  
 Best Local Similarity 54.4%; Pred. No. 5.8e-24;  
 Matches 56; Conservative 16; Mismatches 30; Indels 1; Gaps 1;

QY 5 APSVIFPPSDEQLKSGTASVWCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDS 64  
 DB 5 APSVLLFPPSDEQLKSGTASVWCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDS 64

QY 65 TYSLSSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 107

Db 65 TYSLSSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 106

RESULT 6  
 KAC4\_RABIT  
 ID KAC4\_RABIT STANDARD; PRT; 103 AA.  
 AC P01840;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE IG kappa-B4 chain C region.  
 DE IG kappa-B4 chain C region.  
 OS Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 OX NCBI\_TaxID=9986;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=83300036; PubMed=6412231;  
 RA Emorine L., Dreher K.L., Kindt T.J., Max E.E.;  
 RT "Rabbit immunoglobulin kappa genes: structure of a germline b4  
 allele type J-C locus and evidence for several b4-related sequences in  
 the rabbit genome.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 80:5709-5713(1983).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=82060334; PubMed=6795636;  
 RA Heidmann O., Auffray C., Cazenave P.-A., Rougeon F.;  
 RT "Nucleotide sequence of constant and 3' untranslated regions of a  
 kappa immunoglobulin light chain mRNA of a homozygous b4 rabbit.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 78:5802-5806(1981).  
 RN [3]  
 RP SEQUENCE.  
 RX MEDLINE=75133568; PubMed=1091650;  
 RA Chen K.C.S., Kindt T.J., Krause R.M.;  
 RT "Primary structure of the L chain from a rabbit homogeneous antibody  
 to streptococcal carbohydrate. II. Sequence determination of peptides  
 from tryptic and peptic digests.";  
 RL J. Biol. Chem. 250:3289-3296(1975).  
 CC -1- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM ANTIBODY TO THE  
 SPECIFIC CARBOHYDRATE OF GROUP C STREPTOCOCCI & WAS ISOLATED FROM  
 THE SERUM OF A SINGLE RABBIT.  
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
 CC  
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 CC  
 CC EMBL; X00231; CAA25051.1; -  
 DR PIR; A93971; K4RB.  
 DR HSP; P01842; 7FAB.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig\_c1.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00407; IGc1; 1.  
 DR PROSITE; PS00835; IG\_LIKE; 1.  
 DR PROSITE; PS00290; IG\_MHC; FALSE NEG.  
 KW Immunoglobulin domain; Immunoglobulin C region.  
 FT NON TER 1 95 IG-LIKE.  
 FT DOMAIN 5 95  
 FT DISULFID 26 85  
 FT DISULFID 103 103 INTERCHAIN (WITH A HEAVY CHAIN).  
 FT CONFLICT 58 58 N -> D (IN REF. 3).  
 SQ SEQUENCE 103 AA; 11043 MW; 5FCSACCB60E68DB CRC64;

Query Match 46.6%; Score 257.5; DB 1; Length 103;  
 Best Local Similarity 48.5%; Pred. No. 4.4e-19;  
 Matches 50; Conservative 21; Mismatches 29; Indels 3; Gaps 3;

QY 5 APSVFIFPPSDQLKSGTASVVLNNFYPRKAVQWVNDALQSGNSQESVTEQDSKDS 64  
 DB 4 APTVLFFPAPQVAIGTVIIVCVANKYFP-DVTVTWEVDGTTQTGTIENSKTPQNSADC 62  
 QY 65 TYSLSTLTLSKADYEHKHYKACEVTHQGLSSPVTKSFNRGEC 107  
 DB 63 TYNLSSTLTSTQYNSHKEYTCKVT-QGTTTS-VVQSFNRGDC 103

## RESULT 7

KAC9\_RABIT  
 ID KAC6\_RABIT STANDARD; PRT; 104 AA.  
 AC P01838;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE IG kappa-B3 chain C region.  
 OS Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 OX NCBI\_TaxID=9986;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=76176480; PubMed=817288;  
 RA Farnsworth V., Goodflesh R., Rodkey S., Hood L.;  
 RT "Immunoglobulin allotypes of rabbit kappa chains: polymorphism of a  
 RT control mechanism regulating closely linked duplicated genes?";  
 RL Proc. Natl. Acad. Sci. U.S.A. 73:1293-1296(1976).  
 CC -!- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM POOLED IMMUNOGLOBULIN  
 CC OF HOMOGYOUS B9 RABBITS.  
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.  
 DR PIR; A02120; K9RB.  
 DR HSSP; P01842; 7FAB.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003597; IG\_c1.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR Pfam; PF00047; IG\_1.  
 DR SMART; SM00407; IGc1; 1.  
 DR PROSITE; PS00835; IG-LIKE; 1.  
 DR PROSITE; PS00290; IG\_MHC; FALSE NEG.  
 KW Immunoglobulin domain; Immunoglobulin C region.  
 FT NON\_TER 1  
 FT DOMAIN 6 100 IG-LIKE.  
 FT DISULFID 27 86  
 FT DISULFID 104 104 INTERCHAIN (WITH A HEAVY CHAIN).  
 SQ SEQUENCE 104 AA; 11347 MW; 427B1668B0EC8D98 CRC64;

Query Match 44.6%; Score 246.5; DB 1; Length 104;  
 Best Local Similarity 46.6%; Pred. No. 5.5e-18;  
 Matches 48; Conservative 18; Mismatches 34; Indels 3; Gaps 3;

QY 5 APSVFIFPPSDQLKSGTASVVLNNFYPRKAVQWVNDALQSGNSQESVTEQDSKDS 64  
 DB 5 APTVLFFPAPQVAIGTVIIVCVANKYFP-DVTVTWEVDGTTQTGTIENSKTPQNSADC 62  
 QY 65 TYSLSTLTLSKADYEHKHYKACEVTHQGLSSPVTKSFNRGEC 107  
 DB 65 TYNLSSTLTSTQYNSHKEYTCKVT-QGTTTS-VVQSFNRGDC 103

## RESULT 8

KAC6\_RABIT  
 ID KAC6\_RABIT STANDARD; PRT; 104 AA.  
 AC P03984;  
 DT 23-OCT-1986 (Rel. 02, Created)  
 DT 23-OCT-1986 (Rel. 02, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE IG kappa chain B5 variant C region.  
 OS Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 OX NCBI\_TaxID=9986;

RP SEQUENCE FROM N.A. (CLONE PKB5-F2).  
 RX MEDLINE=84041515; PubMed=6314281;  
 RA Bernstein K.E., Skurla R.M. Jr., Mage R.G.;  
 RT "The sequences of rabbit kappa light chains of b4 and b5 allotypes  
 RT differ more in their constant regions than in their 3' untranslated  
 RT regions";  
 RL Nucleic Acids Res. 11:7205-7214(1983).  
 CC -!- MISCELLANEOUS: THE CDNA FROM WHICH THIS SEQUENCE WAS DERIVED  
 CC CONTAINS A TERMINATOR CODON WITHIN THE V-REGION CODING REGION. THE  
 CC ORIGIN OF THIS CODON AND OF THE DIFFERENCES BETWEEN THIS AND OTHER  
 CC SEQUENCED B5 C REGIONS ARE UNCLEAR. THE CDNA CLONE WAS MADE USING  
 CC MRNA FROM TRYPAZOSOME-INFECTED B5-HOMOGYOUS RABBITS.  
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.  
 CC  
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 CC  
 CC EMBL; K01363; AAA31355.1; -;  
 DR PIR; A02124; KSRBV.  
 DR HSSP; P01842; 2MCG.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003597; IG\_c1.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR Pfam; PF00047; IG\_1.  
 DR SMART; SM00407; IGc1; 1.  
 DR PROSITE; PS00835; IG-LIKE; 1.  
 DR PROSITE; PS00290; IG\_MHC; FALSE NEG.  
 KW Immunoglobulin domain; Immunoglobulin C region.  
 FT NON\_TER 1  
 FT DOMAIN 5 100 IG-LIKE.  
 FT DISULFID 26 85  
 FT DISULFID 104 104 INTERCHAIN (WITH A HEAVY CHAIN).  
 SQ SEQUENCE 104 AA; 11079 MW; 7C71850205381751 CRC64;  
 Query Match 43.6%; Score 241; DB 1; Length 104;  
 Best Local Similarity 46.6%; Pred. No. 2e-17;  
 Matches 48; Conservative 18; Mismatches 35; Indels 2; Gaps 2;  
 QY 5 APSVFIFPPSDQLKSGTASVVLNNFYPRKAVQWVNDALQSGNSQESVTEQDSKDS 64  
 DB 4 APTVLFFPAPQVAIGTVIIVCVANKYFP-DGTVTWQVDGKPLTGTIETSKTPQNSDDC 62  
 QY 65 TYSLSTLTLSKADYEHKHYKACEVTHQGLSSPVTKSFNRGEC 107  
 DB 63 TYNLSSTLTLSKDEYNSHDEYTCQVA-QGSGSPVQVQSFNRKNC 104  
 RESULT 9  
 LAC\_CHICK  
 ID LAC\_CHICK STANDARD; PRT; 103 AA.  
 AC P20763;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE IG lambda chain C region.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=87218480; PubMed=3107981;  
 RA Parvari R., Ziv E., Lerner F., Tel-Or S., Burstein Y., Schechter I.;  
 RT "Analyses of chicken immunoglobulin light chain cDNA clones indicate  
 RT a few germline V lambda genes and allotypes of the C lambda locus";  
 RL EMBL J. 6:97-102(1987).

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CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC -----
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CC -----
DR EMBL; X04768; CAA28461.1; ..
DR PIR; B26167; B26167.
DR HSSP; P01842; 7FAB.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_cl.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; Ig; 1.
DR SMART; SMO0407; Igc1; 1.
DR PROSITE; PS00835; IG LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1
FT DOMAIN 6 99 IG-LIKE.
FT DISULFID 28 85
FT DISULFID 103 103 INTERCHAIN (WITH HEAVY CHAIN).
FT VARIANT 90 N -> D.
FT SEQUENCE 103 AA; 11361 MW; 77BF341B511B91B2 CRC64;
Query Match 41.8%; Score 231; DB 1; Length 103;
Best Local Similarity 43.3%; Pred. No. 1.1e-16;
Matches 45; Conservative 19; Mismatches 34; Indels 6; Gaps 3;
QY 5 APSVFIFPPSDEQLKSGT-ASVVLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKD 63
DB 5 APTTLFPPSKEELNEATKATLVCLINDFVPSPTVDWIDGTRSG---ETTPQRQSN 61
QY 64 STYLSLTLSKADYKHKYACEVTHQGLSPVTKSFNRGEC 107
DB 62 SQYNASSYLSASDWSHETTCRVTHNGTS--ITKTLKRSEC 103

RESULT 10
KAC_RANCA STANDARD; PRT; 108 AA.
AC P11272;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig light chain C region.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE.
RX MEDLINE=89039916; PubMed=3141797;
RA Mikoryak C.A., Steiner L.A.;
RT "Amino acid sequence of the constant region of immunoglobulin light
chains from Rana catesbeiana."
RL Mol. Immunol. 25:695-703(1988).
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A93135; K3FG.
DR HSSP; P01679; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; IG_cl.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; Ig; 1.
DR SMART; SMO0407; Igc1; 1.
DR PROSITE; PS00835; IG LIKE; 1.
DR PROSITE; PS00290; IG_MHC; FALSE NEG.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1
FT DOMAIN 7 102 IG-LIKE.

```

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FT DISULFID 13 106
FT DISULFID 28 86
FT VARIANT 47 47 K -> R (IN HALF OF THE MOLECULES).
SQ SEQUENCE 108 AA; 11808 MW; 60B18F7AF1411F6C CRC64;
Query Match 40.7%; Score 225; DB 1; Length 108;
Best Local Similarity 48.0%; Pred. No. 8.1e-16;
Matches 49; Conservative 16; Mismatches 33; Indels 2; Gaps 2;
QY 6 PSVFIFPPSDEQLKSGTASVVLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDST 65
DB 7 PTVSYCPSLGQRNSGASATVCLVDKFIYFGGAQVTKGDKNVISGVVTSKIKD-KDNT 65
QY 66 YSLSLTSLSKADYKHKYACEVTHQGLSPVTKSFNRGEC 107
DB 66 YSMSTLTMSGEF-KYSTMTCEVTHPTLTLPALAKSFQTSSEC 106

RESULT 11
KAC5_RABIT STANDARD; PRT; 103 AA.
AC P01841;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig kappa-95 chain C region.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE.
RX MEDLINE=83178897; PubMed=6404296;
RA Ayadi H., Dutka S., Paroutaud P., Strosberg A.D.;
RT "Partial amino acid sequence of a rabbit immunoglobulin light chain
of allotype B5."
RL Biochemistry 22:993-998(1983).
RN [2]
RP SEQUENCE OF 4-103.
RX MEDLINE=82057807; PubMed=6795448;
RA Chersi A., Alexander C.B., Mage R.G.;
RT "Partial primary structure of the immunoglobulin light chain constant
region of a single rabbit of B5 allotype."
RL Mol. Immunol. 17:1515-1523(1980).
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A30480; K5RB.
DR HSSP; P01842; 7FAB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; IG_cl.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; Ig; 1.
DR SMART; SMO0407; Igc1; 1.
DR PROSITE; PS00835; IG LIKE; 1.
DR PROSITE; PS00290; IG_MHC; FALSE NEG.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1
FT DOMAIN 5 99 IG-LIKE.
FT DISULFID 26 85
FT DISULFID 103 103 INTERCHAIN (WITH A HEAVY CHAIN).
FT CONFLICT 5 5 MISSING (IN REF. 2).
FT CONFLICT 14 14 P -> S (IN REF. 2).
FT CONFLICT 21 21 A -> T (IN REF. 2).
FT CONFLICT 82 82 E -> Q (IN REF. 2).
FT CONFLICT 87 88 VA -> LP (IN REF. 2).
SQ SEQUENCE 103 AA; 10945 MW; F33800791B031DD3 CRC64;
Query Match 40.4%; Score 223.5; DB 1; Length 103;
Best Local Similarity 44.7%; Pred. No. 1.1e-15;
Matches 46; Conservative 19; Mismatches 35; Indels 3; Gaps 3;
QY 5 APSVFIFPPSDEQLKSGTASVVLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDS 64
DB 4 APTVLIFPPAQLATGAVTIVCVANKYFP-DGVTWEVDGKPLTTGTGTSKTPQNSDDC 62

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RL Biochemistry 13:1295-1302 (1974).  
 RP [6]  
 RN SEQUENCE (DOT).  
 RX MEDLINE=9255298; PubMed=7737190;  
 RA Stoppini M., Ballotti V., Negri A., Merlini G., Garver P., Ferri G.;  
 RT "Characterization of the two unique human anti-flavin monoclonal  
 RL immunoglobulins.";  
 RN Eur. J. Biochem. 228:886-893 (1995).  
 [7]  
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF NEMW.  
 RX MEDLINE=75046825; PubMed=4215080;  
 RA Poljak R.J., Anzel L.M., Avey H.P., Chen B.L., Phizackerley R.P.,  
 RA Saul P.;  
 RT "The three-dimensional structure of the fab' fragment of a human  
 RL myeloma immunoglobulin at 2.0-A resolution.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 71:3440-3444 (1974).  
 [8]  
 RP PARTIAL SEQUENCE (BENCE-JONES PROTEIN MCG).  
 RX MEDLINE=75013804; PubMed=4415202;  
 RA Pett J.W., Deutsch H.F.;  
 RT "Primary structure of the M<sub>g</sub> lambda chain.";  
 RL Biochemistry 13:4102-4114 (1974).  
 [9]  
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF MCG.  
 RX Edmundson A.B., Ely K.R., Abola E.E., Schiffer M.,  
 RA Panagiotopoulos N.;  
 RT "Rotational allomerism and divergent evolution of domains in  
 RL immunoglobulin light chains.";  
 RL Biochemistry 14:3953-3961 (1975).  
 [10]  
 RP X-RAY CRYSTALLOGRAPHY OF MCG.  
 RX MEDLINE=90133913; PubMed=2515285;  
 RA Ely K.R., Herron J.N., Harker M., Edmundson A.B.;  
 RT "Three-dimensional structure of a light chain dimer crystallized in  
 RL water. Conformational flexibility of a molecule in two crystal  
 RL forms.";  
 RL J. Mol. Biol. 210:601-615 (1989).  
 [11]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=82080690; PubMed=6273747;  
 RA Hieter P.A., Hollis G.F., Korsmeyer S.J., Waldmann T.A., Leder P.;  
 RT "Clustered arrangement of immunoglobulin lambda constant region genes  
 RL in man.";  
 RL Nature 294:536-540 (1981).  
 CC -1- MISCELLANEOUS: THE SEQUENCE SHOWN IS THE KERN-/OZ-/MCG- CHAIN  
 CC FOUND IN PROTEINS SH, X, AND NIG-64. THE KERN PROTEIN HAS THE  
 CC KERN+ MARKER, THE NEMW PROTEIN HAS THE OZ+ MARKER, THE MCG PROTEIN  
 CC HAS THE KERN+ MARKER, AND THE MCG+ MARKER.  
 CC -1- MISCELLANEOUS: SIX TANDEM LAMBDA-TYPE GENES WERE IDENTIFIED & THE  
 CC 3 MOST 5' WERE SEQUENCED. THESE CORRESPOND TO THE MCG SEQUENCE  
 CC (LAMBDA-1), THE KERN-/OZ- SEQUENCE (LAMBDA-2) & THE KERN-/OZ+  
 CC SEQUENCE (LAMBDA-3).  
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
 CC -----  
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 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC -----  
 CC EMBL: J00253; AA059107.1;  
 CC EMBL: L38562; AAB36581.1; ALT\_INIT.  
 CC EMBL: X51754; CAB38569.1; ALT\_INIT.  
 CC EMBL: X51755; CAA36049.1;  
 CC EMBL: X51755; CAA36051.1;  
 CC FIR: A92057; L2HU.  
 CC PDB: 2MCG; 15-JUL-92.  
 CC PDB: 7FAB; 31-JAN-94.  
 CC PDB: 1AOK; 04-FEB-98.  
 CC PDB: 1LIL; 15-MAY-97.  
 CC Genew; HGNC:5855; IGLC1.

DR Genew; HGNC:5855; IGLC2.  
 DR Genew; HGNC:5857; IGLC3.  
 DR MIN; 147220; --  
 DR GO; GO:0003823; F:antigen binding activity; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig\_c1.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00407; IGL1; 1.  
 DR PROSITE; PS00835; IG\_LIKE; 1.  
 DR PROSITE; PS00290; IG\_MHC; 1.  
 KW Immunoglobulin domain; Immunoglobulin C region; Bence-Jones protein;  
 KW 3D-structure.  
 FT NON TER 1 1  
 FT DOMAIN 6 100 IG-LIKE.  
 FT DISULFID 27 86 INTERCHAIN (WITH HEAVY CHAIN).  
 FT DISULFID 104 104 A -> N (IN MCG+ MARKER).  
 FT VARIANT 5 5 /FTID=VAR\_003898.  
 FT VARIANT 7 7 S -> T (IN MCG+ MARKER).  
 FT VARIANT 45 45 S -> G (IN KERN+ MARKER).  
 FT VARIANT 56 56 T -> K (IN MCG+ MARKER).  
 FT VARIANT 82 82 R -> K (IN OZ+ MARKER).  
 FT STRAND 8 11 /FTID=VAR\_003901.  
 FT HELIX 15 19 /FTID=VAR\_003902.  
 FT TURN 20 21  
 FT STRAND 24 32  
 FT STRAND 38 43  
 FT TURN 44 45  
 FT STRAND 46 48  
 FT TURN 61 62  
 FT STRAND 65 72  
 FT HELIX 75 80  
 FT STRAND 84 89  
 FT STRAND 94 99  
 SQ SEQUENCE 105 AA; 11236 MW; DCD9C7C201C13CC2 CRC64;  
 Query Match 37.7%; Score 208.5; DB 1; Length 105;  
 Best Local Similarity 40.0%; Pred. No. 3.5e-14;  
 Matches 42; Conservative 27; Mismatches 31; Indels 5; Gaps 3;  
 QY 4 AASVFIPEPSDEOLKSGTASVVCLLNNFYPREAKVQWYDNA-LQSGNSQBSVTEQDSK 62  
 Db 4 AASVTLFPSSSELOQANKATLVCLISDFYGAVTAMKADSSPVKAG--VETTFPSKQS 61  
 QY 63 DSTYSLSTLTLSKADYERKHYVACEVTHQGLSSPVTKSFNRGEC 107  
 Db 62 NNKYAASSYLSLTPEQWKSHRSYSCQVTHEG--STVEKTVAPTEC 104  
 RESULT 14  
 LAC RABIT STANDARD; PRT; 105 AA.  
 ID LAC RABIT AC P01847;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Ig lambda chain C region.  
 OS Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 OX NCBI\_TaxID=9986;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=82091105; PubMed=6797414;  
 RA Garcia I., Jaton J.-C.;  
 RT "The primary structure of the constant region of Basilea-rabbit

RT immunoglobulin lambda-chains.";  
 RL Biochem. J. 197;177-183(1981).  
 CC -!- MISCELLANEOUS: THIS LAMBDA CHAIN EXPRESSES THE C7 ALLOTYPIC  
 CC -!- SPECIFICITY. CONTAINS 1 IMMUNOGLOBULIN-LIKE DOMAIN.  
 CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE DOMAIN.  
 DR HSP; P01842; 7FAB.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig\_c1.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00407; Igcl; 1.  
 DR PROSITE; PS0835; IG\_LIKE; 1.  
 DR PROSITE; PS0290; IG\_MHC; FALSE NEG.  
 KW Immunoglobulin domain; Immunoglobulin C region.  
 FT NON\_TER 1  
 FT DOMAIN 6 100 IG-LIKE.  
 FT DISULFID 27 86  
 FT DISULFID 104 104 INTERCHAIN (WITH HEAVY CHAIN).  
 SQ SEQUENCE 105 AA; 11484 MW; B427513272E8663D CRC64;

Query Match 36.8%; Score 203.5; DB 1; Length 105;  
 Best Local Similarity 44.3%; Pred. No. 1.1e-13;  
 Matches 47; Conservative 15; Mismatches 33; Indels 11; Gaps 4;  
 QY 6 PSVIFPPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNS--QESVTEQDSKD 63  
 DB 6 PSVILFPSPSEELKDKATLVCLISDFYPRTVKYNKAD-----GNSVTQGVDTTPSKQ 60  
 QY 64 ST--YSLSSLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 107  
 DB 61 SNKYAASSFLHLTANQKWSQSVTCQVTHEG--HTVEKSLAPAE 104

RESULT 15  
 LAC1 RAT  
 ID LAC1 RAT STANDARD; PRT; 104 AA.  
 AC P20766;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Ig lambda-1 chain C region.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=87305594; PubMed=3114047;  
 RA Steen M.L., Hellman L., Pettersson U.;  
 RT "The immunoglobulin lambda locus in rat consists of two C lambda  
 RL genes and a single v lambda gene.";  
 RL Gene 55:75-84(1987).  
 CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE DOMAIN.  
 CC -----  
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 CC or send an email to [licenses@isb-sib.ch](mailto:licenses@isb-sib.ch)).  
 CC -----  
 CC EMBL; M22520; AAA41419.1; ALT\_INIT.  
 DR HSP; P01842; 7FAB.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig\_c1.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00407; Igcl; 1.  
 DR PROSITE; PS0835; IG\_LIKE; 1.  
 DR PROSITE; PS0290; IG\_MHC; 1.  
 KW Immunoglobulin domain; Immunoglobulin C region.  
 FT NON\_TER 1

FT DOMAIN 6 99 IG-LIKE.  
 FT DISULFID 27 85  
 FT DISULFID 103 103 INTERCHAIN (WITH HEAVY CHAIN).  
 SQ SEQUENCE 104 AA; 11565 MW; CB71811F4BC878A CRC64;  
 Query Match 34.4%; Score 190; DB 1; Length 104;  
 Best Local Similarity 39.0%; Pred. No. 2.4e-12;  
 Matches 41; Conservative 20; Mismatches 38; Indels 6; Gaps 3;  
 QY 4 AAPSVPFPPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA-LQSGNSQESVTEQDSK 62  
 DB 4 ATPSVTLFPSPSEELKDKATLVCMVDFYPGVMTVVMKADGTPITQGVETTQPFKQNNK 63  
 QY 63 DSTYSLSSLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 107  
 DB 64 ---YMAISYLLLTAKAWETHSNYSQVTHE--ENTVEKSLAPAE 103

Search completed: January 13, 2004, 12:39:29  
 Job time : 5.67249 secs

GenCore version 5.1.1.6  
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OM protein - protein search, using sw model

Run on: January 13, 2004, 12:20:44 ; Search time 19.1572 Seconds  
(without alignments)  
1441.318 Million cell updates/sec

Title: US-09-990-586-99

Perfect score: 553

Sequence: 1 RTVAAPSVFIPPPSDEQLKS.....EVTHQGLSSPVTKSFNRGEC 107

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 23.1\*

- 1: sp\_archaea.\*
- 2: sp\_bacteria.\*
- 3: sp\_fungi.\*
- 4: sp\_human.\*
- 5: sp\_invertebrate.\*
- 6: sp\_mammal.\*
- 7: sp\_mhc.\*
- 8: sp\_organelle.\*
- 9: sp\_phage.\*
- 10: sp\_plant.\*
- 11: sp\_rodent.\*
- 12: sp\_virus.\*
- 13: sp\_vertibrate.\*
- 14: sp\_unclassified.\*
- 15: sp\_virus.\*
- 16: sp\_bacteriap.\*
- 17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	553	100.0	234	Q8NEK1	Q8NEK1 homo sapien
2	553	100.0	239	Q8TCD0	Q8TCD0 homo sapien
3	549	99.3	239	Q8NEK0	Q8NEK0 homo sapien
4	352	63.7	233	Q91WS9	Q91WS9 mus musculus
5	352	63.7	234	Q8R028	Q8R028 mus musculus
6	352	63.7	234	Q91WF8	Q91WF8 mus musculus
7	352	63.7	234	Q8R062	Q8R062 mus musculus
8	352	63.7	234	Q8VCP0	Q8VCP0 mus musculus
9	352	63.7	235	Q91W12	Q91W12 mus musculus
10	352	63.7	238	Q8VCI6	Q8VCI6 mus musculus
11	352	63.7	238	Q99M37	Q99M37 mus musculus
12	352	63.7	239	Q8VC55	Q8VC55 mus musculus
13	352	63.7	239	Q8K0F8	Q8K0F8 mus musculus
14	347	62.7	214	Q91IA5	Q91IA5 mus musculus
15	211.5	38.2	106	Q8TGC5	Q8TGC5 homo sapien
16	211.5	38.2	233	Q8TBC9	Q8TBC9 homo sapien

17	211.5	38.2	236	4	Q8NEJ1	Q8NEJ1 homo sapien
18	210.5	38.1	130	11	Q9D8W4	Q9D8W4 mus musculus
19	208.5	37.7	233	4	Q8N5F4	Q8N5F4 homo sapien
20	208.5	37.7	234	4	Q8N355	Q8N355 homo sapien
21	208.5	37.7	237	4	Q8WUK4	Q8WUK4 homo sapien
22	208.5	37.7	237	4	Q8WTU6	Q8WTU6 homo sapien
23	208.5	37.7	240	4	Q8WUK3	Q8WUK3 homo sapien
24	199.5	36.1	235	11	Q99M11	Q99M11 mus musculus
25	192.5	34.8	233	4	Q96169	Q96169 mus musculus
26	192.5	34.8	236	4	Q96E61	Q96E61 homo sapien
27	174	31.5	105	11	Q99JCI	Q99JCI mus musculus
28	159.5	28.8	473	11	Q9D8L4	Q9D8L4 mus musculus
29	153.5	27.8	468	11	Q99L31	Q99L31 mus musculus
30	153.5	27.8	473	11	Q99L25	Q99L25 mus musculus
31	151	27.3	473	4	Q8TGC3	Q8TGC3 homo sapien
32	149	26.9	509	4	Q8NF17	Q8NF17 homo sapien
33	149	26.9	521	4	Q8N4Y9	Q8N4Y9 homo sapien
34	148	26.8	471	4	Q8TC77	Q8TC77 homo sapien
35	148	26.8	701	4	Q96PQ8	Q96PQ8 homo sapien
36	144	26.0	473	11	Q91Z05	Q91Z05 mus musculus
37	144	26.0	474	11	Q8R3H6	Q8R3H6 mus musculus
38	143	25.9	463	11	Q99LC4	Q99LC4 mus musculus
39	142	25.7	437	11	Q91IA4	Q91IA4 mus musculus
40	142	25.7	469	11	Q8R3V9	Q8R3V9 mus musculus
41	139.5	25.2	337	6	Q95M34	Q95M34 equus caball
42	136	24.6	613	11	Q8VCX7	Q8VCX7 mus musculus
43	134	24.2	684	13	Q90544	Q90544 ginglymoato
44	127.5	23.1	267	13	Q90529	Q90529 ginglymoato
45	127.5	23.1	268	13	Q90524	Q90524 ginglymoato

#### ALIGNMENTS

RESULT 1  
Q8NEK1  
ID Q8NEK1 PRELIMINARY; PRT; 234 AA.  
AC Q8NEK1;  
DT 01-OCT-2002 (TREMREL. 22, Created)  
DT 01-OCT-2002 (TREMREL. 22, Last sequence update)  
DT 01-VAR-2003 (TREMREL. 23, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
RX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lung;  
RA Strausberg R.;  
RL Submitted (JUN-2002) to the EMBL/GenBank/DBSJ databases.  
DR EMBL; BC030813; AAH30813.1; -.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003597; IG\_c1.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_v.  
DR Pfam; PF00047; IG; 2.  
DR SMART; SM00407; IGc1; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG LIKE; 2.  
DR PROSITE; PS00290; IG\_MHC; 1.  
KW Hypothetical protein.  
SQ SEQUENCE 234 AA; 25530 MW; 6316B8DEF8D132F8 CRC64;  
Query Match 100.0%; Score 553; DB 4; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.7e-49;  
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 RTVAAPSVFIPPPSDEQLKSGTASVCLNNFYPREAKVQVKVDNALQSGNSQESVTEQ 60  
Db 128 RTVAAPSVFIPPPSDEQLKSGTASVCLNNFYPREAKVQVKVDNALQSGNSQESVTEQ 187  
QY 61 SKDSTYLSLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 107

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Db 188 SKDSTYLSSTLTLSKADYKHKYACVTHQGLSSPVTKSFNRGEC 234
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RESULT 2
Q8TCDO PRELIMINARY; PRT; 239 AA.
AC Q8TCDO;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 239 AA; 26234 MW; F5E20AD3B0552C0A CRC64;

Query Match 100.0%; Score 553; DB 4; Length 239;
Best Local Similarity 100.0%; Pred. No. 1.8e-49;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
133 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 192
61 SKDSTYLSSTLTLSKADYKHKYACVTHQGLSSPVTKSFNRGEC 107
193 SKDSTYLSSTLTLSKADYKHKYACVTHQGLSSPVTKSFNRGEC 239

Db 188 SKDSTYLSSTLTLSKADYKHKYACVTHQGLSSPVTKSFNRGEC 234
|||||
RESULT 3
Q8NEKO PRELIMINARY; PRT; 239 AA.
AC Q8NEKO;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Prostate;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 239 AA; 26234 MW; F5E20AD3B0552C0A CRC64;

Query Match 100.0%; Score 553; DB 4; Length 239;
Best Local Similarity 100.0%; Pred. No. 1.8e-49;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
133 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 192
61 SKDSTYLSSTLTLSKADYKHKYACVTHQGLSSPVTKSFNRGEC 107
193 SKDSTYLSSTLTLSKADYKHKYACVTHQGLSSPVTKSFNRGEC 239

Db 188 SKDSTYLSSTLTLSKADYKHKYACVTHQGLSSPVTKSFNRGEC 234
|||||
RESULT 4
Q91WS9 PRELIMINARY; PRT; 233 AA.
AC Q91WS9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical 25.8 kDa protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RA Strausberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC013496; AH13496.1; -.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
FT NON_TER 1
RN [1]
RP SEQUENCE 233 AA; 25781 MW; B1C184DA149A16EB CRC64;

Query Match 63.7%; Score 352; DB 11; Length 233;
Best Local Similarity 60.7%; Pred. No. 1.3e-28;
Matches 65; Conservative 15; Mismatches 27; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
127 RADAAPTVGIFFPPSSBQLTSGGASVVCFLNNFYPKIDINVKWKIDGERQNGVLNSWTDQD 186
61 SKDSTYLSSTLTLSKADYKHKYACVTHQGLSSPVTKSFNRGEC 107
187 SKDSTYMSSTLTLTDKDEYRHSNYTCEATHKTSTSPIVKSFNRNEC 233

Db 187 SKDSTYMSSTLTLTDKDEYRHSNYTCEATHKTSTSPIVKSFNRNEC 233
|||||
RESULT 5
Q8R028 PRELIMINARY; PRT; 234 AA.
AC Q8R028;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical 25.7 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Mammary gland;
RA Strausberg R.;
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RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC028540; AAH28540.1; -.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG_2.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 234 AA; 25702 MW; 148377F9C1CD0AEE CRC64;

Query Match 63.7%; Score 352; DB 11; Length 234;
Best Local Similarity 60.7%; Pred. No. 1.3e-28;
Matches 65; Conservative 15; Mismatches 27; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 128 RADAAPTQSVIFPPSDEQLTSGGASVVCFLNFPKDINVKWKIDGSRQGVLSWTDQD 187

QY 61 SKDSTYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 107
Db 188 SKDSTYMSSTLTLTDEYERHNSYTCETHKTSTSPIVKSFNRNEC 234

RESULT 6
Q91WF8 PRELIMINARY; PRT; 234 AA.
AC Q91WF8;
CA TISSUE=Colon;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC015292; AAH15292.1; -.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR InterPro; IPR001865; Ribosomal_S2.
DR Pfam; PF00047; IG_2.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS00290; IG_MHC; 1.
DR PROSITE; PS00362; RIBOSOMAL_S2_1; 1.
KW Hypothetical protein.
SQ SEQUENCE 234 AA; 25929 MW; B0D0B0E6B7812D2 CRC64;

Query Match 63.7%; Score 352; DB 11; Length 234;
Best Local Similarity 60.7%; Pred. No. 1.3e-28;
Matches 65; Conservative 15; Mismatches 27; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 128 RADAAPTQSVIFPPSDEQLTSGGASVVCFLNFPKDINVKWKIDGSRQGVLSWTDQD 187

QY 61 SKDSTYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 107
Db 188 SKDSTYMSSTLTLTDEYERHNSYTCETHKTSTSPIVKSFNRNEC 234

RESULT 7
Q8R062 PRELIMINARY; PRT; 234 AA.
AC Q8R062;
CA TISSUE=Colon;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC015292; AAH15292.1; -.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR InterPro; IPR001865; Ribosomal_S2.
DR Pfam; PF00047; IG_2.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS00290; IG_MHC; 1.
DR PROSITE; PS00362; RIBOSOMAL_S2_1; 1.
KW Hypothetical protein.
SQ SEQUENCE 234 AA; 25929 MW; B0D0B0E6B7812D2 CRC64;

Query Match 63.7%; Score 352; DB 11; Length 234;
Best Local Similarity 60.7%; Pred. No. 1.3e-28;
Matches 65; Conservative 15; Mismatches 27; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 128 RADAAPTQSVIFPPSDEQLTSGGASVVCFLNFPKDINVKWKIDGSRQGVLSWTDQD 187

QY 61 SKDSTYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 107
Db 188 SKDSTYMSSTLTLTDEYERHNSYTCETHKTSTSPIVKSFNRNEC 234

RESULT 8
Q8VCP0 PRELIMINARY; PRT; 234 AA.
AC Q8VCP0;
CA TISSUE=Colon;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC019474; AAH19474.1; -.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG_2.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS00290; IG_MHC; 1.
DR PROSITE; PS00362; RIBOSOMAL_S2_1; 1.
KW Hypothetical protein.
SQ SEQUENCE 234 AA; 25702 MW; 102551C59AC2FA9P CRC64;

Query Match 63.7%; Score 352; DB 11; Length 234;
Best Local Similarity 60.7%; Pred. No. 1.3e-28;
Matches 65; Conservative 15; Mismatches 27; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 128 RADAAPTQSVIFPPSDEQLTSGGASVVCFLNFPKDINVKWKIDGSRQGVLSWTDQD 187

QY 61 SKDSTYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 107
Db 188 SKDSTYMSSTLTLTDEYERHNSYTCETHKTSTSPIVKSFNRNEC 234

RESULT 9
Q91W12 PRELIMINARY; PRT; 234 AA.
AC Q91W12;
CA TISSUE=Colon;
RA Strausberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC027418; AAH27418.1; -.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG_2.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS00290; IG_MHC; 1.
DR PROSITE; PS00362; RIBOSOMAL_S2_1; 1.
KW Hypothetical protein.
SQ SEQUENCE 234 AA; 25857 MW; 4EB08C81426AEAB1 CRC64;

Query Match 63.7%; Score 352; DB 11; Length 234;
Best Local Similarity 60.7%; Pred. No. 1.3e-28;
Matches 65; Conservative 15; Mismatches 27; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 128 RADAAPTQSVIFPPSDEQLTSGGASVVCFLNFPKDINVKWKIDGSRQGVLSWTDQD 187

QY 61 SKDSTYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 107
Db 188 SKDSTYMSSTLTLTDEYERHNSYTCETHKTSTSPIVKSFNRNEC 234
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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RA Strausberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC027418; AAH27418.1; -.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG_2.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS00290; IG_MHC; 1.
DR PROSITE; PS00362; RIBOSOMAL_S2_1; 1.
KW Hypothetical protein.
SQ SEQUENCE 234 AA; 25857 MW; 4EB08C81426AEAB1 CRC64;

Query Match 63.7%; Score 352; DB 11; Length 234;
Best Local Similarity 60.7%; Pred. No. 1.3e-28;
Matches 65; Conservative 15; Mismatches 27; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 128 RADAAPTQSVIFPPSDEQLTSGGASVVCFLNFPKDINVKWKIDGSRQGVLSWTDQD 187

QY 61 SKDSTYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 107
Db 188 SKDSTYMSSTLTLTDEYERHNSYTCETHKTSTSPIVKSFNRNEC 234

RESULT 8
Q8VCP0 PRELIMINARY; PRT; 234 AA.
AC Q8VCP0;
CA TISSUE=Colon;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC019474; AAH19474.1; -.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG_2.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS00290; IG_MHC; 1.
DR PROSITE; PS00362; RIBOSOMAL_S2_1; 1.
KW Hypothetical protein.
SQ SEQUENCE 234 AA; 25702 MW; 102551C59AC2FA9P CRC64;

Query Match 63.7%; Score 352; DB 11; Length 234;
Best Local Similarity 60.7%; Pred. No. 1.3e-28;
Matches 65; Conservative 15; Mismatches 27; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 128 RADAAPTQSVIFPPSDEQLTSGGASVVCFLNFPKDINVKWKIDGSRQGVLSWTDQD 187

QY 61 SKDSTYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 107
Db 188 SKDSTYMSSTLTLTDEYERHNSYTCETHKTSTSPIVKSFNRNEC 234

RESULT 9
Q91W12 PRELIMINARY; PRT; 234 AA.
AC Q91W12;
CA TISSUE=Colon;
RA Strausberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC027418; AAH27418.1; -.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG_2.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS00290; IG_MHC; 1.
DR PROSITE; PS00362; RIBOSOMAL_S2_1; 1.
KW Hypothetical protein.
SQ SEQUENCE 234 AA; 25857 MW; 4EB08C81426AEAB1 CRC64;

Query Match 63.7%; Score 352; DB 11; Length 234;
Best Local Similarity 60.7%; Pred. No. 1.3e-28;
Matches 65; Conservative 15; Mismatches 27; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 128 RADAAPTQSVIFPPSDEQLTSGGASVVCFLNFPKDINVKWKIDGSRQGVLSWTDQD 187

QY 61 SKDSTYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 107
Db 188 SKDSTYMSSTLTLTDEYERHNSYTCETHKTSTSPIVKSFNRNEC 234
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ID Q91W12 PRELIMINARY; PRT; 235 AA.
AC Q91W12;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Unknown (Protein for MGC:16582).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CN NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAUSBERG R.;
RA Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC006643; AAH06643.1; -.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG-LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
SQ SEQUENCE 235 AA; 26021 MW; 5FC73BDEBD5E8FEF CRC64;

Query Match 63.7%; Score 352; DB 11; Length 235;
Best Local Similarity 60.7%; Pred. No. 1.3e-28;
Matches 65; Conservative 15; Mismatches 27; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
DB 129 RADAAPTQSVIFPPSSQSLTSGGASVVCFLNNFYPKDIIVKWKIDGSRQNGVLSWTDQD 186

QY 61 SKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC 107
DB 189 SKDSTYSMSSTLTLTCKDEYERHNSYTCETHTKTSTPIVKSFNREC 235

RESULT 10
Q8VC16 PRELIMINARY; PRT; 238 AA.
ID Q8VC16;
AC Q8VC16;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical 26.2 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CN NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC019760; AAH19760.1; -.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 238 AA; 26224 MW; 35EC08E3DE5414AD CRC64;

Query Match 63.7%; Score 352; DB 11; Length 238;
Best Local Similarity 60.7%; Pred. No. 1.3e-28;
Matches 65; Conservative 15; Mismatches 27; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
DB 132 RADAAPTQSVIFPPSSQSLTSGGASVVCFLNNFYPKDIIVKWKIDGSRQNGVLSWTDQD 191

QY 61 SKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC 107
DB 189 SKDSTYSMSSTLTLTCKDEYERHNSYTCETHTKTSTPIVKSFNREC 235

RESULT 11
Q99M37 PRELIMINARY; PRT; 238 AA.
ID Q99M37;
AC Q99M37;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical 26.3 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CN NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC002035; AAH02035.1; -.
DR HSP; P01679; 2FBJ.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG-LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 238 AA; 26344 MW; FB2B06A0B801330A CRC64;

Query Match 63.7%; Score 352; DB 11; Length 238;
Best Local Similarity 60.7%; Pred. No. 1.3e-28;
Matches 65; Conservative 15; Mismatches 27; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
DB 132 RADAAPTQSVIFPPSSQSLTSGGASVVCFLNNFYPKDIIVKWKIDGSRQNGVLSWTDQD 191

QY 61 SKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC 107
DB 192 SKDSTYSMSSTLTLTCKDEYERHNSYTCETHTKTSTPIVKSFNREC 238

RESULT 12
Q8VC55 PRELIMINARY; PRT; 239 AA.
ID Q8VC55;
AC Q8VC55;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical 26.3 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CN NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RA Strausberg R.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC021781; AAH21781.1; -.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 239 AA; 26303 MW; C16119CACA25C337 CRC64;

Query Match 63.7%; Score 352; DB 11; Length 239;
Best Local Similarity 60.7%; Pred. No. 1.4e-28;
Matches 65; Conservative 15; Mismatches 27; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
DB 132 RADAAPTQSVIFPPSSQSLTSGGASVVCFLNNFYPKDIIVKWKIDGSRQNGVLSWTDQD 191

QY 61 SKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC 107
DB 189 SKDSTYSMSSTLTLTCKDEYERHNSYTCETHTKTSTPIVKSFNREC 235
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DB 192 SKDSTYSMSSTLTLTCKDEYERHNSYTCETHTKTSTPIVKSFNREC 238

RESULT 11
Q99M37 PRELIMINARY; PRT; 238 AA.
ID Q99M37;
AC Q99M37;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical 26.3 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CN NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC002035; AAH02035.1; -.
DR HSP; P01679; 2FBJ.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG-LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 238 AA; 26344 MW; FB2B06A0B801330A CRC64;

Query Match 63.7%; Score 352; DB 11; Length 238;
Best Local Similarity 60.7%; Pred. No. 1.3e-28;
Matches 65; Conservative 15; Mismatches 27; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
DB 132 RADAAPTQSVIFPPSSQSLTSGGASVVCFLNNFYPKDIIVKWKIDGSRQNGVLSWTDQD 191

QY 61 SKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC 107
DB 192 SKDSTYSMSSTLTLTCKDEYERHNSYTCETHTKTSTPIVKSFNREC 238

RESULT 12
Q8VC55 PRELIMINARY; PRT; 239 AA.
ID Q8VC55;
AC Q8VC55;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical 26.3 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CN NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RA Strausberg R.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC021781; AAH21781.1; -.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 239 AA; 26303 MW; C16119CACA25C337 CRC64;

Query Match 63.7%; Score 352; DB 11; Length 239;
Best Local Similarity 60.7%; Pred. No. 1.4e-28;
Matches 65; Conservative 15; Mismatches 27; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
DB 132 RADAAPTQSVIFPPSSQSLTSGGASVVCFLNNFYPKDIIVKWKIDGSRQNGVLSWTDQD 191

QY 61 SKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC 107
DB 192 SKDSTYSMSSTLTLTCKDEYERHNSYTCETHTKTSTPIVKSFNREC 238
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Matches 65; Conservative 15; Mismatches 27; Indels 0; Gaps 0;
QY 1 RTVAAPSVFIIPPSDEQLKSGTASVVCCLNNFYPRKAVQWKVDNALQSGNSQESVTEQD 60
DB 133 RADAAPTQSVFIIPPSDEQLTSGASVVCFLNNFYPKDINVKKIDGSRQNGVLNSWTDQD 192
QY 61 SKDSTYSLSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 107
DB 193 SKDSTYMSSTLTLTQDEYERHNSYTCETHKTSTSPVKSFNRGEC 239

RESULT 13
Q8KOF8 PRELIMINARY; PRT; 239 AA.
AC Q8KOF8
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-MAY-2000 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Breast tumor;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC031498; AA31498.1; -.
DR InterPro; IPR002198; ADH_short.
DR InterPro; IPR003599; IG.
DR InterPro; IPR003597; IG_cl.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; IG_2.
DR SMART; SMC0409; IG; 2.
DR SMART; SMC0407; IGcl; 1.
DR SMART; SMC0406; IG; 1.
DR PROSITE; PS00061; ADH_SHORT; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 239 AA; 26366 MW; D7B884398AA341F0 CRC64;

Query Match 63.7%; Score 352; DB 11; Length 239;
Best Local Similarity 60.7%; Pred. No. 1.4e-28;
Matches 65; Conservative 15; Mismatches 27; Indels 0; Gaps 0;
QY 1 RTVAAPSVFIIPPSDEQLKSGTASVVCCLNNFYPRKAVQWKVDNALQSGNSQESVTEQD 60
DB 133 RADAAPTQSVFIIPPSDEQLTSGASVVCFLNNFYPKDINVKKIDGSRQNGVLNSWTDQD 192
QY 61 SKDSTYSLSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 107
DB 193 SKDSTYMSSTLTLTQDEYERHNSYTCETHKTSTSPVKSFNRGEC 239

RESULT 14
Q9RIAS PRELIMINARY; PRT; 214 AA.
AC Q9RIAS
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Kappa light chain of Mab7 (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Wilde K.G.; Yu X.; Ekraddoullah A.K.M.; Misra S.;
RT "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
antibody (Mab 7, its light and heavy chains) and construction of a
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RT single chain antibody (scFv).";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF152371; RAD40242.1; -.
DR HSP; P01679; 2PB1.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; IG_2.
DR SMART; SMC0406; IG; 1.
DR PROSITE; PS50835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
FT NON_TER 214 214
FT NON_TER 1 1
SQ SEQUENCE 214 AA; 23922 MW; 52BA205FDE995E2A CRC64;

Query Match 62.7%; Score 347; DB 11; Length 214;
Best Local Similarity 59.8%; Pred. No. 3.9e-28;
Matches 64; Conservative 15; Mismatches 28; Indels 0; Gaps 0;
QY 1 RTVAAPSVFIIPPSDEQLKSGTASVVCCLNNFYPRKAVQWKVDNALQSGNSQESVTEQD 60
DB 108 RADAAPTQSVFIIPPSDEQLTSGASVVCFLNNFYPKDINVKKIDGSRQNGVLNSWTDQD 167
QY 61 SKDSTYSLSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 107
DB 168 SKDSTYMSSTLTLTQDEYERHNSYTCETHKTSTSPVKSFNRGEC 214

RESULT 15
Q8TCJ5 PRELIMINARY; PRT; 106 AA.
AC Q8TCJ5
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein (Fragment).
GN DKFZP667J0810.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph node;
RA Duesterhoeft A.; Lauber J.; Mewes H.W.; Weil B.; Wiemann S.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL713800; CAD28551.1; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; IG_cl.
DR Pfam; PF00047; IG; 1.
DR SMART; SMC0407; IGcl; 1.
DR PROSITE; PS50835; IG LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
FT NON_TER 1 1
SQ SEQUENCE 106 AA; 11265 MW; 145272BBE65F4565 CRC64;

Query Match 38.2%; Score 211.5; DB 4; Length 106;
Best Local Similarity 41.0%; Pred. No. 2e-14;
Matches 43; Conservative 26; Mismatches 31; Indels 5; Gaps 3;
QY 4 AAPSVTLPSPSDEQLKSGTASVVCCLNNFYPRKAVQWKVDNALQSGNSQESVTEQD 62
DB 5 AAPSVTLPSPSDEQLKSGTASVVCCLNNFYPRKAVQWKVDNALQSGNSQESVTEQD 62
QY 63 DSTYSLSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 107
DB 63 NKRYAASSYLSLTPEQWKSHKSYSCQVTHEG--STVEKTVAPTEC 105

Search completed: January 13, 2004, 12:43:10
Job time : 20.1572 secs
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 13, 2004, 12:18:44 ; Search time 24.9511 Seconds  
(without alignments)  
680.681 Million cell updates/sec

Title: US-09-990-586-99

Perfect score: 553

Sequence: 1 RTVAAPSVFPSPDEQLKS.....EVTHQGLSSPTKSPNRGEC 107

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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- 19: /SIDSL/gcgdata/Geneseq/Geneseq-emb1/AA1998.DAT:\*
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- 24: /SIDSL/gcgdata/Geneseq/Geneseq-emb1/AA2003.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	553	100.0	107	AAW40578	Human kappa CL dom
2	553	100.0	107	AAW50152	Human kappa light
3	553	100.0	107	AAW08745	Human kappa-CL dom
4	553	100.0	107	AAW92425	Human kappa protei
5	553	100.0	107	AAW827000	Human kappa CL dom
6	553	100.0	107	ABG311883	Human kappa CL dom
7	553	100.0	107	ABP98755	Human kappa light
8	553	100.0	143	ABP93559	Sequence of human
9	553	100.0	193	AAW52145	Humanised HMFGL I1

10	553	100.0	201	20	AAW29770	P-selectin ligand
11	553	100.0	212	23	ABP51955	Humanised anti-CD1
12	553	100.0	213	17	AAW04301	Antibody fusion pr
13	553	100.0	213	22	AAE10510	Humanised high pot
14	553	100.0	213	22	AAE10512	Humanised high pot
15	553	100.0	213	22	AAE10514	Humanised high pot
16	553	100.0	213	22	AAE10516	Humanised high pot
17	553	100.0	213	22	AAE10518	Humanised high pot
18	553	100.0	213	22	AAE10520	Humanised high pot
19	553	100.0	213	22	AAE10522	Humanised high pot
20	553	100.0	213	22	AAE10524	Humanised high pot
21	553	100.0	213	22	AAE10526	Humanised high pot
22	553	100.0	213	22	AAE10528	Humanised high pot
23	553	100.0	213	23	ABP66563	Ganglioside GM2 an
24	553	100.0	213	23	ABP66565	Human RSV antibody
25	553	100.0	213	23	ABP66567	Human RSV antibody
26	553	100.0	213	23	ABP66569	Human RSV antibody
27	553	100.0	213	23	ABP66571	Human RSV antibody
28	553	100.0	213	23	ABP66573	Human RSV antibody
29	553	100.0	213	23	ABP66575	Human RSV antibody
30	553	100.0	213	23	ABP66577	Human RSV antibody
31	553	100.0	213	23	ABP66579	Human RSV antibody
32	553	100.0	213	23	ABP66581	Human RSV antibody
33	553	100.0	213	23	ABP66583	Human RSV antibody
34	553	100.0	213	23	ABP66585	Human RSV antibody
35	553	100.0	213	23	ABP66587	Human RSV antibody
36	553	100.0	213	23	ABP66589	Human RSV antibody
37	553	100.0	213	23	ABP66591	Human RSV antibody
38	553	100.0	213	23	ABP66593	Human RSV antibody
39	553	100.0	213	23	ABP66595	Human RSV antibody
40	553	100.0	213	23	ABP66597	Human RSV antibody
41	553	100.0	213	23	ABP66599	Human RSV antibody
42	553	100.0	213	23	ABP66601	Human RSV antibody
43	553	100.0	213	23	ABP66603	Human RSV antibody
44	553	100.0	213	23	ABP66605	Human RSV antibody
45	553	100.0	213	23	ABP66607	Human RSV antibody

#### ALIGNMENTS

#### RESULT 1

AAW40578  
ID AAW40578 standard; protein; 107 AA.

XX AAW40578;

XX 21-JUL-1998 (first entry)

XX Human kappa CL domain protein fragment.

DE Immunoglobulin G; IgG molecule; human; Fc region; LFA-1 receptor;

XX disorder; salvage receptor binding epitope; cell adherence interaction;

XX lymphocyte; T cell inflammatory response.

XX Homo sapiens.

XX US5739277-A.

XX 14-APR-1998.

XX 14-APR-1995; 95US-0422101.

XX 14-APR-1995; 95US-0422101.

XX (GETH ) GENENTECH INC.

XX Presta LG, Snedecor BR;

XX WPI, 1998-250490/22.

XX Polypeptide(s) that are not Fc fragments and have an increased

XX half-life - are useful for the treatment of LFA-1 mediated disorders

XX Disclosure; Fig 2; 38pp; English.

XX This protein fragment is derived from a human immunoglobulin kappa CL

CC domain and is used to describe a novel method to produce polypeptides

CC which contain an epitope from the Fc region of an IgG molecule and a

CC mutated salvage receptor binding epitope. They are useful for the

CC treatment of LFA-1 mediated disorders. These are conditions caused by

CC cell adherence interactions involving the LFA-1 receptor on lymphocytes,

CC e.g. T cell inflammatory responses. The mutated salvage receptor sequence

CC in the polypeptides means that they have increased in vivo circulatory

CC half-lives when compared to normal Fc regions of IgG molecules.

XX Sequence 107 AA;

XX Query Match 100.0%; Score 553; DB 19; Length 107;

XX Best Local Similarity 100.0%; Pred. No. 6.4e-49;

XX Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

DB 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

QY 61 SKDSTVLSSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC 107

DB 61 SKDSTVLSSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC 107

RESULT 2

AAAY50152

ID AAY50152 standard; Protein; 107 AA.

AC AAY50152;

DT 31-JAN-2000 (first entry)

DE Human kappa light chain constant region.

XX Antibody; monoclonal; F19; fibrinogen activation protein alpha; FAP;

KW humanisation; complementarity determining region; CDR; CDR grafting;

KW reshaped; reactive stroma; fibroblast; epithelial cancer;

KW diagnosis; immune response; framework sequence; constant region;

KW variable region; producibility; treatment; cancer; colorectal; lung;

KW breast; head; neck; ovarian; lung; bladder; pancreatic; metastasis;

KW detection; wound healing; skin inflammation; tumour; immunogenicity;

KW light chain.

OS Homo sapiens.

XX EP953639-A1.

XX 03-NOV-1999.

XX 30-APR-1998; 98EP-0107925.

XX 30-APR-1998; 98EP-0107925.

XX (BOEH ) BOEHRINGER INGELHEIM INT GMBH.

XX Park JE, Garin-Chesa P, Bamberger U, Leger O, Saldanha J;

PI Rettig WJ;

XX WPI; 1999-621833/54.

DR N-PSDB; AA232777.

XX New antibody protein, useful for treating cancer and for imaging

PT presence of activated stromal fibroblasts in healing wound or inflamed

PT skin -

XX Disclosure; Fig 20; 143pp; English.

XX This sequence represents a human kappa light chain, the cDNA of which

CC was used in the construction of a nucleotide encoding the light chain

CC of a human reshaped monoclonal antibody F19. F19 (ATCC Accession number

CC HB 8269) is a murine monoclonal antibody against fibroblast

CC activation protein alpha (FAP). FAP is a cell surface molecule

CC of reactive stromal fibroblasts, and its induction is a highly

CC consistent molecular trait of the reactive stroma of many types of

CC epithelial cancer. Although F19 may be useful in vitro, e.g., for

CC diagnosis, its applications for in vivo use in humans are problematic

CC as it elicits a human anti-mouse response which reduces the efficacy of

CC the antibody in patients and impairs continued administration. The novel

CC human reshaped F19 was humanised by grafting the murine complementarity

CC determining regions (CDRs) of F19 onto human variable region framework

CC sequences, and then joining these "reshaped human" variable regions to

CC human constant regions. These modifications also result in the improved

CC producibility in eukaryotic cell culture systems as compared to a

CC chimeric antibody having the entire variable regions of F19 joined to

CC human constant regions. The human reshaped F19 antibody has low

CC immunogenicity for humans and is useful for treating cancers e.g.,

CC colorectal cancers, non-small cell lung cancers, breast cancers, head

CC and neck cancers, ovarian cancers, lung cancers, bladder cancers,

CC pancreatic cancers and metastatic cancers. It is also useful for the

CC detection of activated stromal fibroblasts in a healing wound, inflamed

CC skin or a tumour in a human patient.

XX Sequence 107 AA;

XX Query Match 100.0%; Score 553; DB 20; Length 107;

XX Best Local Similarity 100.0%; Pred. No. 6.4e-49;

XX Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

DB 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

QY 61 SKDSTVLSSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC 107

DB 61 SKDSTVLSSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC 107

RESULT 3

AAAY08745

ID AAY08745 standard; protein; 107 AA.

XX AAY08745;

XX 10-AUG-1999 (first entry)

XX Human Kappa-CL domain.

XX IgG; immunoglobulin G; CH1 domain; human; anti-CD18; IgG1; IgG2; IgG3;

KW IgG4; Kappa-CL domain; lambda-CL domain; focal ischaemic stroke;

KW cerebroprotective; cerebral artery obstruction; blood flow; infarct;

KW CD18 extracellular domain; endothelium; CD11b/CD18 complex dissociation;

KW antibody.

XX Homo sapiens.

XX US5914112-A.

XX 22-JUN-1999.

XX 22-JAN-1997; 97US-0788800.

XX 23-JAN-1996; 96US-0093038.

XX 22-JAN-1997; 97US-0788800.

XX (SETH ) GENENTECH INC.

XX (UYVE-) UNIV VERMONT & STATE AGRIC COLLEGE.

XX Bednar WM, Gross CE, Thomas GR;

XX WPI; 1999-370483/31.

XX Anti-CD18 antibodies in stroke

XX Disclosure; Fig 4A-B; 25pp; English.

XX This invention describes a method for improving the clinical outcome in focal ischaemic stroke by administering novel anti-CD18 antibody which has cerebroprotective properties. The invention particularly describes a method of treating focal ischaemic stroke caused by the obstruction of a main cerebral artery which comprises administering an anti-CD18 antibody to increase the blood flow or reduce the infarct size, where: (1) the antibody binds to an extracellular domain of CD18 and inhibits or reduces the ability of the cell expressing CD18 to bind to endothelium, (2) the antibody binds CD18 with an affinity of less than 4 nm, or (3) the antibody dissociates CD18/CD18 complex. This sequence represents the human kappa-CL domain which is used to illustrate the method of the invention.

XX Sequence 107 AA;

Query Match 100.0%; Score 553; DB 20; Length 107;  
Best Local Similarity 100.0%; Pred. No. 6.4e-49;  
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60  
DB 1 RTVAAPSVFIPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

QY 61 SKDSTYLSSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 107  
DB 61 SKDSTYLSSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 107

RESULT 4  
AAW92425  
ID AAW92425 standard; peptide; 107 AA.

XX Homo sapiens.

XX US5869046-A.

XX 09-FEB-1999.

XX 14-APR-1995; 95US-0422092.

XX 14-APR-1995; 95US-0422092.

XX (GETH ) GENENTECH INC.

XX Presta LG, Snedecor BR;

XX WPI; 1999-152694/13.

XX Production of antibody fragments with reduced renal clearance - by introducing salvage receptor binding epitope into CH1 or CL region

XX Disclosure; Column 55-58; 38pp; English.

XX This invention describes a method for preparing a variant Fab or F(ab')<sub>2</sub> polypeptide having increased half-life in vivo, where the polypeptide contains an Ig or Ig-like domain comprising a CH1 and/or CL region, is cleaved from the kidneys and does not contain an IGC FC region. The method involves altering the polypeptide within the CH1 or CL region to incorporate a salvage receptor binding epitope taken from two loops of a CH2 domain of an IGC FC region. The polypeptides have a reduced renal

CC clearance rate and an increased circulatory half-life. This sequence represents a human kappa protein CL domain used in the method of the invention.

XX Sequence 107 AA;

Query Match 100.0%; Score 553; DB 20; Length 107;  
Best Local Similarity 100.0%; Pred. No. 6.4e-49;  
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60  
DB 1 RTVAAPSVFIPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

QY 61 SKDSTYLSSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 107  
DB 61 SKDSTYLSSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 107

RESULT 5  
AAB27000  
ID AAB27000 standard; Protein; 107 AA.

XX AAB27000;

XX 25-JAN-2001 (first entry)

XX Human kappa CL domain.

XX Salvage receptor binding epitope; immunomodulator; LFA-1 agonist; mutagenesis; anti-CD18 Fab H52; immunoglobulin; Ig; Crohn's disease; psoriasis; meningitis; allergy; eczema; B-cell lymphoma; wound repair; inflammation; vaccine.

XX Homo sapiens.

XX US6121022-A.

XX 19-SEP-2000.

XX 14-APR-1995; 95US-0422112.

XX 14-APR-1995; 95US-0422112.

XX (GETH ) GENENTECH INC.

XX Presta LG, Snedecor BR;

XX WPI; 2000-610925/58.

XX New nucleic acid encoding new modified polypeptides with increased circulatory half-life useful for preventing/treating LFA-1-mediated disorders, e.g. reducing inflammatory responses or inducing tolerance to immunostimulants -

XX Disclosure; Fig 2; 38pp; English.

XX The present sequence was used in a method for improving the in vivo half-life of polypeptides. The polypeptides comprise an Ig constant domain or an Ig-like constant domain, and a salvage receptor binding epitope within the Ig or Ig-like domain. The salvage receptor epitope is taken from two loops of the CH2 domain of an FC region of an Ig molecule. The modified polypeptides are useful for preventing or treating LFA-1-mediated disorders, e.g. Crohn's disease, psoriasis, meningitis, allergic conditions (e.g. eczema), antigen-antibody complex mediated diseases, B-cell lymphomas. They are also useful for wound repair, reducing inflammatory responses and inducing tolerance to immunostimulants. They may also be used in diagnostic assays. The nucleic acids and modified polypeptides are useful for the passive immunisation of patients, as well as for affinity purification of an antigen from recombinant cell culture or natural sources.

XX Sequence 107 AA;

Query Match 100.0%; Score 553; DB 21; Length 107;  
 Best Local Similarity 100.0%; Pred. No. 6.4e-49;  
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 1 RTVAAPSVFIPPSDEQLKSGTASVCLNNFYPRKQVQKVDNALQSGNSQESVTEQD 60

Qy 61 SKDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107  
 Db 61 SKDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107

Qy 61 SKDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107  
 Db 61 SKDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107

RESULT 6  
 ID ABG31883 standard; protein; 107 AA.  
 XX ABG31883;  
 AC ABG31883;  
 XX 05-NOV-2002 (first entry)  
 DT Human kappa CL domain.  
 XX Human; cytostatic; antitumour; immunosuppressive; antiallergic;  
 KW humanised; antibody; fibroblast activation protein alpha; FAPalpha;  
 KW cancer; monoclonal antibody F19; colorectal cancer;  
 KW non-small cell lung carcinoma; breast cancer; pancreatic cancer;  
 KW tumour; systemic autoimmune disease; allergy; light chain;  
 KW constant region.  
 XX Homo sapiens.  
 OS  
 XX US2002081294-A1.  
 PN 27-JUN-2002.  
 PD 20-DEC-2000; 2000US-0811384.  
 XX 23-JAN-1996; 96US-093038P.  
 PR 17-FEB-1999; 99US-0251652.  
 PR 22-JAN-1997; 97US-0788800.  
 XX (GETH ) GENENTECH INC.  
 PA Bednar MM, Gross CE, Thomas GR, Gross LJ;  
 PI WPI; 2002-626528/67.  
 XX Increasing cerebral blood flow and/or reducing infarct size in focal  
 PT ischaemic stroke using anti-CD18 antibody and tissue plasminogen  
 PT activator is useful to improve clinical outcome in acute ischaemic  
 PT stroke -  
 XX Disclosure; Fig 4; 27pp; English.  
 PS The invention relates to a method of increasing cerebral blood flow and/  
 CC or reducing infarct size in focal ischaemic stroke caused by obstruction  
 CC of a main cerebral artery in a human, comprising co-administering tissue  
 CC plasminogen activator and anti-CD18 antibody about 3-5 hours after the  
 CC stroke. The method is used to improve the clinical outcome in acute  
 CC ischaemic stroke and to provide an alternative to thrombolytic therapy  
 CC for treating thromboembolic stroke, particularly where thrombolytic  
 CC therapy has been unsuccessful or is contra-indicated. The present  
 CC sequence represents the human kappa CL domain used in the method of the  
 CC invention.  
 XX SQ Sequence 107 AA;

Query Match 100.0%; Score 553; DB 23; Length 107;  
 Best Local Similarity 100.0%; Pred. No. 6.4e-49;  
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFIPPSDEQLKSGTASVCLNNFYPRKQVQKVDNALQSGNSQESVTEQD 60  
 Db 1 RTVAAPSVFIPPSDEQLKSGTASVCLNNFYPRKQVQKVDNALQSGNSQESVTEQD 60

Db 1 RTVAAPSVFIPPSDEQLKSGTASVCLNNFYPRKQVQKVDNALQSGNSQESVTEQD 60  
 Qy 61 SKDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107  
 Db 61 SKDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107

RESULT 7  
 ID ABB98755 standard; Protein; 107 AA.  
 XX ABB98755;  
 AC ABB98755;  
 XX 23-JAN-2003 (first entry)  
 DT Human kappa light constant chain.  
 XX Human; cytostatic; antitumour; immunosuppressive; antiallergic;  
 KW humanised; antibody; fibroblast activation protein alpha; FAPalpha;  
 KW cancer; monoclonal antibody F19; colorectal cancer;  
 KW non-small cell lung carcinoma; breast cancer; pancreatic cancer;  
 KW tumour; systemic autoimmune disease; allergy; light chain;  
 KW constant region.  
 XX Homo sapiens.  
 OS  
 XX WO200283171-A2.  
 PN 24-OCT-2002.  
 PD 11-APR-2002; 2002WO-EP04041.  
 PF 12-APR-2001; 2001US-283868P.  
 PR (BOEH ) BOEHRINGER INGELHEIM INT GMBH.  
 PA (BOEH ) BOEHRINGER INGELHEIM PHARM INC.  
 XX Amelsberg A, Scott A, Tanswell P;  
 PI WPI; 2003-058609/05.  
 DR N-PSDB; ABV74601.  
 XX Use of a humanized antibody which specifically binds to fibroblast  
 PT activation protein alpha for manufacturing a medicament for treating  
 PT cancer -  
 XX Claim 7; Page 55; 57pp; English.  
 PS The present invention relates to the use of a humanised antibody (I),  
 CC which specifically binds to fibroblast activation protein alpha  
 CC (FAPalpha), for manufacturing a medicament for treating cancer. (I) has  
 CC the complementary determining region (CDR) of the monoclonal antibody  
 CC F19, but has framework modifications resulting in improved producibility  
 CC in host cells as compared to a chimeric antibody having the variable  
 CC regions of F19 and foreign constant regions. To generate (I), a chimeric  
 CC antibody was constructed having variable regions of the light and heavy  
 CC chains of F19 and human light and heavy constant regions. (I) is useful  
 CC for treating a patient suffering from a pathological condition  
 CC characterised by expression of FAPalpha, such as colorectal cancer,  
 CC non-small cell lung carcinoma, breast cancer, pancreatic cancer, tumours,  
 CC systemic autoimmune diseases and allergies. The present sequence is  
 CC human kappa light constant chain which was used to produce (I).  
 XX SQ Sequence 107 AA;

Query Match 100.0%; Score 553; DB 24; Length 107;  
 Best Local Similarity 100.0%; Pred. No. 6.4e-49;  
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFIPPSDEQLKSGTASVCLNNFYPRKQVQKVDNALQSGNSQESVTEQD 60  
 Db 1 RTVAAPSVFIPPSDEQLKSGTASVCLNNFYPRKQVQKVDNALQSGNSQESVTEQD 60



QY 61 SKDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107  
 |||||  
 DB 61 SKDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107

RESULT 8  
 AAP93559  
 ID AAP93559 standard; protein; 143 AA.

XX AC AAP93559;  
 XX 25-MAR-2003 (updated)  
 DT 28-JAN-1991 (first entry)  
 XX Sequence of human kappa light chain fragment.

XX HIV; antiviral; therapy; diagnosis.

XX Homo sapiens.

XX FH Key Location/Qualifiers  
 XX Region 1..37  
 FT /label=  
 FT /note="light variable and joining"  
 FT 38..38  
 FT /note="light constant"  
 FT 37..38  
 FT /note="insert site"

XX WO902922-A.

XX 06-APR-1989.

XX 03-OCT-1988; 88WO-US03414.

XX 02-OCT-1987; 87US-0104329.

XX 28-SEP-1988; 88US-0250785.

XX (GETH ) GENENTECH INC.

XX Capon DJ, Gregory TJ;

XX WPI; 1989-1114397/15.

XX P-PSDB; AAP93559.

XX New nucleic acid sequences encoding adhesion, esp. CD4, variants -  
 PT partic. with trans-membrane domain inactivated or fused to other  
 PT peptide, useful esp. for treating HIV infections

XX Example; Figure Fig 5; 78pp; English.

XX It is employed in the prepn. of CD4 fusions. The insert site is  
 CC given in the Features Table. CD4 fusion proteins can have antiviral and  
 CC immunomodulatory activity are esp. useful for treating HIV infections,  
 CC regardless of genetic variation within the virus. They and antibodies  
 CC raised against them can also be used diagnostically for assaying adhesions  
 CC and their ligands.

CC (Updated on 25-MAR-2003 to correct PR field.)

CC (Updated on 25-MAR-2003 to correct PA field.)

XX Sequence 143 AA;

Query Match 100.0%; Score 553; DB 10; Length 143;  
 Best Local Similarity 100.0%; Pred. No. 9.2e-49;  
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIFFPPSDQLKSGTASVVCLLNFPYPRKQVQKVDNALQSGNSQESVTEQD 60  
 |||||  
 DB 37 RTVAAPSVFIFFPPSDQLKSGTASVVCLLNFPYPRKQVQKVDNALQSGNSQESVTEQD 96

QY 61 SKDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107

97 SKDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 143

RESULT 9  
 AAM52145  
 ID AAM52145 standard; Protein; 193 AA.

XX AC AAM52145;

XX DT 05-FEB-2002 (first entry)

XX Humanised HMFG1 light chain.

XX Humanised monoclonal antibody; polymorphic epithelial mucin; PEM1;  
 KW cytotoxic; endonuclease; DNase I; human; cytostatic; cancer; apoptosis.  
 XX Synthetic.

XX WO200174905-A1.

XX 11-OCT-2001.

XX 26-MAR-2001; 2001WO-GB01324.

XX 03-APR-2000; 2000GB-0008049.

XX 02-OCT-2000; 2000US-237159P.

XX (ANTI-) ANTISOMA RES LTD.

XX Young RJ;

XX WPI; 2001-662969/76.

XX Novel compound used to treat cancer has target cell-specific portion  
 PT comprising humanised monoclonal antibody having specificity for  
 PT polymorphic epithelial mucin, and cytotoxic portion having  
 PT endonucleolytic activity

XX Claim 20; Figure 3; 176pp; English.

XX The invention relates to a compound which comprises a target  
 CC cell-specific portion, comprising an humanised monoclonal antibody,  
 CC having specificity for polymorphic epithelial mucin (PEM) or its antigen  
 CC binding fragment and a cytotoxic portion having endonucleolytic activity,  
 CC exemplified by AAM52154-AAM52168 and encoded by ABA02682-ABA02728. The  
 CC compound has cytostatic activity useful for treating cancer and acting as  
 CC a potential inducer of apoptosis.

XX Sequence 193 AA;

Query Match 100.0%; Score 553; DB 22; Length 193;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-48;  
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIFFPPSDQLKSGTASVVCLLNFPYPRKQVQKVDNALQSGNSQESVTEQD 60

DB 87 RTVAAPSVFIFFPPSDQLKSGTASVVCLLNFPYPRKQVQKVDNALQSGNSQESVTEQD 146

QY 61 SKDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107

DB 147 SKDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 193

RESULT 10  
 AAY29770  
 ID AAY29770 standard; Protein; 201 AA.

XX AC AAY29770;

XX DT 04-NOV-1999 (first entry)

XX P-selectin ligand and kappa chain constant region fusion protein.

XX Human; P-selectin ligand; glycoprotein; fusion protein; infection;

KW inflammation; intercellular adhesion; ulcerative colitis; asthma;  
 KW diabetes; transplant rejection; myocardial infarction; thermal injury;  
 KW metastatic condition; autoimmune thyroiditis; multiple sclerosis;  
 KW Reynaud's syndrome; neutrophilic dermatosis; Sweet's syndrome;  
 KW Grave's disease; glomerulonephritis; gingivitis; periodontitis;  
 KW Crohn's disease; necrotising enterocolitis.  
 OS Homo sapiens.  
 OS Synthetic.  
 XX WO9943834-A2.  
 XX 02-SEP-1999.  
 XX 25-FEB-1999; 99WO-US04302.  
 XX 27-FEB-1998; 98US-0032080.  
 XX (GEMY ) GENETICS INST INC.  
 XX Camphausen R, Chang X, Cumming D, Davis M, Kumar R;  
 PI Larsen GR, Sako DS, Shaw G, Veldman GW;  
 DR WPI; 1999-527628/44.  
 DR N-PSDB; AA208843.  
 XX New P-selectin ligand fusion proteins, used for treating e.g.  
 PT inflammation, infections, asthma, diabetes, ulcerative colitis or  
 PT transplant rejection  
 XX Claim 66; Page 128-129; 145pp; English.  
 XX The present invention describes P-selectin ligand fusion proteins  
 CC comprising amino acids 42-60, 42-402, 42-310, 42-88, 42-118 or 42-189  
 CC of the P-selectin ligand protein. The fusion proteins comprising a  
 CC P-selectin ligand act as ligands for P-selectin on human endothelial  
 CC cells and platelets. The isolated P-selectin ligand proteins may be  
 CC useful in treating conditions characterized by P-, E- or L-selectin  
 CC mediated intercellular adhesion e.g. myocardial infarction, bacterial  
 CC or viral infection, metastatic conditions, inflammatory disorders,  
 CC thermal injury such as burns or frostbite, autoimmune thyroiditis,  
 CC experimental allergic encephalomyelitis, multiple sclerosis, multiple  
 CC organ injury syndrome secondary to trauma, diabetes, Reynaud's syndrome,  
 CC neutrophilic dermatosis (Sweet's syndrome), inflammatory bowel disease,  
 CC Grave's disease, glomerulonephritis, gingivitis, periodontitis,  
 CC haemolytic uraemic syndrome, ulcerative colitis, Crohn's disease,  
 CC necrotising enterocolitis, granulocyte transfusion associated syndrome,  
 CC or cytokine-induced toxicity. Isolated P-selectin ligand proteins may  
 CC also be useful in organ transplantation, both to prepare organs for  
 CC transplantation and to quell organ transplant rejection. P-selectin  
 CC ligand proteins may be used to treat haemodialysis and leukophoresis  
 CC patients or used as an antimetastatic agent. The fusion proteins can  
 CC also be used to treat a condition which is affected by the protein to  
 CC which the P-selectin ligand protein is fused. The fusion proteins can be  
 CC used for the production of antibodies for use in therapy, detection,  
 CC diagnosis and drug screening. AA208839 to AA208850 encode specifically  
 CC claimed fusion proteins from the present invention, which are given in  
 CC RAY29766 to RAY29777.  
 XX  
 SQ Sequence 201 AA;  
 Query Match 100.0%; Score 553; DB 20; Length 201;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-48;  
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 RTVAAPSVIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60  
 DB 95 RTVAAPSVIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 154  
 QY 61 SKDSTYISLSSTLTLSKADYKHKVACEVTHGQLSSPYTKSFNRGEC 107  
 DB 155 SKDSTYISLSSTLTLSKADYKHKVACEVTHGQLSSPYTKSFNRGEC 201

RESULT 11  
 ABP51955  
 ID ABP51955 standard; Protein; 212 AA.  
 XX  
 AC ABP51955;  
 XX  
 DT 09-OCT-2002 (first entry)  
 XX  
 DE Humanised anti-CD18 kappa LC sequence SEQ ID NO:5.  
 XX  
 KW Bacterial host; protease; degp; prc; spr; anti-VEGF antibody; antibody;  
 KW humanised; Apo2 ligand; anti-CD18; anti-tissue factor; 2C4; anti-CD20;  
 KW anti-vascular endothelial growth factor; anti-Her-2; anti-CD40; Fab;  
 KW anti-CD11a; Fab'; Fab'; Fab'; Fab'; Fab'; Fab'; Fab'; Fab'; Fab'; Fab';  
 XX Homo sapiens.  
 OS Synthetic.  
 XX WO200248376-A2.  
 XX 20-JUN-2002.  
 XX 07-DEC-2001; 2001WO-US47581.  
 XX 14-DEC-2000; 2000US-256162P.  
 XX (GETH ) GENENTECH INC.  
 XX Chen CY;  
 PI WPI; 2002-583522/62.  
 DR Novel Escherichia coli strain useful for producing polypeptide,  
 PT deficient in degp and prc encoding protease, and harboring mutant spr  
 PT gene, product of gene suppresses growth phenotypes of strains harboring  
 PT prc mutants  
 XX Example 1; Fig 10; 63pp; English.  
 XX The present invention describes an Escherichia coli strain (I) deficient  
 CC in chromosomal degp and prc encoding protease Degp and Prc, respectively,  
 CC and harbouring a mutant spr gene, the product of mutant spr gene  
 CC suppresses growth phenotypes exhibited by strains harbouring prc mutants.  
 CC (I) is useful for producing a polypeptide, by culturing (I) comprising  
 CC nucleic acid encoding the polypeptide, which is heterologous to the  
 CC strain, such that the nucleic acid is expressed, and recovering the  
 CC heterologous polypeptide from the strain. The heterologous polypeptide is  
 CC proteolytically sensitive. Culturing of (I) is performed in a fermentor  
 CC under conditions of high- or low-cell density fermentation. The  
 CC polypeptide is recovered from the periplasm or culture medium of the  
 CC strain. The polypeptide is an antibody (humanised or full-length  
 CC antibody) or Apo2 ligand. The antibody is an anti-CD18, anti-vascular  
 CC endothelial growth factor (VEGF), anti-tissue factor, 2C4, anti-Her-2,  
 CC anti-CD20, anti-CD40, or anti-CD11a antibody. The antibody is also an  
 CC antibody fragment having a light chain (kappa light chain). The antibody  
 CC fragment is a Fab, Fab', Fab'/2 or Fab'/2-leucine zipper fusion, anti-CD18  
 CC Fab'/2-leucine zipper fusion, anti-tissue factor Fab'/2-leucine zipper  
 CC fusion or anti-VEGF Fab, with or without a histidine or lysine tag,  
 CC or anti-tissue factor Fab'/2-leucine zipper fusion with a 6-histidine tag,  
 CC or anti-CD18 Fab'/2-leucine zipper fusion with a 6-histidine tag, and  
 CC anti-CD18 Fab'/2-leucine zipper fusion with a 6-lysine tag. The present  
 CC sequence represents a humanised anti-CD18 kappa LC sequence from the  
 CC present invention.  
 XX  
 SQ Sequence 212 AA;  
 Query Match 100.0%; Score 553; DB 23; Length 212;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-48;  
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 RTVAAPSVIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

Db 106 RTVAAPSVFIIPPSPDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 165

QY 61 SKDSTYLSSTLTLSKADYEKHKYACEVTHQGLSSPVTKSFNRGEC 107

Db 166 SKDSTYLSSTLTLSKADYEKHKYACEVTHQGLSSPVTKSFNRGEC 212

RESULT 12

AAW04301

ID AAW04301 standard; Protein; 213 AA.

XX

AC AAW04301;

XX

DT 25-MAR-2003 (updated)

DT 14-FEB-1997 (first entry)

XX

DE Antibody fusion protein.

XX

KW Antibody; fusion protein; recombinant antibody; tumour therapy; prodrug.

KW

XX

OS Synthetic.

XX

PN EP737747-A2.

XX

PD 16-OCT-1996.

XX

PF 13-MAR-1996; 96EP-0103913.

XX

PR 11-APR-1995; 95DE-1013676.

XX

PA (BEHW ) BEHRINGWERKE AG.

XX

FI Bosslet K, Czech J, Oppen M;

XX

DR WPI; 1996-457328/45.

XX

DR N-PSDB; AAT38397.

XX

XX

PT Prodn. of recombinant antibody (Ab), Ab fragment or Ab/enzyme fusion protein - by cytoplasmic expression in thio:redoxin:reductase deficient E. coli

PT

XX

PS Example 1; Figure 5a; 12pp; German.

XX

CC Production of recombinant antibodies (Ab), Ab fragments or Ab fragment/enzyme fusion proteins can be used for tumour therapy, especially when the fusion protein comprises a tumour-specific Ab fragment and an enzyme capable of converting a non-toxic prodrug to a toxic drug. The fusion proteins are constructed in expression vectors and expressed in thiorodoxinreductase deficient E.coli, allowing expression products to be isolated in soluble functional form without renaturation. The Ab fragment is an FAb fragment or an antigen binding region. In the fusion protein, the Ab component is humanised and the enzyme component is a human cytoplasmic enzyme. This fusion protein comprises the antibody constant and variable light chain regions.

CC

CC (Updated on 25-MAR-2003 to correct PR field.)

XX

SQ Sequence 213 AA;

Query Match 100.0%; Score 553; DB 17; Length 213;

Best Local Similarity 100.0%; Pred. No. 1.5e-48;

Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIIPPSPDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

Db 107 RTVAAPSVFIIPPSPDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 166

QY 61 SKDSTYLSSTLTLSKADYEKHKYACEVTHQGLSSPVTKSFNRGEC 107

Db 167 SKDSTYLSSTLTLSKADYEKHKYACEVTHQGLSSPVTKSFNRGEC 213

RESULT 14

AAE10512

ID AAE10512 standard; Protein; 213 AA.

XX

AC AAE10512;

XX

RESULT 13

AAE10510

ID AAE10510 standard; Protein; 213 AA.

XX

AC AAE10510;

XX

DT 10-DEC-2001 (first entry)

XX

DE Humanised high potency antibody clone 25 full length light chain.

XX

KW Human; light chain; respiratory syncytial virus infection; virucide; parainfluenza virus; therapy; high potency antibody; drug; cocaine; cancer cell; toxic substance.

KW

XX

OS Homo sapiens.

OS Synthetic.

XX

PN WO200164751-A2.

XX

PD 07-SEP-2001.

XX

PF 01-MAR-2001; 2001WO-US06815.

XX

PR 01-MAR-2000; 2000US-0186252.

XX

PA (MEDI-) MEDIMMUNE INC.

XX

PI Young JF, Keenig S, Johnson LS, Huse WD, Wu H, Watkins JD;

XX

DR WPI; 2001-582150/65.

XX

XX

PT High potency recombinant antibody, useful for preventing and treating diseases induced or caused by viruses, especially respiratory syncytial virus and parainfluenza virus, has high kinetic association rate constant

PT

XX

PS Claim 23; Page 75-76; 98pp; English.

XX

CC The invention relates to a high potency antibody including its immunologically active portions, fragments and segments other than vitamin. The antibody has increased potency, high rate constant for antibody-antigen complex formation and high affinity for any desired antigen. The high potency antibody is also useful for nullifying or ameliorating the effects of addictive drugs, such as cocaine. The high potency has specificity for antigenic determinants found on microbes such as viruses, bacteria or fungi, antigens found on cancer cells and toxic substances or product of toxic substances. The high potency antibody is useful for preventing or treating a disease caused by a virus such as respiratory syncytial virus (RSV) and parainfluenza virus (PIV). The present sequence is humanised high potency antibody full length light chain variable region.

CC

SQ Sequence 213 AA;

Query Match 100.0%; Score 553; DB 22; Length 213;

Best Local Similarity 100.0%; Pred. No. 1.5e-48;

Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIIPPSPDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

Db 107 RTVAAPSVFIIPPSPDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 166

QY 61 SKDSTYLSSTLTLSKADYEKHKYACEVTHQGLSSPVTKSFNRGEC 107

Db 167 SKDSTYLSSTLTLSKADYEKHKYACEVTHQGLSSPVTKSFNRGEC 213

RESULT 14

AAE10512

ID AAE10512 standard; Protein; 213 AA.

XX

AC AAE10512;

XX

DT 10-DEC-2001 (first entry)  
 XX Humanised high potency antibody clone 26 full length light chain.  
 DE  
 DE  
 KW Human; light chain; respiratory syncytial virus infection; virucide;  
 KW parainfluenza virus; therapy; high potency antibody; drug; cocaine;  
 KW cancer cell; toxic substance.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX WO200164751-A2.  
 XX  
 XX 07-SEP-2001.  
 XX  
 XX 01-MAR-2001; 2001WO-US06815.  
 XX  
 XX 01-MAR-2000; 2000US-0186252.  
 XX  
 XX (MEDI-) MEDIMUNE INC.  
 PA  
 PI Young JF, Koenig S, Johnson LS, Huse WD, Wu H, Watkins JD;  
 XX WPI; 2001-582150/65.  
 DR  
 XX High potency recombinant antibody, useful for preventing and treating  
 PT diseases induced or caused by viruses, especially respiratory syncytial  
 PT virus and parainfluenza virus, has high kinetic association rate  
 PT constant -  
 XX  
 PS Claim 23; Page 78-79; 98pp; English.  
 CC The invention relates to a high potency antibody including its  
 CC immunologically active portions, fragments and segments other than  
 CC vitaxin. The antibody has increased potency, high rate constant for  
 CC antibody-antigen complex formation and high affinity for any desired  
 CC antigen. The high potency antibody is also useful for nullifying or  
 CC ameliorating the effects of addictive drugs, such as cocaine. The high  
 CC potency has specificity for antigenic determinants found on microbes  
 CC such as viruses, bacteria or fungi, antigens found on cancer cells and  
 CC toxic substances or product of toxic substances. The high potency  
 CC antibody is useful for preventing or treating a disease caused by a  
 CC virus such as respiratory syncytial virus (RSV) and parainfluenza  
 CC virus (PIV). The present sequence is humanised high potency antibody  
 CC full length light chain variable region.  
 XX  
 SQ Sequence 213 AA;  
 Query Match 100.0%; Score 553; DB 22; Length 213;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-48;  
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60  
 Db 107 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 166  
 QY 61 SKDSTYSLSTLTLSKADYERKHVYACEVTHQGLSPVTKSFNRGEC 107  
 Db 167 SKDSTYSLSTLTLSKADYERKHVYACEVTHQGLSPVTKSFNRGEC 213  
 QY 61 SKDSTYSLSTLTLSKADYERKHVYACEVTHQGLSPVTKSFNRGEC 107  
 Db 167 SKDSTYSLSTLTLSKADYERKHVYACEVTHQGLSPVTKSFNRGEC 213  
 RESULT 15  
 AAEL0514  
 ID AAE10514 standard; Protein; 213 AA.  
 XX  
 AC AAE10514;  
 XX  
 DT 10-DEC-2001 (first entry)  
 XX  
 XX Humanised high potency antibody clone 18 full length light chain.  
 DE  
 DE  
 KW Human; light chain; respiratory syncytial virus infection; virucide;  
 KW parainfluenza virus; therapy; high potency antibody; drug; cocaine;

KW cancer cell; toxic substance.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX WO200164751-A2.  
 XX  
 XX 07-SEP-2001.  
 XX  
 XX 01-MAR-2001; 2001WO-US06815.  
 XX  
 XX 01-MAR-2000; 2000US-0186252.  
 XX  
 XX (MEDI-) MEDIMUNE INC.  
 PA  
 PI Young JF, Koenig S, Johnson LS, Huse WD, Wu H, Watkins JD;  
 XX WPI; 2001-582150/65.  
 DR  
 XX High potency recombinant antibody, useful for preventing and treating  
 PT diseases induced or caused by viruses, especially respiratory syncytial  
 PT virus and parainfluenza virus, has high kinetic association rate  
 PT constant -  
 XX  
 PS Claim 23; Page 80-81; 98pp; English.  
 CC The invention relates to a high potency antibody including its  
 CC immunologically active portions, fragments and segments other than  
 CC vitaxin. The antibody has increased potency, high rate constant for  
 CC antibody-antigen complex formation and high affinity for any desired  
 CC antigen. The high potency antibody is also useful for nullifying or  
 CC ameliorating the effects of addictive drugs, such as cocaine. The high  
 CC potency has specificity for antigenic determinants found on microbes  
 CC such as viruses, bacteria or fungi, antigens found on cancer cells and  
 CC toxic substances or product of toxic substances. The high potency  
 CC antibody is useful for preventing or treating a disease caused by a  
 CC virus such as respiratory syncytial virus (RSV) and parainfluenza  
 CC virus (PIV). The present sequence is humanised high potency antibody  
 CC full length light chain variable region.  
 XX  
 SQ Sequence 213 AA;  
 Query Match 100.0%; Score 553; DB 22; Length 213;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-48;  
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60  
 Db 107 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 166  
 QY 61 SKDSTYSLSTLTLSKADYERKHVYACEVTHQGLSPVTKSFNRGEC 107  
 Db 167 SKDSTYSLSTLTLSKADYERKHVYACEVTHQGLSPVTKSFNRGEC 213  
 Search completed: January 13, 2004, 12:38:27  
 Job time : 24.9511 secs

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OM protein - protein search, using sw model

Run on: January 13, 2004, 12:43:20 ; Search time 17.1013 Seconds  
(without alignments)  
1260.812 Million cell updates/sec

Title: US-09-990-586-99

Perfect score: 553

Sequence: 1 RTVAAPSVFPPSDEQLKS.....EVTHQGLSSPVTKSFNRGEC 107

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747907 seqs, 201509753 residues

Total number of hits satisfying chosen parameters: 747907

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

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2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep.\*  
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17: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*  
18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	553	100.0	107	9	US-09-811-384-5
2	553	100.0	107	11	US-09-990-586-99
3	553	100.0	107	11	US-09-990-586-99
4	553	100.0	107	12	US-10-159-006-20
5	553	100.0	107	12	US-10-310-113-166
6	553	100.0	107	12	US-10-310-113-166
7	553	100.0	107	12	US-10-310-113-168
8	553	100.0	107	12	US-10-230-880-97
9	553	100.0	107	12	US-10-230-880-99
10	553	100.0	107	12	US-10-366-709-54
11	553	100.0	107	15	US-10-121-464-18
12	553	100.0	107	15	US-10-269-805-67
13	553	100.0	212	14	US-10-320-231A-77
14	553	100.0	212	14	US-10-011-125-5
15	553	100.0	213	9	US-09-796-848A-38
	553	100.0	213	9	US-09-796-848A-40

Sequence 42, Appl  
Sequence 44, Appl  
Sequence 46, Appl  
Sequence 48, Appl  
Sequence 50, Appl  
Sequence 52, Appl  
Sequence 54, Appl  
Sequence 209, App  
Sequence 211, App  
Sequence 211, App  
Sequence 215, App  
Sequence 217, App  
Sequence 219, App  
Sequence 221, App  
Sequence 223, App  
Sequence 225, App  
Sequence 227, App  
Sequence 229, App  
Sequence 231, App  
Sequence 233, App  
Sequence 235, App  
Sequence 237, App  
Sequence 239, App  
Sequence 241, App  
Sequence 243, App  
Sequence 245, App  
Sequence 247, App  
Sequence 251, App  
Sequence 253, App  
Sequence 255, App

16 553 100.0 213 9 US-09-796-848A-42  
17 553 100.0 213 9 US-09-796-848A-44  
18 553 100.0 213 9 US-09-796-848A-46  
19 553 100.0 213 9 US-09-796-848A-48  
20 553 100.0 213 9 US-09-796-848A-50  
21 553 100.0 213 9 US-09-796-848A-52  
22 553 100.0 213 9 US-09-796-848A-54  
23 553 100.0 213 10 US-09-996-288-209  
24 553 100.0 213 10 US-09-996-288-211  
25 553 100.0 213 10 US-09-996-288-213  
26 553 100.0 213 10 US-09-996-288-215  
27 553 100.0 213 10 US-09-996-288-217  
28 553 100.0 213 10 US-09-996-288-219  
29 553 100.0 213 10 US-09-996-288-221  
30 553 100.0 213 10 US-09-996-288-223  
31 553 100.0 213 10 US-09-996-288-225  
32 553 100.0 213 10 US-09-996-288-227  
33 553 100.0 213 10 US-09-996-288-229  
34 553 100.0 213 10 US-09-996-288-231  
35 553 100.0 213 10 US-09-996-288-233  
36 553 100.0 213 10 US-09-996-288-235  
37 553 100.0 213 10 US-09-996-288-237  
38 553 100.0 213 10 US-09-996-288-239  
39 553 100.0 213 10 US-09-996-288-241  
40 553 100.0 213 10 US-09-996-288-243  
41 553 100.0 213 10 US-09-996-288-245  
42 553 100.0 213 10 US-09-996-288-247  
43 553 100.0 213 10 US-09-996-288-251  
44 553 100.0 213 10 US-09-996-288-253  
45 553 100.0 213 10 US-09-996-288-255

#### ALIGNMENTS

#### RESULT 1

US-09-811-384-5  
; Sequence 5, Application US/09811384  
; Patent No. US20020081294A1  
; GENERAL INFORMATION:  
; APPLICANT: Bednar, Martin M.  
; Thomas, G. Roger  
; Gross, Cordell E.  
; TITLE OF INVENTION: ANTI-CD18 ANTIBODIES IN STROKE  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/811,384  
; FILING DATE: 20-Dec-2000  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/251652  
; FILING DATE: 17-FEB-2000  
; APPLICATION NUMBER: 08/788900  
; FILING DATE: 22-JAN-1997  
; APPLICATION NUMBER: 60/093038  
; FILING DATE: 23-JAN-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Love, Richard B.  
; REGISTRATION NUMBER: 34,659  
; REFERENCE/DOCKET NUMBER: P1729C1  
; TELECOMMUNICATION INFORMATION:

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; TELEPHONE: 650/225-5530
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 107 amino acids
;   TYPE: Amino Acid
;   TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-811-384-5

Query Match      100.0%; Score 553; DB 9; Length 107;
Best Local Similarity 100.0%; Pred. No. 6.5e-53;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFPPSPDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 1 RTVAAPSVFPPSPDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

Qy 61 SKDSTVSLSTLTLSKADYEKKHKVYACEVTHQGLSSPVTKSFNRGEC 107
Db 61 SKDSTVSLSTLTLSKADYEKKHKVYACEVTHQGLSSPVTKSFNRGEC 107

RESULT 2
US-09-990-586-97
; Sequence 97, Application US/09990586
; Publication No. US20030109680A1
; GENERAL INFORMATION:
; APPLICANT: JIAO, JIN-AN
; APPLICANT: WONG, HING C.
; TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD COAGULATION AND METHODS
; FILE REFERENCE: 71758/46943-CIP2
; CURRENT APPLICATION NUMBER: US/09/990,586
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 09/293,854
; PRIOR FILING DATE: 1999-04-16
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 97
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-990-586-97

Query Match      100.0%; Score 553; DB 11; Length 107;
Best Local Similarity 100.0%; Pred. No. 6.5e-53;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFPPSPDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 1 RTVAAPSVFPPSPDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

Qy 61 SKDSTVSLSTLTLSKADYEKKHKVYACEVTHQGLSSPVTKSFNRGEC 107
Db 61 SKDSTVSLSTLTLSKADYEKKHKVYACEVTHQGLSSPVTKSFNRGEC 107

RESULT 3
US-09-990-586-99
; Sequence 99, Application US/09990586
; Publication No. US20030109680A1
; GENERAL INFORMATION:
; APPLICANT: JIAO, JIN-AN
; APPLICANT: WONG, HING C.
; TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD COAGULATION AND METHODS
; FILE REFERENCE: 71758/46943-CIP2
; CURRENT APPLICATION NUMBER: US/09/990,586
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 09/293,854
; PRIOR FILING DATE: 1999-04-16
; NUMBER OF SEQ ID NOS: 102
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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 99
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-990-586-99

Query Match      100.0%; Score 553; DB 11; Length 107;
Best Local Similarity 100.0%; Pred. No. 6.5e-53;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFPPSPDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 1 RTVAAPSVFPPSPDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

Qy 61 SKDSTVSLSTLTLSKADYEKKHKVYACEVTHQGLSSPVTKSFNRGEC 107
Db 61 SKDSTVSLSTLTLSKADYEKKHKVYACEVTHQGLSSPVTKSFNRGEC 107

RESULT 4
US-10-159-006-20
; Sequence 20, Application US/10159006
; Publication No. US20030143229A1
; GENERAL INFORMATION:
; APPLICANT: Park, John E.
; APPLICANT: Garin-Chesa, Pilar
; APPLICANT: Bamberger, Uwe
; APPLICANT: Leger, Olivier
; APPLICANT: Saldanha, Jose W.
; APPLICANT: Rettig, Wolfgang J.
; TITLE OF INVENTION: FAPA-specific Antibody with Improved Producibility
; FILE REFERENCE: 0652.1890002
; CURRENT APPLICATION NUMBER: US/10/159,006
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US 09/301,593
; PRIOR FILING DATE: 1999-04-29
; PRIOR APPLICATION NUMBER: EP 98107925.4
; PRIOR FILING DATE: 1998-04-30
; PRIOR APPLICATION NUMBER: US 60/086,049
; PRIOR FILING DATE: 1998-05-18
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-159-006-20

Query Match      100.0%; Score 553; DB 12; Length 107;
Best Local Similarity 100.0%; Pred. No. 6.5e-53;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFPPSPDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 1 RTVAAPSVFPPSPDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

Qy 61 SKDSTVSLSTLTLSKADYEKKHKVYACEVTHQGLSSPVTKSFNRGEC 107
Db 61 SKDSTVSLSTLTLSKADYEKKHKVYACEVTHQGLSSPVTKSFNRGEC 107

RESULT 5
US-10-310-113-166
; Sequence 166, Application US/10310113
; Publication No. US20030176664A1
; GENERAL INFORMATION:
; APPLICANT: JIAO, JIN-AN
; APPLICANT: WONG, HING C.
; APPLICANT: NIEVES, ESPERANZA LILIANA
; APPLICANT: MOSQUERA, LUIS A.
; TITLE OF INVENTION: USE OF ANTI-TISSUE FACTOR ANTIBODIES FOR TREATING
; TITLE OF INVENTION: THROMBOSES
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; FILE REFERENCE: 58122(71758)
; CURRENT APPLICATION NUMBER: US/10/310,113
; CURRENT FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: 09/990,586
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/343,306
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/293,854
; PRIOR FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: 08/814,806
; PRIOR FILING DATE: 1997-03-10
; NUMBER OF SEQ ID NOS: 169
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 166
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-310-113-166

Query Match      100.0%; Score 553; DB 12; Length 107;
Best Local Similarity 100.0%; Pred. No. 6.5e-53;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIFFPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
DB 1 RTVAAPSVFIFFPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
QY 61 SKDSTYLSSTLTLSKADYKHKYKVIACEVTHQGLSSPVTKSFNRGEC 107
DB 61 SKDSTYLSSTLTLSKADYKHKYKVIACEVTHQGLSSPVTKSFNRGEC 107

RESULT 6
US-10-310-113-168
; Sequence 168, Application US/10310113
; Publication No. US20030176664A1
; GENERAL INFORMATION:
; APPLICANT: JIAO, JIN-AN
; APPLICANT: WONG, HING C.
; APPLICANT: NIEVES, ESPERANZA LILIANA
; APPLICANT: MOSQUERA, LUIS A.
; TITLE OF INVENTION: USE OF ANTI-TISSUE FACTOR ANTIBODIES FOR TREATING
; TITLE OF INVENTION: THROMBOSES
; FILE REFERENCE: 58122(71758)
; CURRENT APPLICATION NUMBER: US/10/310,113
; CURRENT FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: 09/990,586
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/343,306
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/293,854
; PRIOR FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: 08/814,806
; PRIOR FILING DATE: 1997-03-10
; NUMBER OF SEQ ID NOS: 169
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 168
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-310-113-168

Query Match      100.0%; Score 553; DB 12; Length 107;
Best Local Similarity 100.0%; Pred. No. 6.5e-53;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIFFPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
DB 1 RTVAAPSVFIFFPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
QY 61 SKDSTYLSSTLTLSKADYKHKYKVIACEVTHQGLSSPVTKSFNRGEC 107
DB 61 SKDSTYLSSTLTLSKADYKHKYKVIACEVTHQGLSSPVTKSFNRGEC 107
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RESULT 7
US-10-230-880-97
; Sequence 97, Application US/10230880
; Publication No. US20030190705A1
; GENERAL INFORMATION:
; APPLICANT: WONG, HING C.
; APPLICANT: STINSON, JEFFREY L.
; APPLICANT: MOSQUERA, LUIS A.
; TITLE OF INVENTION: METHOD OF HUMANIZING IMMUNE SYSTEM MOLECULES
; FILE REFERENCE: 71758/58066
; CURRENT APPLICATION NUMBER: US/10/230,880
; CURRENT FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: 09/990,586
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/343,306
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/293,854
; PRIOR FILING DATE: 1999-04-16
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 97
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-230-880-97

Query Match      100.0%; Score 553; DB 12; Length 107;
Best Local Similarity 100.0%; Pred. No. 6.5e-53;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIFFPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
DB 1 RTVAAPSVFIFFPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
QY 61 SKDSTYLSSTLTLSKADYKHKYKVIACEVTHQGLSSPVTKSFNRGEC 107
DB 61 SKDSTYLSSTLTLSKADYKHKYKVIACEVTHQGLSSPVTKSFNRGEC 107

RESULT 8
US-10-230-880-99
; Sequence 99, Application US/10230880
; Publication No. US20030190705A1
; GENERAL INFORMATION:
; APPLICANT: WONG, HING C.
; APPLICANT: STINSON, JEFFREY L.
; APPLICANT: MOSQUERA, LUIS A.
; TITLE OF INVENTION: METHOD OF HUMANIZING IMMUNE SYSTEM MOLECULES
; FILE REFERENCE: 71758/58066
; CURRENT APPLICATION NUMBER: US/10/230,880
; CURRENT FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: 09/990,586
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/343,306
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/293,854
; PRIOR FILING DATE: 1999-04-16
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 99
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-230-880-99

Query Match      100.0%; Score 553; DB 12; Length 107;
Best Local Similarity 100.0%; Pred. No. 6.5e-53;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIFFPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
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Db 1 RTVAAPSVFI PPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60  
QY 61 SKDSTYSLSTLTLSKADYKHKVYACEVTHOGLSSPVTKSFNRGEC 107  
Db 61 SKDSTYSLSTLTLSKADYKHKVYACEVTHOGLSSPVTKSFNRGEC 107

RESULT 9  
US-10-366-709-54  
; Sequence 54, Application US/10366709  
; Publication No. US20030219433A1  
; GENERAL INFORMATION:  
; APPLICANT: HANSEN, HANS  
; APPLICANT: QU, ZHENGXING  
; APPLICANT: GOLDENBERG, DAVID M.  
; TITLE OF INVENTION: ANTI-CD20 ANTIBODIES AND FUSION PROTEINS THEREOF AND  
; FILE REFERENCE: 18733/115  
; CURRENT APPLICATION NUMBER: US/10/366,709  
; CURRENT FILING DATE: 2003-02-14  
; PRIOR APPLICATION NUMBER: 60/356,132  
; PRIOR FILING DATE: 2002-02-14  
; PRIOR APPLICATION NUMBER: 60/416,232  
; PRIOR FILING DATE: 2002-10-07  
; NUMBER OF SEQ ID NOS: 55  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 54  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-366-709-54

Query Match 100.0%; Score 553; DB 12; Length 107;  
Best Local Similarity 100.0%; Pred. No. 6.5e-53;  
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFI PPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60  
Db 1 RTVAAPSVFI PPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60  
QY 61 SKDSTYSLSTLTLSKADYKHKVYACEVTHOGLSSPVTKSFNRGEC 107  
Db 61 SKDSTYSLSTLTLSKADYKHKVYACEVTHOGLSSPVTKSFNRGEC 107

RESULT 10  
US-10-121-464-18  
; Sequence 18, Application US/10121464  
; Publication No. US20030103968A1  
; GENERAL INFORMATION:  
; APPLICANT: Boehringer Ingelheim International GmbH  
; APPLICANT: Boehringer Ingelheim Pharmaceuticals, Inc.  
; TITLE OF INVENTION: Cancer treatment by using FAP-alpha specific antibodies  
; FILE REFERENCE: 1-1203ff  
; CURRENT APPLICATION NUMBER: US/10/121,464  
; CURRENT FILING DATE: 2002-11-15  
; PRIOR APPLICATION NUMBER: US 60/283,868  
; PRIOR FILING DATE: 2001-04-12  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 18  
; LENGTH: 107  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Antibody  
US-10-121-464-18

Query Match 100.0%; Score 553; DB 15; Length 107;  
Best Local Similarity 100.0%; Pred. No. 6.5e-53;  
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFI PPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60  
Db 1 RTVAAPSVFI PPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60  
QY 61 SKDSTYSLSTLTLSKADYKHKVYACEVTHOGLSSPVTKSFNRGEC 107  
Db 61 SKDSTYSLSTLTLSKADYKHKVYACEVTHOGLSSPVTKSFNRGEC 107

RESULT 11  
US-10-269-805-67  
; Sequence 67, Application US/10269805  
; Publication No. US20030124129A1  
; GENERAL INFORMATION:  
; APPLICANT: OLINER, JONATHAN D.  
; TITLE OF INVENTION: ANGIOPOIETIN-2 SPECIFIC BINDING AGENTS  
; FILE REFERENCE: A-722  
; CURRENT APPLICATION NUMBER: US/10/269,805  
; CURRENT FILING DATE: 2002-10-10  
; PRIOR APPLICATION NUMBER: US 60/328,604  
; PRIOR FILING DATE: 2001-10-11  
; NUMBER OF SEQ ID NOS: 76  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 67  
; LENGTH: 107  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-269-805-67

Query Match 100.0%; Score 553; DB 15; Length 107;  
Best Local Similarity 100.0%; Pred. No. 6.5e-53;  
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFI PPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60  
Db 1 RTVAAPSVFI PPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60  
QY 61 SKDSTYSLSTLTLSKADYKHKVYACEVTHOGLSSPVTKSFNRGEC 107  
Db 61 SKDSTYSLSTLTLSKADYKHKVYACEVTHOGLSSPVTKSFNRGEC 107

RESULT 12  
US-10-320-231A-77  
; Sequence 77, Application US/10320231A  
; Publication No. US20030194405A1  
; GENERAL INFORMATION:  
; APPLICANT: Neben, Steven  
; APPLICANT: Takeuchi, Toshihiko  
; APPLICANT: Tomkinson, Adrian  
; TITLE OF INVENTION: Antibody Inhibiting Stem Cell Factor Activity And Use For  
; TITLE OF INVENTION: Treatment Of Asthma  
; FILE REFERENCE: 7430\*163  
; CURRENT APPLICATION NUMBER: US/10/320,231A  
; CURRENT FILING DATE: 2002-12-19  
; PRIOR APPLICATION NUMBER: US 60/342,174  
; PRIOR FILING DATE: 2001-12-17  
; NUMBER OF SEQ ID NOS: 85  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 77  
; LENGTH: 212  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: synthetic sequence  
US-10-320-231A-77

Query Match 100.0%; Score 553; DB 12; Length 212;  
Best Local Similarity 100.0%; Pred. No. 1.5e-52;  
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFI PPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60



QY 1 RTVAAPSVFIPPSPDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60  
DB 107 RTVAAPSVFIPPSPDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 166  
QY 61 SKDSTYSLSTLTLSKADYKHKYKHYACEVTHQGLSSPVTKSFNRGEC 107  
DB 167 SKDSTYSLSTLTLSKADYKHKYKHYACEVTHQGLSSPVTKSFNRGEC 213

RESULT 15

US-09-796-848A-40  
; Sequence 40, Application US/09796848A  
; Patent No. US20020098189A1  
; GENERAL INFORMATION:  
; APPLICANT: Young, James F.  
; APPLICANT: Johnson, Leslie S.  
; APPLICANT: Huse, William D.  
; APPLICANT: Wu, Herren  
; APPLICANT: Watkins, Jeffrey D.  
; TITLE OF INVENTION: High Potency Recombinant Antibodies and Methods of  
; FILE REFERENCE: 469201-526  
; CURRENT APPLICATION NUMBER: US/09/796,848A  
; PRIOR FILING DATE: 2001-10-30  
; PRIOR APPLICATION NUMBER: U.S. 60/186,252  
; NUMBER OF SEQ ID NOS: 59  
; SOFTWARE: Patent in Ver. 2.1  
; SEQ ID NO 40  
; LENGTH: 213  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Light chain of  
; OTHER INFORMATION: high potency antibody.  
US-09-796-848A-40

Query Match 100.0%; Score 553; DB 9; Length 213;  
Best Local Similarity 100.0%; Pred. No. 1.5e-52;  
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIPPSPDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60  
DB 107 RTVAAPSVFIPPSPDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 166  
QY 61 SKDSTYSLSTLTLSKADYKHKYKHYACEVTHQGLSSPVTKSFNRGEC 107  
DB 167 SKDSTYSLSTLTLSKADYKHKYKHYACEVTHQGLSSPVTKSFNRGEC 213

Search completed: January 13, 2004, 13:13:46  
Job time : 18.1013 secs

DB 106 RTVAAPSVFIPPSPDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 165  
QY 61 SKDSTYSLSTLTLSKADYKHKYKHYACEVTHQGLSSPVTKSFNRGEC 107  
DB 166 SKDSTYSLSTLTLSKADYKHKYKHYACEVTHQGLSSPVTKSFNRGEC 212

RESULT 13

US-10-011-125-5  
; Sequence 5, Application US/10011125  
; Publication No. US20020142389A1  
; GENERAL INFORMATION:  
; APPLICANT: Chen, Christina Yu-Ching  
; TITLE OF INVENTION: BACTERIAL HOST STRAINS  
; FILE REFERENCE: P1804K1  
; CURRENT APPLICATION NUMBER: US/10/011,125  
; CURRENT FILING DATE: 2001-12-07  
; PRIOR APPLICATION NUMBER: US 60/256,162  
; PRIOR FILING DATE: 2000-12-14  
; NUMBER OF SEQ ID NOS: 10  
; SEQ ID NO 5  
; LENGTH: 212  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Sequence is synthesized.  
US-10-011-125-5

Query Match 100.0%; Score 553; DB 14; Length 212;  
Best Local Similarity 100.0%; Pred. No. 1.5e-52;  
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIPPSPDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60  
DB 106 RTVAAPSVFIPPSPDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 165  
QY 61 SKDSTYSLSTLTLSKADYKHKYKHYACEVTHQGLSSPVTKSFNRGEC 107  
DB 166 SKDSTYSLSTLTLSKADYKHKYKHYACEVTHQGLSSPVTKSFNRGEC 212

RESULT 14

US-09-796-848A-38  
; Sequence 38, Application US/09796848A  
; Patent No. US20020098189A1  
; GENERAL INFORMATION:  
; APPLICANT: Young, James F.  
; APPLICANT: Johnson, Leslie S.  
; APPLICANT: Huse, William D.  
; APPLICANT: Wu, Herren  
; APPLICANT: Watkins, Jeffrey D.  
; TITLE OF INVENTION: High Potency Recombinant Antibodies and Methods of  
; FILE REFERENCE: 469201-526  
; CURRENT APPLICATION NUMBER: US/09/796,848A  
; CURRENT FILING DATE: 2001-10-30  
; PRIOR APPLICATION NUMBER: U.S. 60/186,252  
; PRIOR FILING DATE: 2000-03-01  
; NUMBER OF SEQ ID NOS: 59  
; SOFTWARE: Patent in Ver. 2.1  
; SEQ ID NO 38  
; LENGTH: 213  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Light chain of  
; OTHER INFORMATION: high potency antibody.  
US-09-796-848A-38

Query Match 100.0%; Score 553; DB 9; Length 213;  
Best Local Similarity 100.0%; Pred. No. 1.5e-52;  
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 13, 2004, 12:33:50 ; Search time 9.25153 Seconds  
(without alignments)  
489.353 Million cell updates/sec

Title: US-09-990-586-99  
Perfect score: 553  
Sequence: 1 RTVAAPSVFIPPSDEQLKS.....EVTHGGLSSPVTKSNRGEK 107

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA.\*  
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3: /cgn2\_6/ptodata/1/1aa/6A.COMB.pdp.\*  
4: /cgn2\_6/ptodata/1/1aa/6B.COMB.pdp.\*  
5: /cgn2\_6/ptodata/1/1aa/PTUS.COMB.pdp.\*  
6: /cgn2\_6/ptodata/1/1aa/backfiles.pdp.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	553	100.0	107	1	US-08-422-101-8
2	553	100.0	107	1	US-08-422-091-8
3	553	100.0	107	2	US-08-422-092-8
4	553	100.0	107	2	US-08-788-800-5
5	553	100.0	107	3	US-08-422-093-8
6	553	100.0	107	3	US-08-422-112-8
7	553	100.0	107	4	US-09-301-593-20
8	553	100.0	213	3	US-08-630-820-6
9	553	100.0	213	1	US-08-397-411-12
10	553	100.0	214	1	US-08-458-516-12
11	553	100.0	214	2	US-07-934-373C-24
12	553	100.0	214	2	US-07-934-373C-39
13	553	100.0	214	2	US-07-934-373C-40
14	553	100.0	214	2	US-08-480-753-6
15	553	100.0	214	2	US-08-788-800-11
16	553	100.0	214	3	US-09-041-889-11
17	553	100.0	214	3	US-08-437-642B-24
18	553	100.0	214	3	US-08-437-642B-39
19	553	100.0	214	3	US-08-437-642B-40
20	553	100.0	214	3	US-08-837-058-11
21	553	100.0	214	3	US-09-097-309-2
22	553	100.0	214	3	US-08-397-411-5
23	553	100.0	214	3	US-09-097-171A-2
24	553	100.0	214	4	US-09-247-352-4
25	553	100.0	214	4	US-09-460-587-2
26	553	100.0	214	4	US-09-679-397-1
27	553	100.0	214	4	US-08-146-206C-24

28	553	100.0	214	4	US-09-466-635-4	Sequence 4, Appl
29	553	100.0	214	4	US-09-680-148-1	Sequence 1, Appl
30	553	100.0	214	4	US-09-289-942A-6	Sequence 6, Appl
31	553	100.0	214	4	US-09-304-465A-1	Sequence 1, Appl
32	553	100.0	214	4	US-09-417-264-11	Sequence 11, Appl
33	553	100.0	214	5	PCT-US93-07832-24	Sequence 24, Appl
34	553	100.0	214	5	PCT-US93-07832-39	Sequence 39, Appl
35	553	100.0	214	5	PCT-US93-07832-40	Sequence 40, Appl
36	553	100.0	215	2	US-08-480-753-8	Sequence 8, Appl
37	553	100.0	218	2	US-08-887-352B-13	Sequence 13, Appl
38	553	100.0	218	2	US-08-887-352B-15	Sequence 15, Appl
39	553	100.0	218	2	US-08-887-352B-17	Sequence 17, Appl
40	553	100.0	218	2	US-08-887-352B-19	Sequence 19, Appl
41	553	100.0	218	2	US-08-887-352B-24	Sequence 24, Appl
42	553	100.0	218	3	US-08-466-151-9	Sequence 9, Appl
43	553	100.0	218	3	US-09-109-207C-13	Sequence 13, Appl
44	553	100.0	218	3	US-09-109-207C-15	Sequence 15, Appl
45	553	100.0	218	3	US-09-109-207C-17	Sequence 17, Appl

ALIGNMENTS

RESULT 1  
US-08-422-101-8  
; Sequence 8, Application US/08422101  
; Patent No. 5732277  
; GENERAL INFORMATION:  
; APPLICANT: Leonard Presta  
; APPLICANT: Brad Snedecor  
; TITLE OF INVENTION: Altered Polypeptides with Increased  
; TITLE OF INVENTION: Half-Life  
; NUMBER OF SEQUENCES: 31  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: patin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/422,101  
; FILING DATE: 14-APR-1995  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lee, Wendy M.  
; REGISTRATION NUMBER:  
; REFERENCE/DOCKET NUMBER: 932-3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415/225-1994  
; TELEFAX: 415/952-9881  
; TELEX: 910/371-7168  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 107 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
US-08-422-101-8

Query Match 100.0%; Score 553; DB 1; Length 107;  
Best Local Similarity 100.0%; Pred. No. 4.9e-57;  
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 RTVAAPSVFIPPSDEQLKSGTASVVCLLNNFYPREAKVQMKVNDALQSGNSQSVTQD 60  
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Db 1 RTVAAPSVFIIPPDSDEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQSVTEQD 60  
 QY 61 SKDSTYLSSTLTLSKADYKHKYVACEVTHQGLSSPVTXSFNRGEC 107  
 Db 61 SKDSTYLSSTLTLSKADYKHKYVACEVTHQGLSSPVTXSFNRGEC 107

## RESULT 2

US-08-422-091-8  
 ; Sequence 8, Application US/08422091  
 ; Patent No. 5747035  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Leonard Presta  
 ; APPLICANT: Brad Snedecor  
 ; TITLE OF INVENTION: Altered Polypeptides with Increased  
 ; TITLE OF INVENTION: Half-Life  
 ; NUMBER OF SEQUENCES: 31  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Genentech, Inc.  
 ; STREET: 460 Point San Bruno Blvd  
 ; CITY: South San Francisco  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 94080  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: patin (Genentech)  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/422,091  
 ; FILING DATE: 14-APR-1995  
 ; CLASSIFICATION: 424  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER:  
 ; FILING DATE:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Lee, Wendy M.  
 ; REGISTRATION NUMBER:  
 ; REFERENCE/DOCKET NUMBER: 932-6  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 415/225-1994  
 ; TELEFAX: 415/952-9881  
 ; TELEX: 910/371-7168  
 ; INFORMATION FOR SEQ ID NO: 8:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 107 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; APPLICATION NUMBER:  
 ; FILING DATE:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Lee, Wendy M.  
 ; REGISTRATION NUMBER:  
 ; REFERENCE/DOCKET NUMBER: 932-6  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 415/225-1994  
 ; TELEFAX: 415/952-9881  
 ; TELEX: 910/371-7168  
 ; INFORMATION FOR SEQ ID NO: 8:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 107 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear

## US-08-422-091-8

Query Match 100.0%; Score 553; DB 1; Length 107;  
 Best Local Similarity 100.0%; Pred. No. 4.9e-57;  
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIIPPDSDEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQSVTEQD 60  
 Db 1 RTVAAPSVFIIPPDSDEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQSVTEQD 60  
 QY 61 SKDSTYLSSTLTLSKADYKHKYVACEVTHQGLSSPVTXSFNRGEC 107  
 Db 61 SKDSTYLSSTLTLSKADYKHKYVACEVTHQGLSSPVTXSFNRGEC 107

## RESULT 3

US-08-422-092-8  
 ; Sequence 8, Application US/08422092  
 ; Patent No. 5869046  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Leonard Presta  
 ; APPLICANT: Brad Snedecor  
 ; TITLE OF INVENTION: Altered Polypeptides with Increased  
 ; TITLE OF INVENTION: Half-Life

NUMBER OF SEQUENCES: 31  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Genentech, Inc.  
 STREET: 460 Point San Bruno Blvd  
 CITY: South San Francisco  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94080  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: patin (Genentech)  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/422,092  
 FILING DATE: 14-APR-1995  
 CLASSIFICATION: 530  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER:  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Lee, Wendy M.  
 REGISTRATION NUMBER:  
 REFERENCE/DOCKET NUMBER: 932-4  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 415/225-1994  
 TELEFAX: 415/952-9881  
 TELEX: 910/371-7168  
 INFORMATION FOR SEQ ID NO: 8:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 107 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 APPLICATION NUMBER:  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Lee, Wendy M.  
 REGISTRATION NUMBER:  
 REFERENCE/DOCKET NUMBER: 932-4  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 415/225-1994  
 TELEFAX: 415/952-9881  
 TELEX: 910/371-7168  
 INFORMATION FOR SEQ ID NO: 8:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 107 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear

## US-08-422-092-8

Query Match 100.0%; Score 553; DB 2; Length 107;  
 Best Local Similarity 100.0%; Pred. No. 4.9e-57;  
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIIPPDSDEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQSVTEQD 60  
 Db 1 RTVAAPSVFIIPPDSDEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQSVTEQD 60  
 QY 61 SKDSTYLSSTLTLSKADYKHKYVACEVTHQGLSSPVTXSFNRGEC 107  
 Db 61 SKDSTYLSSTLTLSKADYKHKYVACEVTHQGLSSPVTXSFNRGEC 107

## RESULT 4

US-08-788-800-5  
 ; Sequence 5, Application US/08788800  
 ; Patent No. 5914112  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bednar, Martin M.  
 ; APPLICANT: Thomas, G. Roger  
 ; APPLICANT: Gross, Cordell E.  
 ; TITLE OF INVENTION: ANTI-CD18 ANTIBODIES IN STROKE  
 ; NUMBER OF SEQUENCES: 15  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Genentech, Inc.  
 ; STREET: 460 Point San Bruno Blvd  
 ; CITY: South San Francisco  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 94080  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: WinPatin (Genentech)  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/788,800  
 ; FILING DATE: 22-Jan-1997

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CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0987r1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: Amino acid
TOPOLOGY: Linear
US-08-788-800-5

Query Match 100.0%; Score 553; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 4.9e-57;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFIIPPSPDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 1 RTVAAPSVFIIPPSPDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Qy 61 SKDSTYSLSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 107
Db 61 SKDSTYSLSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 107

RESULT 5
US-08-422-093-8
Sequence 8, Application US/08422093
Patent No. 6096871
GENERAL INFORMATION:
APPLICANT: Leonard Presta
TITLE OF INVENTION: Altered Polypeptides with Increased
TITLE OF INVENTION: Half-Life
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patin (Genentech)
CURRENT APPLICATION DATA:
FILING DATE: 14-APR-1995
CLASSIFICATION: 536
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 932-1
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-422-093-8

Query Match 100.0%; Score 553; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 4.9e-57;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFIIPPSPDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 1 RTVAAPSVFIIPPSPDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Qy 61 SKDSTYSLSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 107
Db 61 SKDSTYSLSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 107

RESULT 6
US-08-422-112-8
Sequence 8, Application US/08422112
Patent No. 6121022
GENERAL INFORMATION:
APPLICANT: Leonard Presta
TITLE OF INVENTION: Altered Polypeptides with Increased
TITLE OF INVENTION: Half-Life
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patin (Genentech)
CURRENT APPLICATION DATA:
FILING DATE: 14-APR-1995
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 932-1
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-422-112-8

Query Match 100.0%; Score 553; DB 3; Length 107;
Best Local Similarity 100.0%; Pred. No. 4.9e-57;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFIIPPSPDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 1 RTVAAPSVFIIPPSPDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Qy 61 SKDSTYSLSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 107
Db 61 SKDSTYSLSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 107

RESULT 7
US-09-301-593-20
Sequence 20, Application US/09301593A
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Query Match 100.0%; Score 553; DB 3; Length 107;
Best Local Similarity 100.0%; Pred. No. 4.9e-57;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFIIPPSPDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 1 RTVAAPSVFIIPPSPDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Qy 61 SKDSTYSLSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 107
Db 61 SKDSTYSLSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 107

RESULT 6
US-08-422-112-8
Sequence 8, Application US/08422112
Patent No. 6121022
GENERAL INFORMATION:
APPLICANT: Leonard Presta
TITLE OF INVENTION: Altered Polypeptides with Increased
TITLE OF INVENTION: Half-Life
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patin (Genentech)
CURRENT APPLICATION DATA:
FILING DATE: 14-APR-1995
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 932-1
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-422-112-8

Query Match 100.0%; Score 553; DB 3; Length 107;
Best Local Similarity 100.0%; Pred. No. 4.9e-57;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFIIPPSPDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 1 RTVAAPSVFIIPPSPDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Qy 61 SKDSTYSLSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 107
Db 61 SKDSTYSLSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 107

RESULT 7
US-09-301-593-20
Sequence 20, Application US/09301593A
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Patent No. 6455677  
GENERAL INFORMATION:  
APPLICANT: Park, John E.  
APPLICANT: Garin-Chesa, Pilar  
APPLICANT: Bamberger, Uwe  
APPLICANT: Leget, Olivier  
APPLICANT: Saldanha, Jose W.  
APPLICANT: Rettig, Wolfgang J.  
TITLE OF INVENTION: FAP-specific Antibody with Improved Producibility  
FILE REFERENCE: 0652.189001  
CURRENT APPLICATION NUMBER: US/09/301,593A  
CURRENT FILING DATE: 1999-04-29  
EARLIER APPLICATION NUMBER: EP 98107925.4  
EARLIER FILING DATE: 1998-04-30  
EARLIER APPLICATION NUMBER: US 60/086,049  
EARLIER FILING DATE: 1998-05-18  
NUMBER OF SEQ ID NOS: 108  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 20  
LENGTH: 107  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-301-593-20

Query Match 100.0%; Score 553; DB 4; Length 107;  
Best Local Similarity 100.0%; Pred. No. 4.9e-57; Indels 0; Gaps 0;  
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIFFPSDEQLKSGTASVVLNNFYPREAKVQWVDNALQSGNSQESVTEQD 60  
Db 1 RTVAAPSVFIFFPSDEQLKSGTASVVLNNFYPREAKVQWVDNALQSGNSQESVTEQD 60

QY 61 SKDSTYSLSTLTSLKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 107  
Db 61 SKDSTYSLSTLTSLKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 107

RESULT 8  
US-08-630-820-6  
Sequence 6, Application US/08630820  
Patent No. 6008023  
GENERAL INFORMATION:  
APPLICANT: Oppen, Martin  
APPLICANT: BOSSLET, Klaus  
APPLICANT: CZECH, Joerg  
TITLE OF INVENTION: CYTOLASMIC EXPRESSION OF ANTIBODIES,  
TITLE OF INVENTION: ANTIBODY FRAGMENTS AND ANTIBODY FRAGMENT FUSION MOLECULES  
TITLE OF INVENTION: IN E. COLI  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/630,820  
FILING DATE: 10-APR-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE 19513676.4  
FILING DATE: 11-APR-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: GRANADOS, Patricia D.  
REGISTRATION NUMBER: 33,683  
REFERENCE/DOCKET NUMBER: 18749/306  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300

TELEFAX: (202)672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 213 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-630-820-6

Query Match 100.0%; Score 553; DB 3; Length 213;  
Best Local Similarity 100.0%; Pred. No. 1.2e-56; Indels 0; Gaps 0;  
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIFFPSDEQLKSGTASVVLNNFYPREAKVQWVDNALQSGNSQESVTEQD 60  
Db 107 RTVAAPSVFIFFPSDEQLKSGTASVVLNNFYPREAKVQWVDNALQSGNSQESVTEQD 166

QY 61 SKDSTYSLSTLTSLKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 107  
Db 167 SKDSTYSLSTLTSLKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 213

RESULT 9  
US-08-397-411-12  
Sequence 12, Application US/08397411  
Patent No. 6129914  
GENERAL INFORMATION:  
APPLICANT: Weiner, George  
APPLICANT: Gingsrich, Roger  
APPLICANT: Link, Brian  
APPLICANT: Tso, J. Yun  
TITLE OF INVENTION: Bispecific Antibody Effective to Treat  
TITLE OF INVENTION: B-Cell Lymphoma and Cell Line  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew  
STREET: One Market Plaza, Steuart Tower, Suite 2000  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/397,411  
FILING DATE: 01-MAR-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/859,583  
FILING DATE: 27-MAR-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 011823-004901  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-326-2400  
TELEFAX: 415-326-2422  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 213 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-397-411-12

Query Match 100.0%; Score 553; DB 3; Length 213;  
Best Local Similarity 100.0%; Pred. No. 1.2e-56; Indels 0; Gaps 0;  
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIFFPSDEQLKSGTASVVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQD 60  
| | | | |  
Db 107 RTVAAPSVFIFFPSDEQLKSGTASVVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQD 166  
| | | | |  
QY 61 SKDSTYLSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107  
| | | | |  
Db 167 SKDSTYLSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 213  
| | | | |

RESULT 10  
US-08-458-516-12  
; Sequence 12, Application US/08458516  
; Patent No. 5777085  
; GENERAL INFORMATION:  
; APPLICANT: Co, Man Sung  
; APPLICANT: Tso, J. Yun  
; TITLE OF INVENTION: Humanized Antibodies Reactive with  
; TITLE OF INVENTION: GPIIb/IIIa  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: William M. Smith  
; STREET: One Market Plaza, Steuart Tower, Suite 2000  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94105

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/458,516  
; FILING DATE:  
; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/059,159  
; FILING DATE: 03-MAY-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M.  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 11823-37-3  
; TELEPHONE: 415-326-2400  
; TELEFAX: 415-326-2422  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 214 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein

US-08-458-516-12

Query Match 100.0%; Score 553; DB 1; Length 214;  
Best Local Similarity 100.0%; Pred. No. 1.2e-56;  
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIFFPSDEQLKSGTASVVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQD 60  
| | | | |  
Db 108 RTVAAPSVFIFFPSDEQLKSGTASVVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQD 167  
| | | | |  
QY 61 SKDSTYLSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107  
| | | | |  
Db 168 SKDSTYLSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 214  
| | | | |

RESULT 11  
US-07-934-373C-24  
; Sequence 24, Application US/07934373C  
; Patent No. 5821337  
; GENERAL INFORMATION:

; APPLICANT: Paul J. Carter  
; APPLICANT: Leonard G. Presta  
; TITLE OF INVENTION: Immunoglobulin Variants  
; NUMBER OF SEQUENCES: 48  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/934,373C  
; FILING DATE: 21-Aug-1992  
; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US92/05126  
; FILING DATE: 15-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/715272  
; FILING DATE: 14-JUN-1991  
; ATTORNEY/AGENT INFORMATION:

; NAME: Lee, Wendy M.  
; REGISTRATION NUMBER: 40,378  
; REFERENCE/DOCKET NUMBER: P0709P2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-1994  
; TELEFAX: 650/952-9881

; INFORMATION FOR SEQ ID NO: 24:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 214 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear

US-07-934-373C-24

Query Match 100.0%; Score 553; DB 2; Length 214;  
Best Local Similarity 100.0%; Pred. No. 1.2e-56;  
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIFFPSDEQLKSGTASVVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQD 60  
| | | | |  
Db 108 RTVAAPSVFIFFPSDEQLKSGTASVVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQD 167  
| | | | |  
QY 61 SKDSTYLSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107  
| | | | |  
Db 168 SKDSTYLSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 214  
| | | | |

RESULT 12  
US-07-934-373C-39  
; Sequence 39, Application US/07934373C  
; Patent No. 5821337  
; GENERAL INFORMATION:

; APPLICANT: Paul J. Carter  
; APPLICANT: Leonard G. Presta  
; TITLE OF INVENTION: Immunoglobulin Variants  
; NUMBER OF SEQUENCES: 48  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS

```

SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/934,373C
FILING DATE: 21-AUG-1992
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P2
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 214 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-07-934-373C-39

Query Match 100.0%; Score 553; DB 2; Length 214;
Best Local Similarity 100.0%; Pred. No. 1.2e-56;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIPPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
DB 108 RTVAAPSVFIPPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 167
QY 61 SKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 107
DB 168 SKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 214

RESULT 14
US-07-934-373C-6
Sequence 6, Application US/08480753
Patent No. 5830675
GENERAL INFORMATION:
APPLICANT: Targan M.D., Stephan R.
APPLICANT: Vidrich Ph.D., Alda M.
TITLE OF INVENTION: METHODS FOR SELECTIVELY DETECTING
PERINUCLEAR ANTI-NEUTROPHIL CYTOPLASMIC ANTIBODY OF
TITLE OF INVENTION: ULCERATIVE COLITIS, PRIMARY SCLEROSING CHOLANGITIS,
TITLE OF INVENTION: TYPE I AUTOIMMUNE HEPATITIS
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wendy A. Whiteford, Esq.
STREET: 444 South Flower Street, Suite 2000
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patencin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,753
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Whiteford, Wendy A.
REGISTRATION NUMBER: 36,964
REFERENCE/DOCKET NUMBER: P07 33571
TELEPHONE: (213) 622-7700
TELEFAX: (213) 489-4210
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 214 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-480-753-6

Query Match 100.0%; Score 553; DB 2; Length 214;
Best Local Similarity 100.0%; Pred. No. 1.2e-56;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIPPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
DB 108 RTVAAPSVFIPPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 167
QY 61 SKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 107
DB 168 SKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 214

RESULT 13
US-07-934-373C-40
Sequence 40, Application US/07934373C
Patent No. 5821337
GENERAL INFORMATION:
APPLICANT: Paul J. Carter
APPLICANT: Leonard G. Presta
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/934,373C
FILING DATE: 21-AUG-1992
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P2

```

QY 61 SKDSTYSLSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 107  
Db 168 SKDSTYSLSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 214

## RESULT 15

US-08-788-800-11  
; Sequence 11, Application US/08788800  
; Patent No. 5914112  
; GENERAL INFORMATION:  
; APPLICANT: Bednar, Martin M.  
; APPLICANT: Thomas, G. Roger  
; APPLICANT: Gross, Cordell E.  
; TITLE OF INVENTION: ANTI-CD18 ANTIBODIES IN STROKE  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/788,800  
; FILING DATE: 22-Jan-1997  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lee, Wendy M.  
; REGISTRATION NUMBER: 40,378  
; REFERENCE/DOCKET NUMBER: P0987r1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415/225-1994  
; TELEFAX: 415/952-9881  
; TELEX: 910/371-7168  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 214 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
US-08-788-800-11

Query Match 100.0%; Score 553; DB 2; Length 214;  
Best Local Similarity 100.0%; Pred. No. 1.2e-56;  
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIIPPDEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQESVTEQD 60  
Db 108 RTVAAPSVFIIPPDEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQESVTEQD 167  
QY 61 SKDSTYSLSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 107  
Db 168 SKDSTYSLSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 214

Search completed: January 13, 2004, 12:46:35  
Job time : 9.25153 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 13, 2004, 12:22:35 ; Search time 23.8489 Seconds  
(without alignments)  
1326.664 Million cell updates/sec

Title: US-09-990-586-100

Perfect score: 1754

Sequence: 1 EFASKGPSVFPLAPCSRST.....MHEALNHYTKSLSLSLK 329

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR\_76.\*

1: Pir1.\*

2: Pir2.\*

3: Pir3.\*

4: Pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1743	99.4	327	1	G4HU	Ig gamma-4 chain C
2	1605.5	91.5	326	1	G8HU	Ig gamma-2 chain C
3	1590.5	90.7	330	1	G8HU	Ig gamma-1 chain C
4	1585	90.4	377	2	A50764	Ig gamma-3 chain C
5	1575	89.8	377	2	A23511	Ig gamma-3 chain C
6	1289.5	73.5	328	2	I47159	Ig gamma 2a chain
7	1283.5	73.2	328	2	I47160	Ig gamma 2b chain
8	1264.5	72.1	328	2	I47161	Ig gamma 1 chain C
9	1240.5	70.7	328	2	I47158	Ig gamma 1 chain C
10	1199	68.4	323	1	GHRB	Ig gamma chain C r
11	1189	68.4	472	2	S31459	Ig gamma-1 chain -
12	1185	66.6	470	2	S22080	Ig heavy chain pre
13	1158	66.0	329	1	G2GP	Ig gamma-2 chain C
14	1147	65.4	308	2	S30554	Ig heavy chain C r
15	1143	65.2	374	2	S69339	Ig heavy chain V r
16	1139.5	65.0	255	4	S31866	Ig gamma-1 chain C
17	1129.5	64.4	234	2	PT0207	Ig gamma chain C r
18	1124	64.1	333	2	P80018	Ig gamma-2b chain C
19	1118.5	63.8	326	2	P80017	Ig gamma-1 chain C
20	1118.5	63.8	444	2	P4436	monoclonal antibody
21	1108.5	63.2	289	1	G3HUW1	Ig gamma-3 heavy c
22	1108	63.2	329	2	S00847	Ig gamma-2c chain C
23	1106.5	63.1	324	1	G1MS	Ig gamma-1 chain C
24	1106.5	63.1	330	1	G2MSA	Ig gamma-2a chain
25	1106.5	63.1	469	2	S37483	Ig gamma-2a chain
26	1103	62.9	327	2	S06611	Ig gamma-2 chain C
27	1101.5	62.8	393	1	G1MSM	Ig gamma-1 chain C
28	1101.5	62.8	399	1	G2MSAB	Ig gamma-2a chain
29	1099	62.7	335	1	G2MSAB	Ig gamma-2a chain

30	1098.5	62.6	329	1	G3MSC	Ig gamma-3 chain C
31	1091.5	62.2	446	2	S40295	Ig gamma-2a chain
32	1090.5	62.2	398	1	G3MSM	Ig gamma-3 chain C
33	1085.5	61.9	277	2	I47162	Ig gamma 4 chain c
34	1084.5	61.8	322	2	P80019	Ig gamma-2a chain
35	1049.5	59.8	405	1	G2MSBM	Ig gamma-2b chain
36	1032	58.8	474	1	G2MS11	Ig gamma-2b chain
37	1027.5	58.6	475	2	S01321	Ig gamma-2b chain
38	684	39.0	180	2	I46732	Ig gamma heavy cha
39	644	36.7	548	2	S38864	Ig epsilon chain VHI
40	568.5	32.4	249	2	S69340	Ig heavy chain pre
41	566.5	32.3	549	2	S04845	Ig heavy chain pre
42	553.5	31.6	241	2	S69131	Ig heavy chain (DO
43	551	31.4	152	2	S14236	Ig gamma-1 chain C
44	549	31.3	218	2	A36040	Ig heavy chain V-I
45	496	28.3	429	1	EHRT	Ig epsilon chain C

## ALIGNMENTS

### RESULT 1

G4HU

Ig gamma-4 chain C region - human

C:Species: Homo sapiens (man)

C>Date: 02-Apr-1982 #sequence revision 02-Apr-1982 #text\_change 16-Jul-1999

A:Accession: A90933; A90249; A02150

R:Ellison, J.; Buxbaum, J.; Hood, L.

DNA 1, 11-18, 1981

A:Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.

A:Reference number: A90933; MUID:83157104; PMID:6299662

A:Accession: A90933

A:Molecule type: DNA

A:Residues: 1-327 <ELL>

A>Note: the sequence was determined from the germline gene

R:Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.

Biochem. J. 117, 33-47, 1970

A:Title: Human immunoglobulin subclasses. Partial amino acid sequence of the constant r

A:Reference number: A90249; MUID:70207560; PMID:4192699

A:Accession: A90249

A:Molecule type: protein

A:Residues: 1-30; 81-326 <PIN>

C:Genetics:

A:Gene: GDB:IGHG4

A:Cross-references: GDB:119340; OMIM:147130

A:Map position: 14q32.33-14q32.33

A:Introns: 95/1; 111/1; 221/1

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap)

chain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into la:

C:Superfamily: immunoglobulin C region; immunoglobulin homology

C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin

F;20-85/Domain: immunoglobulin homology <IM1>

F;99-110/Region: hinge

F;134-203/Domain: immunoglobulin homology <IM2>

F;240-307/Domain: immunoglobulin homology <IM3>

F;14/Disulfide bonds: interchain (to light chain) #status experimental

F;27-93, 141-201, 247-305/Disulfide bonds: #status predicted

F;106, 109/Disulfide bonds: interchain (to heavy chain) #status experimental

F;177/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 99.4%; Score 1743; DB 1; Length 327;

Best Local Similarity 100.0%; Pred. No. 7e-115;

Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ASTKGPSVFPLAPCSRSTSEALGCLVKDYFPPPTVSWNSGALTSGVHTFPAVLQSS 62

Db 1 ASTKGPSVFPLAPCSRSTSEALGCLVKDYFPPPTVSWNSGALTSGVHTFPAVLQSS 60

QY 63 GLYSLSVVTVFSSSLGTYTCNVDPKPSNTKVDKRVESKYGPPCPAPDFLGGPSV 122

Db 61 GLYSLSVVTVFSSSLGTYTCNVDPKPSNTKVDKRVESKYGPPCPAPDFLGGPSV 120

QY 123 FLFPPKPKDTLMSRTPVTCVVVDVSDPEQEDPEVFQFNWYDVGVENVNAKTKPREEQFNSTY 182

Db	121	FLPPKPKDLMISRPVETCVVDVSDQEDPEVQFVWYVDGVEVHNAKTKPREEQFNSTY	180
Qy	183	RVSVSLFVLHODWLMNGKEYCKVSNKGLPSSIEKTKISKAGQPREPQVYTLPPSQEEMTK	242
Db	181	RVSVSLFVLHODWLMNGKEYCKVSNKGLPSSIEKTKISKAGQPREPQVYTLPPSQEEMTK	240
Qy	243	NOVSLTCLVKGFPSPDIAVWESNGQPNENYKTPPVLDSGDSGFFLYSLTLVDKSRWQSG	302
Db	241	NOVSLTCLVKGFPSPDIAVWESNGQPNENYKTPPVLDSGDSGFFLYSLTLVDKSRWQSG	300
Qy	303	NVFCSCVMHEALHNYTKSLSLGK	329
Db	301	NVFCSCVMHEALHNYTKSLSLGK	327
RESULT 2			
GzHU			
Ig gamma-2 chain C region - human			
C:Species: Homo sapiens (man)			
C:Date: 30-Apr-1981 #sequence revision 13-Jun-1983 #text_change 21-Jul-2000			
C:Accession: A93906; A92809; A90752; A93132; A02148			
R:Ellison, J.; Hood, L.			
Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982			
A:Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain con			
A:Reference number: A93906; MUID:82197621; PMID:6804948			
A:Accession: A93906			
A:Molecule type: DNA			
A:Residues: 1-326 <ELL>			
A:Cross-references: GB:V00554; GB:J00230; NID:G32759; PIDN:CAB58438.1; PID:G6066056			
A:Note: Lys-326 is probably removed posttranslationally			
R:Wang, A.C.; Tung, E.; Fudenberg, H.H.			
J. Immunol. 125, 1048-1054, 1980			
A:Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and f			
A:Reference number: A92809; MUID:81007873; PMID:6774012			
A:Contents: myeloma protein Til			
A:Accession: A92809			
A:Molecule type: protein			
A:Residues: 1-19,'Q',21-57,'Z',59,'A',61-193,'D',195-325 <WAN>			
A:Note: Trp-156 is at or near the complement-binding site			
R:Hofmann, G.E.; Parr, D.M.; Hofmann, T.			
Can. J. Biochem. 57, 758-767, 1979			
A:Title: The amino acid sequences of the three heavy chain constant region domains of a			
A:Reference number: A90752; MUID:80001357; PMID:113060			
A:Contents: myeloma protein Zie			
A:Accession: A90752			
A:Molecule type: Protein			
A:Residues: 1-24,'B',26-57,'EV',60-85;132-171,'ZZZ',175,'B',177-193,'D',195-196,'Q',198-			
A:Note: this sequence has since been revised			
R:Hofmann, T.; Parr, D.M.			
Mol. Immunol. 16, 923-925, 1979			
A:Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin g			
A:Reference number: A93132; MUID:80114419; PMID:118920			
A:Contents: Zie			
A:Accession: A93132			
A:Molecule type: protein			
A:Residues: 238-275 <HOP>			
R:Hofmann, T.; Parr, D.M.			
submitted to the Atlas, March 1980			
A:Reference number: A94591			
A:Contents: annotation; Zie, revisions to residues 25, 59, 60, and 264-268			
A:Note: the revised sequence differs from that shown in having 60-Ala and in the amidati-			
ned			
R:Milstein, C.; Frangione, B.			
Biochem. J. 121, 217-225, 1971			
A:Title: Disulfide bridges of the heavy chain of human immunoglobulin G2.			
A:Reference number: A90253; MUID:72033500; PMID:4940472			
A:Contents: annotation; myeloma protein Sa, disulfide bonds			
R:Frangione, B.; Milstein, C.; Fink, J.R.L.			
Nature 221, 145-148, 1969			
A:Title: Structural studies of immunoglobulin G.			
A:Reference number: A93157; MUID:69064124; PMID:5782707			
A:Contents: annotation; Sa, disulfide bonds			
C:Genetics:			
A:Gene: GDB:IGHG2			
A:Cross-references: GDB:119338; OMIM:147110			
A:Map position: 14q32.33-14q32.33			
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kai			
chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into li			
C:Superfamily: immunoglobulin C region; immunoglobulin homology			
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin			
F:20-85/Domain: immunoglobulin homology <IM1>			
F:133-202/Domain: immunoglobulin homology <IM2>			
F:239-306/Domain: immunoglobulin homology <IM3>			
F:14/Disulfide bonds: interchain (to light chain) #status experimental			
F:27-83;140-200,246-304/Disulfide bonds: #status experimental			
F:102,103,106,109/Disulfide bonds: interchain (to heavy chain) #status experimental			
F:176/Binding site: carbohydrate (Asn) (covalent) #status predicted			
Query Match			
Best Local Similarity 91.5%; Score 1605.5; DB 1; Length 326;			
Matches 302; Conservative 10; Mismatches 14; Indels 1; Gaps 1;			
Qy	3	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS	62
Db	1	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS	60
Qy	63	GLYSLSVVTVFSSSLGKTTCNVDPKPSNTKVDKVESKYGPPCPSCPAPELFGPSV	122
Db	61	GLYSLSVVTVFSSNFGQTTCNVDPKPSNTKVDKVERKCCVCCPCAPP-VAGPSV	119
Qy	123	FLFPPKPKDLMISRPVETCVVDVSDQEDPEVQFVWYVDGVEVHNAKTKPREEQFNSTY	182
Db	120	FLFPPKPKDLMISRPVETCVVDVSDQEDPEVQFVWYVDGVEVHNAKTKPREEQFNSTF	179
Qy	183	RVSVSLTVLHODWLMNGKEYCKVSNKGLPSSIEKTKISKAGQPREPQVYTLPPSQEEMTK	242
Db	180	RVSVSLTVLHODWLMNGKEYCKVSNKGLPAPIEKTKISKAGQPREPQVYTLPPSQEEMTK	239
Qy	243	NOVSLTCLVKGFPSPDIAVWESNGQPNENYKTPPVLDSGDSGFFLYSLTLVDKSRWQEG	302
Db	240	NOVSLTCLVKGFPSPDIAVWESNGQPNENYKTPPMLDSGDSGFFLYSLTLVDKSRWQOG	299
Qy	303	NVFCSCVMHEALHNYTKSLSLGK	329
Db	300	NVFCSCVMHEALHNYTKSLSLGK	326
RESULT 3			
GHU			
Ig gamma-1 chain C region - human			
C:Species: Homo sapiens (man)			
C:Date: 31-Jan-1981 #sequence revision 18-Aug-1982 #text change 16-Jul-1999			
C:Accession: A93433; S36861; S3887; B90563; A90564; B91668; A91723; A02146			
R:Ellison, J.W.; Berson, B.J.; Hood, L.E.			
Nucleic Acids Res. 10, 4071-4079, 1982			
A:Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.			
A:Reference number: A93433; MUID:82274238; PMID:6287432			
A:Accession: A93433			
A:Molecule type: DNA			
A:Residues: 1-330 <ELL>			
A:Cross-references: EMBL:Z17370			
A:Note: this sequence has the G1m(17) allotypic marker, 97-Lys, and the G1m(1) markers,			
A:Note: Lys-330 is removed after translation			
R:Harris, L.J.			
submitted to the EMBL Data Library, October 1992			
A:Reference number: S33904			
A:Accession: S36861			
A:Molecule type: DNA			
A:Residues: 2-330 <HAR>			
A:Cross-references: EMBL:Z17370			
R:Takahashi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Honjo, T.			
Cell 29, 671-679, 1982			
A:Title: Structure of human immunoglobulin gamma genes: implications for evolution of a			
A:Reference number: S33887; MUID:83001943; PMID:6811139			
A:Accession: S33887			

A:Molecule type: DNA  
A:Residues: 88-113:235-330 <TAK>  
A:Cross-references: EMBL:Z17370  
R:Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman, Biochemistry 9, 3161-3170, 1970  
A:Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid sequence  
A:Reference number: A90563; MUID:71064024; PMID:5489771  
A:Contents: myeloma protein Eu  
A:Accession: B90563  
A:Molecule type: protein  
A:Residues: 1-96, 'R', 98-135 <CUN>  
A:Note: this sequence has the G1m(3) marker; 97-Arg  
R:Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M. Biochemistry 9, 3171-3181, 1970  
A:Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid sequence  
A:Reference number: A90564; MUID:71064025; PMID:5530842  
A:Contents: Eu  
A:Accession: A90564  
A:Molecule type: Protein  
A:Residues: 136-154, 'Q', 156-165, 'Q', 167-176, 'Q', 178-194, 'N', 196-197, 'D', 199-238, 'E', 240, 'A'; Note: this sequence has the G1m(non-1) markers, 239-Glu and 241-Met  
R:Ponstingl, H.; Hilschmann, N.  
Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976  
A:Title: Die Primaerstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Nie), igen Primaerstruktur  
A:Reference number: A91668; MUID:77070269; PMID:826475  
A:Contents: myeloma protein Nie  
A:Accession: B91668  
A:Molecule type: protein  
A:Residues: 1-34, 'Q', 36-96, 'K', 98-115, 'Q', 117-197, 'D', 199-238, 'D', 240, 'L', 242-268, 'E', 270, 'A'; Note: this sequence has the G1m(17) and G1m(1) markers  
R:Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.  
Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983  
A:Title: Die Primaerstruktur des kristallisierten monoklonalen Immunglobulins IgG1 KOL  
A:Reference number: A91723; MUID:83289131; PMID:6884994  
A:Contents: myeloma protein KOL; disulfide bonds  
A:Accession: A91723  
A:Molecule type: protein  
A:Residues: 1-96, 'R', 98-197, 'D', 199-238, 'E', 240, 'M', 242-266, 'D', 268-271, 'D', 273-330 <SCH>  
A:Note: this sequence has the G1m(3) and G1m(non-1) markers  
R:Gall, W.E.; Edelman, G.M.  
Biochemistry 9, 3188-3196, 1970  
A:Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfide bonds  
A:Reference number: A90565; MUID:71064027; PMID:4923144  
A:Contents: annotation; disulfide bonds  
R:Dreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.  
Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976  
A:Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglobulin  
A:Reference number: A91667; MUID:77070267; PMID:1002129  
A:Contents: annotation; disulfide bonds  
C:Genetics:  
A:Gene: GDB:IGHG1  
A:Cross-references: GDB:120085; OMIM:147100  
A:Map position: 14q32.33-14q32.33  
A:Introns: 99/1; 114/1; 224/1  
A:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into higher order complexes.  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin  
F:20-85/Domain: immunoglobulin homology <IM1>  
F:137-206/Domain: immunoglobulin homology <IM2>  
F:243-310/Domain: immunoglobulin homology <IM3>  
F:72-83, 144-204, 250-308/Disulfide bonds: #status experimental  
F:103/Disulfide bonds: interchain (to light chain) #status experimental  
F:109, 112/Disulfide bonds: interchain (to heavy chain) #status experimental  
F:180/Binding site: carbohydrate (Asn) (covalent) #status experimental

Db 1 ASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60  
QY 63 GLYSLSVVTVPPSSSLGKTTCNVNDHKPSNTKVDKRVESK---YGPSPCSCPAPEFLGG 119  
Db 61 GLYSLSVVTVPPSSSLGKTTCNVNDHKPSNTKVDKRVESKCDKTHCTCPCPAPELLGG 120  
QY 120 PSVFLFPPPKDITLMISRTPEVTCVVDVSDQEDPEVQFNWVDGVEVHNATKREEOFN 179  
Db 121 PSVFLFPPPKDITLMISRTPEVTCVVDVSHEDPEVQFNWVDGVEVHNATKREEOYN 180  
QY 180 STYRVSVTLTVLHODWLNKGYKCKVSNKGLPSSIEKTIKAKGQPREPQVYTLPPSQEE 239  
Db 181 STYRVSVTLTVLHODWLNKGYKCKVSNKGLPSSIEKTIKAKGQPREPQVYTLPPSRDE 240  
QY 240 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSLRTVDKSRW 299  
Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSLRTVDKSRW 300  
QY 300 CBGKVFSCSVNHEALHNHYTQKSLSLGLK 329  
Db 301 QGQNVFSCSVNHEALHNHYTQKSLSLSPGK 330  
RESULT 4  
A60764  
IG gamma-3 chain C region, form LAT - human  
C:Species: Homo sapiens (man)  
C:Date: 14-May-1993 #sequence\_revision 14-May-1993 #text\_change 16-Jul-1999  
C:Accession: A60764  
R:Huck, S.; Lefranc, G.; Lefranc, M.P.  
Immunogenetics 30, 250-257, 1989  
A:Title: A human immunoglobulin IGHG3 allele (Gmb0, b1, c3, c5, u) with an IGHG4 convert  
A:Reference number: A60764; MUID:90007613; PMID:2571587  
A:Accession: A60764  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-377 <HUC>  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: immunoglobulin  
F:20-85/Domain: immunoglobulin homology <IM>  
Query Match 90.4%; Score 1585; DB 2; Length 377;  
Best Local Similarity 80.6%; Pred. No. 9.9e-104;  
Matches 304; Conservative 8; Mismatches 15; Indels 50; Gaps 1;  
QY 3 ASTKGPSVFPLAPCSRSSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 62  
Db 1 ASTKGPSVFPLAPCSRSSTSGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60  
QY 63 GLYSLSVVTVPPSSSLGKTTCNVNDHKPSNTKVDKRVESK---YGPSPCSCPAPEFLGG 120  
Db 61 GLYSLSVVTVPPSSSLGKTTCNVNDHKPSNTKVDKRVESK---YGPSPCSCPAPEFLGG 120  
QY 104 -----YGPSPCSCPAPEFLGGPSVFLLFPKPKDT 132  
Db 121 DTPPPCPCPCPCSCDTPPPCPCPCPCDTPPPCPCPCPCDTPPPCPCPCPCDTPPPCPCPCDTP 180  
QY 133 LMSRTPEVTCVVDVSDQEDPEVQFNWVDGVEVHNATKREEOFNSTYRVSVTLTVLH 192  
Db 181 LMSRTPEVTCVVDVSHEDPEVQFNWVDGVEVHNATKREEOFNSTYRVSVTLTVLH 240  
QY 193 QDWLNKGYKCKVSNKGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVK 252  
Db 241 QDWLNKGYKCKVSNKGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVK 300  
QY 253 GFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSLRTVDKSRWQGNVFSVWME 312  
Db 301 GFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSLRTVDKSRWQGNVFSVWME 360  
QY 313 ALHNHYTQKSLSLGLK 329  
Db 361 ALHNHYTQKSLSLSPGK 377

```

RESULT 5
A23511
Ig gamma-3 chain C region (allotype G3m(b)) - human
C:Species: Homo sapiens (man)
C>Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 23-Jul-1999
C:Accession: A23511
R:Huck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.
Nucleic Acids Res. 14, 1779-1789, 1986
A:Title: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene: c
A:Reference number: A23511; MUID:86148507; PMID:3081877
A:Accession: A23511
A:Molecule type: DNA
A:Residues: 1-377 <HUC>
A:Cross-references: GB:X03604; GB:M12958; NID:g33070; PIDN:CAA27268.1; PID:g577056
C:Genetics:
A:Gene: GDB:IGHG3
A:Map position: 14q32.33-14q32.33
A:Introns: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:20-85/Domain: immunoglobulin homology <IMM>

Query Match      89.8%; Score 1575; DB 2; Length 377;
Best Local Similarity 79.6%; Pred. No. 5e-103;
Matches 300; Conservative 12; Mismatches 15; Indels 50; Gaps 1;

QY 3 ASTKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 62
Db 1 ASTKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
QY 63 GLYSLSVVTVFSSSLGKTTCNVDPKSNKVDKVESK----- 103
Db 61 GLYSLSVVTVFSSSLGKTTCNVDPKSNKVDKVESK----- 103
QY 104 -----YGPCCPCAPAFLOGPSVFPFPKPKDT 132
Db 121 DTPPPCPKPCPKSDTPPPCPKPCPKSDTPPPCPKPCPKSDTPPPCPKPCPKDT 180
QY 133 LMISTPVTCTVVDVSDQDEVOFNWYDGVGVHNAKTPREQNSRYRVSVLTVLH 192
Db 181 LMISTPVTCTVVDVSDQDEVOFNWYDGVGVHNAKTPREQNSRYRVSVLTVLH 240
QY 193 QDWLNGKEYCKVKSNKGLPSSIEKTIKAKGQPREPOVYTPPPSQQEMTKNQVSLTCLVK 252
Db 241 QDWLNGKEYCKVKSNKGLPAPLPIEKTIKAKGQPREPOVYTPPPSQQEMTKNQVSLTCLVK 300
QY 253 GYPSDIAVEESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQSGNVFSCSMHE 312
Db 301 GYPSDIAVEESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQSGNVFSCSMHE 360
QY 313 ALHNHYTQKSLSLGLK 329
Db 361 ALHNRYTQKSLSLSPGK 377

RESULT 6
I47159
Ig gamma 2a chain constant region - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C:Accession: I47159
R:Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A:Title: Five putative subclasses of swine Igg identified from the cDNA sequences of a
A:Reference number: I47158; MUID:95015845; PMID:7930579
A:Accession: I47159
A:Molecule type: mRNA
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Residues: 1-328 <KAC>
A:Cross-references: EMBL:U03779; NID:g433123; PIDN:AAA52217.1; PID:g433124
C:Superfamily: immunoglobulin C region; immunoglobulin homology
F:133-202/Domain: immunoglobulin homology <IMM>

Query Match      73.2%; Score 1283.5; DB 2; Length 328;
Best Local Similarity 71.7%; Pred. No. 1.1e-82;
Matches 236; Conservative 39; Mismatches 51; Indels 3; Gaps 2;

QY 3 ASTKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 62
Db 1 AKTAPLVYPLAPCGRDTSGPNVALGCLASSYFPPEPVTVSWNSGALTSGVHTFPAVLQSS 60
QY 63 GLYSLSVVTVFSSSLGKTTCNVDPKSNKVDKVESKYPGPCPCAPAFELGPGSV 122
Db 61 GLYSLSVVTVFSSSLGKTTCNVDPKSNKVDKVESKYPGPCPCAPAFELGPGSV 119
QY 123 FLPPPKPKDTLMISRTPEVTCVVVDVSDQDEPPVQVFNWYDGVGVHNAKTPREQNSRY 182
Db 120 FIFPPKPKDTLMISRTPEVTCVVVDVSDQDEPPVQVFNWYDGVGVHNAKTPREQNSRY 179
QY 183 RVSVLTVLHQDWLNGKEYCKVKSNKGLPSSIEKTIKAKGQPREPOVYTPPPSQQEMTK 242
Db 180 RVSVLTPIHQDWLNGKEYCKVKSNKGLPAPLPIEKTIKAKGQPREPOVYTPPPHAEELSR 239

RESULT 7
I47160
Ig gamma 2b chain constant region - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C:Accession: I47160
R:Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A:Title: Five putative subclasses of swine Igg identified from the cDNA sequences of a
A:Reference number: I47158; MUID:95015845; PMID:7930579
A:Accession: I47160
A:Molecule type: mRNA
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Residues: 1-328 <KAC>
A:Cross-references: EMBL:U03780; NID:g433125; PIDN:AAA52218.1; PID:g433126
C:Superfamily: immunoglobulin C region; immunoglobulin homology
F:133-202/Domain: immunoglobulin homology <IMM>

Query Match      73.2%; Score 1283.5; DB 2; Length 328;
Best Local Similarity 71.7%; Pred. No. 1.1e-82;
Matches 236; Conservative 39; Mismatches 51; Indels 3; Gaps 2;

QY 3 ASTKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 62
Db 1 AKTAPLVYPLAPCGRDTSGPNVALGCLASSYFPPEPVTVSWNSGALTSGVHTFPAVLQSS 60
QY 63 GLYSLSVVTVFSSSLGKTTCNVDPKSNKVDKVESKYPGPCPCAPAFELGPGSV 122
Db 61 GLYSLSVVTVFSSSLGKTTCNVDPKSNKVDKVESKYPGPCPCAPAFELGPGSV 119
QY 123 FLPPPKPKDTLMISRTPEVTCVVVDVSDQDEPPVQVFNWYDGVGVHNAKTPREQNSRY 182
Db 120 FIFPPKPKDTLMISRTPEVTCVVVDVSDQDEPPVQVFNWYDGVGVHNAKTPREQNSRY 179
QY 183 RVSVLTVLHQDWLNGKEYCKVKSNKGLPSSIEKTIKAKGQPREPOVYTPPPSQQEMTK 242
Db 180 RVSVLTPIHQDWLNGKEYCKVKSNKGLPAPLPIEKTIKAKGQPREPOVYTPPPHAEELSR 239

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in Gamma Globulins, Nobel Symp. 3, Killander, J., ed., pp.109-127, Almqvist and Wiksell, A;Reference number: A94416  
 A;Accession: A94416  
 A;Molecule type: protein  
 A;Residues: 123-131;155-172, 'D', 174-184, 'A', 186, 'E', 188-200, 'D', 202-217, 'E', 219-232, 'Q', 'A';Note: this has the e15 allotypic marker, 185-Ala  
 C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap) chain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into la C;Superfamily: immunoglobulin C region; immunoglobulin homology  
 C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin  
 F;20-82/Domain: immunoglobulin homology <IM1>  
 F;130-193/Domain: immunoglobulin homology <IM2>  
 F;236-303/Domain: immunoglobulin homology <IM3>  
 F;173/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 68.4%; Score 1199; DB 1; Length 323;  
 Best Local Similarity 69.0%; Pred. No. 9e-77;  
 Matches 225; Conservative 35; Mismatches 58; Indels 8; Gaps 3;

QY 6 KPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPTVSNHGALTSVHTFPAVLQSSGLY 65  
 Db 4 KAPSVFPPLAPCGDTPSSVTILGCLVKGYLPEPTVTWNSGTLNGVTRTPSVRQSSGLY 63

QY 66 SLSSVVTVPSSSLGKTTCNVNDHKPSNTKVDKVESKYGPCC--PSCPAPFELGSPSVF 123  
 Db 64 SLSSVSVTSSS---QPVTCNVAHPATNTKVDKVAPS---TCSKPTCPPELLGGPSVF 117

QY 124 LPPPKPKDTLMISRTPEVTCVVDVSDQEDPEVQFNWYVDGVEVNAKTKPREQFNSTYR 183  
 Db 118 LPPPKPKDTLMISRTPEVTCVVDVSDQEDPEVQFNWYVDGVEVNAKTKPREQFNSTIR 177

QY 184 VVSVLTVLHQDLWNGKEYCKVSKNGKLPSSIEKTSKAKGQPREPQVYVTPPSSQEMTKN 243  
 Db 178 VVSTPIPIHQDLWNGKEYCKVSKNGKLPSSIEKTSKAKGQPREPQVYVTPPSSQEMTKN 237

QY 244 QVSLTCLVKGFYPSDIAEVWESNGQPNYKTTTPVLDSDGSEFFLYSLRITVDKSRWQEGN 303  
 Db 238 VSVLTCMNGFYPSDISVEWENKGAEDNYKTTTPVLDSDGSEFFLYSLRITVDKSRWQEGN 297

QY 304 VFSCSVMEALHNHYTKQSLSLGK 329  
 Db 298 VFSCSVMEALHNHYTKQSLSLGK 323

RESULT 11  
 S31459  
 I;Gamma-1 chain - sheep (fragment)  
 C;Species: Ovis orientalis aries; Ovis ammon aries (domestic sheep)  
 C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 16-Jul-1999  
 C;Accession: S31459  
 R;Patri, S.; Nau, F.  
 submitted to the EMBL Data Library, December 1992  
 A;Reference number: S31459  
 A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Residues: 1-472 <PAT>  
 A;Cross-references: EMBL:X6797  
 C;Superfamily: immunoglobulin C region; immunoglobulin homology  
 C;Keywords: immunoglobulin  
 F;277-346/Domain: immunoglobulin homology <IMM>

Query Match 68.4%; Score 1199; DB 2; Length 472;  
 Best Local Similarity 67.5%; Pred. No. 1.5e-76;  
 Matches 226; Conservative 34; Mismatches 63; Indels 12; Gaps 3;

QY 3 ASTKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPTVSNHGALTSVHTFPAVLQSS 62  
 Db 142 ASTTPKPVPLSSCCGDTSSIVTLGCLVSSYMPEPTVTWNSGALTSVHTFPAVLQSS 201

QY 63 GLYSLSVVTVPSSSLGTYTCNVNDHKPSNTKVDKVESKYGPCC-----CPAPEF 116  
 Db 202 GLYSLSVVTVPASTSGAQTFCICNVAHPASTTKVDKVE-----PGCPDPCKRCRCPPEL 257

QY 117 LGSPSVFLPPPKPKDTLMISRTPEVTCVVDVSDQEDPEVQFNWYVDGVEVNAKTKPREE 176  
 Db 258 PGSPSVFLPPPKPKDTLMISRTPEVTCVVDVSDQEDPEVQFNWYVDGVEVNAKTKPREE 317

QY 177 QNSYRVSVLTVLHQDLWNGKEYCKVSKNGKLPSSIEKTSKAKGQPREPQVYVTPPSS 236  
 Db 318 QNSYRVSVLTVLHQDLWNGKEYCKVSKNGKLPSSIEKTSKAKGQPREPQVYVTPPSS 377

QY 237 QEMTKNQVSLTCLVKGFYPSDIAEVWESNGQPNYKTTTPVLDSDGSEFFLYSLRITV 294  
 Db 378 QEELSKSTLSVTCVLTGFPDYIAEVWQKNGQPESEDKYGTTSQDADSGVFLYSLRV 437

QY 295 DKSRWQEGNVPSCSVMEALHNHYTKQSLSLGK 329  
 Db 438 DKNSWQEGDTCVAVVMEALHNHYTKQSLSLGK 472

RESULT 12  
 S22080  
 I;heavy chain precursor (B/WT 4A.17, H5, A5) - bovine  
 N;Alternate names: Ig gamma-1 chain C region (clone 8.10)  
 C;Species: Bos primigenius taurus (cattle)  
 C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 23-Jul-1999  
 C;Accession: S22080; S06610; A31303  
 R;Sanders, P.G.  
 submitted to the EMBL Data Library, November 1991  
 A;Reference number: S22080  
 A;Accession: S22080  
 A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Residues: 1-470 <SAN>  
 A;Cross-references: EMBL:X62916; NID:G439; PIDN:CAA44699.1; PID:G440  
 R;Symons, D.B.A.; Clarkson, C.A.; Beale, D.  
 Mol. Immunol. 26, 841-850, 1989  
 A;Title: Structure of bovine immunoglobulin constant region heavy chain gamma 1 and gam  
 A;Reference number: S06610; MUID:90097956; PMID:2513487  
 A;Accession: S06610  
 A;Molecule type: DNA  
 A;Residues: 142-470 <SYM>  
 A;Cross-references: EMBL:X16701  
 A;Note: the sequence was determined from the germline gene  
 C;Genetics:  
 A;Gene: Ig CH gamma-1  
 A;Introns: 98/1; 111/1; 221/1  
 C;Superfamily: immunoglobulin C region; immunoglobulin homology  
 C;Keywords: glycoprotein; heterotetramer; immunoglobulin; membrane protein  
 F;161-225/Domain: immunoglobulin homology <IMM>  
 F;318/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 67.6%; Score 1185; DB 2; Length 470;  
 Best Local Similarity 67.6%; Pred. No. 1.4e-75;  
 Matches 223; Conservative 35; Mismatches 68; Indels 4; Gaps 3;

QY 3 ASTKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPTVSNHGALTSVHTFPAVLQSS 62  
 Db 142 ASTAPKPVPLSSCCGDXSSIVTLGCLVSSYMPEPTVTWNSGALTSVHTFPAVLQSS 201

QY 63 GLYSLSVVTVPSSSLGTYTCNVNDHKPSNTKVDKVESKYGP-PCSPCAPEFLGGPS 121  
 Db 202 GLYSLSVMTVPSTSG-QTFTCNVAHPASTTKVDKAVDPTCKPSPCDCCPPELPGGGS 260

QY 122 VLFPPPKPKDTLMISRTPEVTCVVDVSDQEDPEVQFNWYVDGVEVNAKTKPREQFNST 181  
 Db 261 VLFPPPKPKDTLMISRTPEVTCVVDVSDQEDPEVQFNWYVDGVEVNAKTKPREQFNST 320

QY 182 YRVSVSVLTVLHQDLWNGKEYCKVSKNGKLPSSIEKTSKAKGQPREPQVYVTPPSSQEMTK 241  
 Db 321 YRVSVSVLTVLHQDLWNGKEYCKVSKNGKLPSSIEKTSKAKGQPREPQVYVTPPSSQEMTK 380

QY 242 KNQVSLTCLVKGFYPSDIAEVWESNGQPNYKTTTPVLDSDGSEFFLYSLRITVDKSRW 299  
 Db 381 KSTVSLTCLVKGFYPSDIAEVWESNGQPNYKTTTPVLDSDGSEFFLYSLRITVDKSRW 440

QY 300 QEGNVFSCVMHEALHNHYTKSLSLGK 329  
 Db 441 QEGDVTTCVMHEALHNHYTKSLSACK 470

## RESULT 13

G2GP

IG gamma-2 chain C region - guinea pig  
 C:Species: Cavia porcellus (guinea pig)  
 C:Date: 07-May-1981 #sequence revision 07-May-1981 #text change 16-Jul-1999  
 C:Accession: A94553; A90352; A90359; A90384; A90385; A03151  
 R./Trischmann, T.M.  
 submitted to the Atlas, April 1975  
 A:Reference number: A94553  
 A:Accession: A94553  
 A:Molecule type: protein  
 A:Residues: 1-3 <TR>  
 R./Birstein, B.K.; Hussein, Q.Z.; Cebra, J.J.  
 Biochemistry 10, 18-25, 1971  
 A:Title: Structure of heavy chain from strain 13 guinea pig immunoglobulin-G(2). III. Am  
 A:Reference number: A90352; MUID:71058471; PMID:5538606  
 A:Accession: A90352  
 A:Molecule type: protein  
 A:Residues: 4-68 <BR>  
 R./Turner, K.J.; Cebra, J.J.  
 Biochemistry 10, 9-17, 1971  
 A:Title: Structure of heavy chain from strain 13 guinea pig immunoglobulin-G(2). II. Am  
 A:Reference number: A90359; MUID:71058486; PMID:5538616  
 A:Accession: A90359  
 A:Molecule type: protein  
 A:Residues: 69-133; 312-329 <TR>  
 R./Tracey, D.E.; Cebra, J.J.  
 Biochemistry 13, 4796-4803, 1974  
 A:Title: Primary structure of the C-H2 homology region from guinea pig IgG2 antibodies.  
 A:Reference number: A90384; MUID:75036072; PMID:4429665  
 A:Accession: A90384  
 A:Molecule type: protein  
 A:Residues: 134-226 <TR>  
 R./Trischmann, T.M.; Cebra, J.J.  
 Biochemistry 13, 4804-4811, 1974  
 A:Title: Primary structure of the C-H3 homology region from guinea pig IgG2 antibodies.  
 A:Reference number: A90385; MUID:75036073; PMID:4609467  
 A:Accession: A90385  
 A:Molecule type: protein  
 A:Residues: 227-311 <TR>  
 R./Oliveira, B.; Lamm, M.E.  
 Biochemistry 10, 26-31, 1971  
 A:Title: Interchain disulfide bridges of guinea pig gamma-2- immunoglobulin.  
 A:Reference number: A90354; MUID:71058474; PMID:4922544  
 A:Contents: annotation; disulfide bonds  
 A:Note: Cys-16 is involved in a heavy-light chain bond  
 A:Comment: This chain was isolated from pooled serum of strain 13 inbred guinea pigs.  
 Chain disulfide bonds. In some cases, such as IGA and IgM, the subunits associate into 14  
 C:Superfamily: immunoglobulin C region; immunoglobulin homology  
 C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin  
 F:128-79/Disulfide bonds: #status experimental  
 F:142-202/Disulfide bonds: #status experimental  
 F:178/Binding site: carbohydrate (Asn) (covalent) #status experimental  
 F:248-308/Disulfide bonds: #status experimental

Query Match 66.0%; Score 1158; DB 1; Length 329;  
 Best Local Similarity 67.3%; Pred. No. 6.9e-74;  
 Matches 224; Conservative 34; Mismatches 63; Indels 12; Gaps 4;

QY 3 ASTKGPSVFPLAPCSRSTSESTAALGLCLVKDYFPEPTVSWNSGALTSVHTFPAVLQSS 62  
 Db 2 ARTTAPSVFPLAASCVDTSGSMATIGCLVKGYFPEPTVKWNSGALTSVHTFPAVLQ-S 60

QY 63 GLYSLSSVWTVPSSSLGKTKYTCNVDPHKPNTKVDKREVSKEYGP-----PCPCPAPPEFL 117  
 Db 61 GLYSLTSMWTVPS-----QKATCNVAHPASSTKVDKTVETIRTPZPBPCCTCPKCPPEL 116  
 QY 118 GGPSVFLPPKPKDTLMISRTPEVTCVVVDVSDPEVQFNWYVDGVGVENAKTKPREEQ 177  
 Db 117 GGPSVFIPLPKPKDTLMISLTPRVTCVVVDVSDPEVQFTWFDNKPVGNAETKPRVEQ 176  
 QY 178 FNSTYRVSVLVTLVHQLDGLANGKEYCKVSNKGPSSIEKTSKAKGQRPQVVTLPSPQ 237  
 Db 177 YNTTFVESVLPIQHODWLRGKEFKCKVYNKALPAIEKTSKAGPRMPDVVTLPPSR 236  
 QY 238 BEMTKNQVSLTCLVKGPYSPDIAVENESNGQP--ENNYKTPPVLDSDGSFFLYSRLTVD 295  
 Db 237 DELSKSKSVTCLINFFPADIHVEMASNRVPVSEKEYKNTPIEDADGSFYLSKLTVD 296  
 QY 296 KSRWQEGNVFSCVMHEALHNHYTKSLSLG 328  
 Db 297 KSANDQGTVTTCVMHEALHNHYTKAISRSPG 329

## RESULT 14

C30554

IG heavy chain C region - sheep (fragment)

C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C:Date: 03-Mar-1989 #sequence revision 03-Mar-1989 #text change 21-Jan-2000

C:Accession: C30554

R./Foley, R.C.; Beh, K.J.

J. Immunol. 142, 708-711, 1989

A:Title: Isolation and sequence of sheep Ig H and L chain cDNA.

A:Reference number: A30554; MUID:89093962; PMID:2492052

A:Accession: C30554

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-308 &lt;FC&gt;

C:Superfamily: immunoglobulin C region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:113-182/Domain: immunoglobulin homology &lt;IMV&gt;

Query Match 65.4%; Score 1147; DB 2; Length 308;

Best Local Similarity 69.1%; Pred. No. 3.7e-73;

Matches 215; Conservative 33; Mismatches 51; Indels 12; Gaps 3;

QY 27 LGCLVKDYFPEPTVSWNSGALTSVHTFPAVLQSSGLYSLSSVTVPSSSLGKTKYTCN 86  
 Db 2 LGCLVSSYNPEPTVWNSGALTSVHTFPAVLQSSGLYSLSSVTVPSSTGACITFCN 61

QY 87 VDHKPSNTKVDKREVSKEYGPSPCS-----CPAPEFLGGPSVFLPPKPKDTLMISRTPE 140  
 Db 62 VAHPASSTKVDKRV-----PCPDPCKHCRCPPELPGPSVFIPLPKDTLTISGTPE 117

QY 141 VTCVVVDVSDPEVQFNWYVDGVGVENAKTKPREQFNSTYRVSVLVTLVHQLDGLNGKE 200  
 Db 118 VTCVVVDVSDPEVQFNWYVDGVGVENAKTKPREQFNSTYRVSVLVTLVHQLDGLNGKE 177

QY 201 YKCKYSNKGLSSSTKTSKAKGQRPQVVTLPSPQEMTKNOVSLTCLVKGFVPSDIA 260  
 Db 178 FKCKVNEALPAIVRTISRTKGQAREPQVTVLAPPQELSKSLVSLTCLVTGFPDYIA 237

QY 261 VEWESNGQP--ENNYKTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCVMHEALHNHY 318  
 Db 238 VEWKNGQPESBKYGTITTSOLDADGSFYLSRLRVDRKNSWQEGDVTACVVMHEALHNHY 297

QY 319 TQKSLSLGK 329

Db 298 TQKSLSKPFGK 308

## RESULT 15

S69339

Ig heavy chain V region precursor - human

C:Species: Homo sapiens (man)

C>Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 01-Dec-2000  
C/Accession: S69339; S72664  
R/Khamilichi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.  
Eur. J. Biochem. 229, 54-60, 1995  
A/Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.  
A/Reference number: S69339; PMID:7744049  
A/Accession: S69339  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-374 <KHA>  
A/Cross-references: EMBL:X81695  
R/Khamilichi, A.A.  
submitted to the EMBL Data Library, September 1994  
A/Reference number: S72664  
A/Accession: S72664  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-140, C', 142-374 <KH2>  
A/Cross-references: EMBL:X81695  
C/Superfamily: immunoglobulin C region; immunoglobulin homology

Query Match 65.2%; Score 1143; DB 2; Length 374;  
Best Local Similarity 76.4%; Pred. No. 9.1e-73;  
Matches 220; Conservative 9; Mismatches 15; Indels 44; Gaps 3;

Qy	42	SWNSGALTSGVHTFPVAVLOSSGLYSLSVTVVFPSSSLGKTKYTCNVVDHKPSNTKYDKRVE	101
Db	131	SWGQGT-----VTYSS-----EPKCDKTH-----	151
Qy	102	SKYGPCPCPAPEFLGGPSVFLPPKPKDTLMISRTPEVTCVVDVSOEDPEVOFNWYV	161
Db	152	-----TCPPCPAPELIGGSPVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYV	206
Qy	162	DGVEVHNATKPREQFNSTYRVSVLTVLHQDLNKGKVKCKVSNKGLPSSIEKTIISKA	221
Db	207	DGVEVHNATKPREQVNSTYRVSVLTVLHQDLNKGKVKCKVSNKALPAPIEKTIISKA	266
Qy	222	KGQPREQVYTLPPSOEEMTKNOVSLTCLVKGYFSPSDIAVEWESNGQPENNYKTTTPPVLD	281
Db	267	KGQPREQVYTLPPSREMTKNQVSLTCLVKGYFSPSDIAVEWESNGQPENNYKTTTPPVLD	326
Qy	282	SDGSFFLYSLTVDKSRWQGNVFCSCVMHEALHNYHTOKSLSLGK	329
Db	327	SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYHTOKSLSLSPGK	374

Search completed: January 13, 2004, 12:44:43  
Job time : 24.8489 secs



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OM protein - protein search, using sw model

Run on: January 13, 2004, 12:19:34 ; Search time 14.3668 Seconds  
(without alignments)  
1076.912 Million cell updates/sec

Title: US-09-990-586-100

Perfect score: 1754

Sequence: 1 EFASKGFSVPFLAPCRST.....MHEALHNHYTKSLSLGK 329

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	1743	99.4	327	GC4_HUMAN	P01861 homo sapien
2	1605.5	91.5	326	GC2_HUMAN	P01859 homo sapien
3	1590.5	90.7	330	GCI_HUMAN	P01857 homo sapien
4	1199	68.4	323	GC_RABIT	P01870 oryctolagus
5	1158	66.0	329	GC2_CAVPO	P01862 cavia porce
6	1124	64.1	333	GC2_RAT	P20761 rattus norv
7	1118.5	63.8	326	GC1_RAT	P20759 rattus norv
8	1113.5	63.5	290	GC3_HUMAN	P01860 homo sapien
9	1108	63.2	329	GC2_RAT	P20762 rattus norv
10	1106.5	63.1	324	GCI_MOUSE	P01868 mus musculu
11	1106.5	63.1	330	GCAA_MOUSE	P01863 mus musculu
12	1101.5	62.8	393	GCIM_MOUSE	P01869 mus musculu
13	1101.5	62.8	399	GCAM_MOUSE	P01865 mus musculu
14	1099	62.7	335	GCAB_MOUSE	P01864 mus musculu
15	1098.5	62.6	329	GC3_MOUSE	P22436 mus musculu
16	1090.5	62.2	398	GC3M_MOUSE	P03987 mus musculu
17	1084.5	61.8	322	GCA_RAT	P20760 rattus norv
18	1054.5	60.1	336	GCB_MOUSE	P01866 mus musculu
19	1049.5	59.8	405	GCB_MOUSE	P01867 mus musculu
20	496	28.3	429	EPC_RAT	P01855 rattus norv
21	482.5	27.5	421	EPC_MOUSE	P06336 mus musculu
22	478.5	27.3	428	EPC_HUMAN	P01854 homo sapien
23	447.5	25.5	454	MUC_HUMAN	P01871 homo sapien
24	433.5	24.7	457	MUC_SUNMU	P20768 suncus murl
25	430.5	24.5	450	MUC_CANFA	P01874 canis famli
26	427.5	24.4	455	MUC_MOUSE	P01872 mus musculu
27	425.5	24.3	458	MUC_RABIT	P03988 oryctolagus
28	422	24.1	454	MUC_MESAU	P06337 mesocricetu
29	417.5	23.8	476	MUC_MOUSE	P01873 mus musculu
30	415.5	23.7	479	MUC_RABIT	P04221 oryctolagus
31	411.5	23.5	391	MUCB_HUMAN	P04220 homo sapien
32	393	22.4	353	ALC1_HUMAN	P01876 homo sapien
33	390.5	22.3	438	HVCS_HETER	P23087 heterodontu

## ALIGNMENTS

RESULT 1									
GC4_HUMAN	34	390	22.2	353	1	ALC1_GORGO	34	390	22.2
ID GC4_HUMAN	AC	P01861	STANDARD;	PRT;	327 AA.				
DT 21-JUL-1986 (Rel. 01, Created)	DT	21-JUL-1986 (Rel. 01, Last sequence update)							
DT 15-SEP-2003 (Rel. 42, Last annotation update)	DT	15-SEP-2003 (Rel. 42, Last annotation update)							
IG gamma-4 chain C region.	DE	IG gamma-4 chain C region.							
GN IGHG4.	GN	IGHG4.							
OS Homo sapiens (Human).	OS	Homo sapiens (Human).							
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;							
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.							
OX NCBI_TaxID:9606;	OX	NCBI_TaxID:9606;							
RN [1]	RN	SEQUENCE FROM N.A.							
RP MEDLINE=83157104; PubMed=6299662;	RP	MEDLINE=83157104; PubMed=6299662;							
RA Ellison J.W., Buxbaum J.N., Hood L.E.;	RA	Ellison J.W., Buxbaum J.N., Hood L.E.;							
RT "Nucleotide sequence of a human immunoglobulin C gamma 4 gene.";	RT	"Nucleotide sequence of a human immunoglobulin C gamma 4 gene.";							
DNA 1:11-18(1981).	RN	DNA 1:11-18(1981).							
[2]									
SEQUENCE OF 1-30 AND 81-326.	RP	SEQUENCE OF 1-30 AND 81-326.							
MEDLINE=70207560; PubMed=4192699;	RP	MEDLINE=70207560; PubMed=4192699;							
Pink J.R.L., Buttery S.H., de Vries G.M., Milstein C.;	RA	Pink J.R.L., Buttery S.H., de Vries G.M., Milstein C.;							
"Human immunoglobulin subclasses. Partial amino acid sequence of the	RT	"Human immunoglobulin subclasses. Partial amino acid sequence of the							
constant region of a gamma 4 chain.";	RT	constant region of a gamma 4 chain.";							
Biochem. J. 117:33-47(1970).	RL	Biochem. J. 117:33-47(1970).							
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or send an email to license@isb-sib.ch).	CC	or send an email to license@isb-sib.ch).							
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EMBL; K01316; AAB59394.1; ALT_INIT.	DR	EMBL; K01316; AAB59394.1; ALT_INIT.							
PIR; A90933; G4HU.	DR	PIR; A90933; G4HU.							
PDB; 1A0Q; 16-SEP-98.	DR	PDB; 1A0Q; 16-SEP-98.							
Genew; HGNC:5528; IGHG4.	DR	Genew; HGNC:5528; IGHG4.							
MIM; 147130; .	DR	MIM; 147130; .							
GO; GO:0005624; Cmembrane fraction; NAS.	DR	GO; GO:0005624; Cmembrane fraction; NAS.							
GO; GO:0003823; F antigen binding activity; TAS.	DR	GO; GO:0003823; F antigen binding activity; TAS.							
GO; GO:0006955; P immune response; NAS.	DR	GO; GO:0006955; P immune response; NAS.							
InterPro; IPR007110; IG-like.	DR	InterPro; IPR007110; IG-like.							
InterPro; IPR003597; IG_c1.	DR	InterPro; IPR003597; IG_c1.							
InterPro; IPR003006; IG_MHC.	DR	InterPro; IPR003006; IG_MHC.							
Pfam; PF00047; ig, 3.	DR	Pfam; PF00047; ig, 3.							
SMART; SM00407; IGC1; 2.	DR	SMART; SM00407; IGC1; 2.							
PROSITE; PS00835; IG_LIKE; 3.	DR	PROSITE; PS00835; IG_LIKE; 3.							
PROSITE; PS00230; IG_MHC; 2.	DR	PROSITE; PS00230; IG_MHC; 2.							
Immunoglobulin domain; Immunoglobulin C region; 3D-structure.	KW	Immunoglobulin domain; Immunoglobulin C region; 3D-structure.							
NON TER 1 98	FT	NON TER 1 98							
DOMAIN 1 98	FT	DOMAIN 1 98							
DOMAIN 99 110	FT	DOMAIN 99 110							
DOMAIN 111 220	FT	DOMAIN 111 220							
DOMAIN 221 327	FT	DOMAIN 221 327							

FT	DISULFID	14	14	INTERCHAIN (WITH A LIGHT CHAIN).
FT	DISULFID	27	83	
FT	DISULFID	106	106	INTERCHAIN (WITH A HEAVY CHAIN).
FT	DISULFID	109	109	INTERCHAIN (WITH A HEAVY CHAIN).
FT	DISULFID	141	201	
FT	DISULFID	247	305	
SQ	SEQUENCE	327 AA;	35940 MW;	3EDBD811EF208E7A CRC64;
Query Match 99.4%; Score 1743; DB 1; Length 327;				
Best Local Similarity 100.0%; Pred. No. 1.2e-123; Indels 0; Gaps 0;				
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
Qy	3	ASTKGPSVFLAPCSRSTSESTAALGCLVKDYDPEPVTVSWNSGALTSGVHTTTPAVLQSS	62	
Dd	1	ASTKGPSVFLAPCSRSTSESTAALGCLVKDYDPEPVTVSWNSGALTSGVHTTTPAVLQSS	60	
Qy	63	GLYSLSSVTVPPSSSLGKTYTCNVDRKPSNTKVDKRVESKYGPPCPSPCAPPEFLGGPSV	122	
Dd	61	GLYSLSSVTVPPSSSLGKTYTCNVDRKPSNTKVDKRVESKYGPPCPSPCAPPEFLGGPSV	120	
Qy	123	FLFPKPKDTLMIKRTPEVTTCVVVDVSDPEQDFVFNVDGVVHNNAKTKPREEQNSTY	182	
Dd	121	FLFPKPKDTLMIKRTPEVTTCVVVDVSDPEQDFVFNVDGVVHNNAKTKPREEQNSTY	180	
Qy	183	RVSGLVTLVHODWLNKGYCKVSKNGLPSIEKTIISKAKGQREPOVYTLPPSQEEMTK	242	
Dd	181	RVSGLVTLVHODWLNKGYCKVSKNGLPSIEKTIISKAKGQREPOVYTLPPSQEEMTK	240	
Qy	243	NOVSLTCLVKGYFSDIAVESNGQPENNYKTTTPVLDSDGFFFLYSLRTVDKSRWQEG	302	
Dd	241	NOVSLTCLVKGYFSDIAVESNGQPENNYKTTTPVLDSDGFFFLYSLRTVDKSRWQEG	300	
Qy	303	NVFCSCVMHEALHNHYTQKSLSLIGK	329	
Dd	301	NVFCSCVMHEALHNHYTQKSLSLIGK	327	
RESULT 2				
GC2_HUMAN	GC2_HUMAN	STANDARD;	PRT;	326 AA.
AC	FOA859;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	IG gamma-2 chain C region.			
GN	IGHG2.			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
[1]				
RP	SEQUENCE OF 2-326 FROM N.A.			
RX	MEDLINE=82197621; PubMed=6804948;			
RA	Ellison J.W., Hood L.E.;			
RT	"Linkage and sequence homology of two human immunoglobulin gamma			
RT	heavy chain constant region genes.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 79:1984-1988(1982).			
[2]				
RP	SEQUENCE OF 88-115 FROM N.A.			
RC	TISSUE=Fetal liver;			
RX	MEDLINE=83001943; PubMed=6811139;			
RA	Takahashi N., Ueda S., Obata M., Nikaide T., Nakai S., Honjo T.;			
RT	"Structure of human immunoglobulin gamma genes: implications for			
RT	evolution of a gene family.";			
RL	Cell 29:671-679(1982).			
[3]				
RP	SEQUENCE OF 99-177 AND 310-326 FROM N.A.			
RC	TISSUE=Petal liver;			
RX	MEDLINE=84235992; PubMed=6329676;			
RA	Krawinkel U., Rabbits T.H.;			
RT	"Comparison of the hinge-coding segments in human immunoglobulin gamma			
RT	heavy chain genes and the linkage of the gamma 2 and gamma 4 subclass			
RT	genes.";			
RL				
FT	DISULFID	14	14	INTERCHAIN (WITH A LIGHT CHAIN).
FT	DISULFID	27	83	
FT	DISULFID	106	106	INTERCHAIN (WITH A HEAVY CHAIN).
FT	DISULFID	109	109	INTERCHAIN (WITH A HEAVY CHAIN).
FT	DISULFID	141	201	
FT	DISULFID	247	305	
SQ	SEQUENCE	327 AA;	35940 MW;	3EDBD811EF208E7A CRC64;
Query Match 99.4%; Score 1743; DB 1; Length 327;				
Best Local Similarity 100.0%; Pred. No. 1.2e-123; Indels 0; Gaps 0;				
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
Qy	3	ASTKGPSVFLAPCSRSTSESTAALGCLVKDYDPEPVTVSWNSGALTSGVHTTTPAVLQSS	62	
Dd	1	ASTKGPSVFLAPCSRSTSESTAALGCLVKDYDPEPVTVSWNSGALTSGVHTTTPAVLQSS	60	
Qy	63	GLYSLSSVTVPPSSSLGKTYTCNVDRKPSNTKVDKRVESKYGPPCPSPCAPPEFLGGPSV	122	
Dd	61	GLYSLSSVTVPPSSSLGKTYTCNVDRKPSNTKVDKRVESKYGPPCPSPCAPPEFLGGPSV	120	
Qy	123	FLFPKPKDTLMIKRTPEVTTCVVVDVSDPEQDFVFNVDGVVHNNAKTKPREEQNSTY	182	
Dd	121	FLFPKPKDTLMIKRTPEVTTCVVVDVSDPEQDFVFNVDGVVHNNAKTKPREEQNSTY	180	
Qy	183	RVSGLVTLVHODWLNKGYCKVSKNGLPSIEKTIISKAKGQREPOVYTLPPSQEEMTK	242	
Dd	181	RVSGLVTLVHODWLNKGYCKVSKNGLPSIEKTIISKAKGQREPOVYTLPPSQEEMTK	240	
Qy	243	NOVSLTCLVKGYFSDIAVESNGQPENNYKTTTPVLDSDGFFFLYSLRTVDKSRWQEG	302	
Dd	241	NOVSLTCLVKGYFSDIAVESNGQPENNYKTTTPVLDSDGFFFLYSLRTVDKSRWQEG	300	
Qy	303	NVFCSCVMHEALHNHYTQKSLSLIGK	329	
Dd	301	NVFCSCVMHEALHNHYTQKSLSLIGK	327	
EMBO J. 1:403-407(1982).				
[4]				
RP	SEQUENCE OF 1-325 (MYELOMA PROTEIN TIL).			
RX	MEDLINE=81007873; PubMed=6774012;			
RA	Wang A.-C., Tung E., Fudenberg H.H.;			
RT	"The primary structure of a human IgG2 heavy chain: genetic,			
RT	evolutionary, and functional implications.";			
RL	J. Immunol. 125:1048-1054(1980).			
[5]				
RP	SEQUENCE OF 1-85 AND 132-325 (MYELOMA PROTEIN ZIE).			
RX	MEDLINE=80001357; PubMed=113060;			
RA	Connell G.E., Parr D.M., Hofmann T.;			
RT	"The amino acid sequences of the three heavy chain constant region			
RT	domains of a human IgG2 myeloma protein.";			
RL	Can. J. Biochem. 57:758-767(1979).			
[6]				
RP	SEQUENCE OF 238-275 (ZIE).			
RX	MEDLINE=80114419; PubMed=118920;			
RA	Hofmann T., Parr D.M.;			
RT	"A note of the amino acid sequence of residues 381-391 of human			
RT	immunoglobulin gamma chains.";			
RL	Mol. Immunol. 16:923-925(1979).			
[7]				
RP	REVISED TO 25; 59; 60 AND 264-268 (ZIE).			
RX	Hofmann T., Parr D.M.;			
RL	Submitted (MAR-1980) to the PIR data bank.			
[8]				
RP	SEQUENCE OF 1-121 (DOT).			
RX	MEDLINE=95255298; PubMed=7737190;			
RA	Stoppini M., Bellotti V., Negri A., Merlini G., Garver P., Ferri G.;			
RT	"Characterization of the two unique human anti-flavin monoclonal			
RT	immunoglobulins.";			
RL	Eur. J. Biochem. 228:886-893(1995).			
[9]				
RP	DISULFIDE BONDS.			
RX	MEDLINE=72033500; PubMed=4940472;			
RA	Milstein C., Frangione B.;			
RT	"Disulphide bridges of the heavy chain of human immunoglobulin G2.";			
RL	Biochem. J. 121:217-225(1971).			
[10]				
RP	DISULFIDE BONDS.			
RX	MEDLINE=69064124; PubMed=5782707;			
RA	Frangione B., Milstein C., Pink J.R.L.;			
RT	"Structural studies of immunoglobulin G.";			
RL	Nature 221:145-148(1969).			
[11]				
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CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).			
CC	-----			
DR	EMBL; J00230; AAB59393.1; ..			
DR	PIR; A93906; G2HU.			
DR	HSSP; P01857; 1FC1.			
DR	Genew; HGNC:5526; IGHG2.			
DR	NTM; 147110; ..			
DR	GO; GO:0005624; C:membrane fraction; NAS.			
DR	GO; GO:0003823; F:antigen binding activity; TAS.			
DR	GO; GO:0006955; P:immune response; NAS.			
DR	InterPro; IPR007110; IG-like.			
DR	InterPro; IPR003597; IG_c1.			
DR	InterPro; IPR003006; IG_MHC.			
DR	Pfam; PF00047; IG; 3.			
DR	SMART; SM00407; IGH1; 2.			
DR	PROSITE; PS00835; IG_LIKE; 3.			
DR	PROSITE; PS00290; IGH1; 2.			
KW	Immunoglobulin domain; Immunoglobulin C region.			
FT	NON TER	1	98	CHI.
FT	DOMAIN	99	110	HINGE.

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FT DOMAIN 111 219
FT DOMAIN 220 326
FT DISULFID 14 14
FT DISULFID 27 83
FT DISULFID 102 102
FT DISULFID 103 103
FT DISULFID 106 106
FT DISULFID 109 109
FT DISULFID 140 200
FT DISULFID 248 304
FT SITE 156 156
FT MOD_RES 326 326
FT VARIANT 60 60
FT CONFLICT 109 109
FT SEQUENCE 326 AA; 35884 MW; 8310878C6878CF9C CRC64;

Query Match 91.5%; Score 1605.5; DB 1; Length 326;
Best Local Similarity 92.4%; Pred. No. 2.4e-113;
Matches 302; Conservative 10; Mismatches 14; Indels 1; Gaps 1;

QY 3 ASTKGPSVFLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 62
DB 1 ASTKGPSVFLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
QY 63 GLYSLSVVTPSSSLGTITTCNVDPKPSNTKVDKRVESKYGPPCPSPAPEFLGGPSV 122
DB 61 GLYSLSVVTPSSSLGTITTCNVDPKPSNTKVDKRVESKYGPPCPSPAPEFLGGPSV 119
QY 123 FLPPPKPKDTLMISRPETVTCVVDVSDQEDPEVFQFNWYDGVGVHNAKTKPREQFNSTY 182
DB 120 FLPPPKPKDTLMISRPETVTCVVDVSDQEDPEVFQFNWYDGVGVHNAKTKPREQFNSTY 179
QY 183 RVSVLTVLHQLDMLNGKEYCKVSKNGLPSSIEKTSKAGQPRPQVYVLPPESEMTK 242
DB 180 RVSVLTVLHQLDMLNGKEYCKVSKNGLPAPTEKTSKAGQPRPQVYVLPPESEMTK 239
QY 243 NQVSLCLVKGFYPSDIAVEWESNGQPENNYKTTPPELSDGSGFFLYSLRTVDKSRWQEG 302
DB 240 NQVSLCLVKGFYPSDIAVEWESNGQPENNYKTTPPELSDGSGFFLYSLRTVDKSRWQEG 299
QY 303 NVFSCSVMEALHNHYTQKSLSLSLK 329
DB 300 NVFSCSVMEALHNHYTQKSLSLSLSPGK 326

RESULT 3
GC1_HUMAN STANDARD; PRT; 330 AA.
AC P01857;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE 19 gamma-I chain C region.
GN IGHG1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=82274238; PubMed=6287432;
RA Ellison J.W., Berson B.J., Hood L.E.;
RT "The nucleotide sequence of a human immunoglobulin C gamma1 gene.";
RL Nucleic Acids Res. 10:4071-4079(1982).
(2)
RP SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).
RX MEDLINE=71064024; PubMed=5489771;
RA Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,
RA Waxdal M.J., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. VII. Amino
RT acid sequence of heavy-chain cyanogen bromide fragments H1-H4.";
RL Biochemistry 9:3161-3170(1970).

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RN SEQUENCE OF 136-329 (EU).
RP MEDLINE=71064025; PubMed=5530842;
RX Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,
RA Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. 8. Amino
RT acid sequence of heavy-chain cyanogen bromide fragments H5-H7.";
RL Biochemistry 9:3171-3181(1970).
(4)
RN SEQUENCE (MYELOMA PROTEIN NIE).
RP MEDLINE=77070269; PubMed=826475;
RX Ponsingl H., Hilschmann N.;
RT "The rule of antibody structure. The primary structure of a
RT monoclonal IgG1 immunoglobulin (myeloma protein NIE). III. The
RT chymotryptic peptides of the H-chain, alignment of the tryptic
RT peptides and discussion of the complete structure.";
RL Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).
(5)
RN SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS.
RP MEDLINE=83289131; PubMed=6884994;
RX Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;
RT "Three-dimensional structure determination of antibodies. Primary
RT structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";
RL Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).
(6)
RN DISULFIDE BONDS.
RP MEDLINE=71064027; PubMed=4923144;
RX Gall W.E., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. X.
RT Intrachain disulfide bonds.";
RL Biochemistry 9:3188-3196(1970).
(7)
RN DISULFIDE BONDS.
RP MEDLINE=77070267; PubMed=1002129;
RX Dreker L., Schwarz J., Reichel W., Hilschmann N.;
RT "Rule of antibody structure. The primary structure of a monoclonal
RT IgG1 immunoglobulin (myeloma protein NIE), I: Purification and
RT characterization of the protein, the L- and H-chains, the
RT cyanogen bromide cleavage products, and the disulfide bridges.";
RL Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
(8)
RN X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
RP MEDLINE=81208100; PubMed=7236608;
RX Deisenhofer J.;
RT "Crystallographic refinement and atomic models of a human Fc fragment
RT and its complex with fragment B of protein A from Staphylococcus
RT aureus at 2.9- and 2.8-A resolution.";
RL Biochemistry 20:2361-2370(1981).
CC -1- MISCELLANEOUS: NIE HAS THE GIM(17) ALLOTYPIC MARKER. 97-K, & THE
CC GIM(1) MARKERS. 239-D & 241-L. KOL & EU SEQUENCES HAVE THE GIM(3)
CC MARKER & THE GIM (NON-1) MARKERS.
CC -1- MISCELLANEOUS: NIE ALSO DIFFERS IN THE AMIDATION STATES OF
CC 35,116,198,269 & 272.
CC -1- MISCELLANEOUS: EU ALSO DIFFERS IN THE AMIDATION STATES OF RESIDUES
CC 155, 166, 177, 195, 198, 269, AND 272 AND IN THE ORDER OF RESIDUES
CC 268-272.
CC -1- MISCELLANEOUS: KOL ALSO DIFFERS IN THE AMIDATION STATES OF
CC RESIDUES 198,267&272.
CC
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CC -----
CC EMBL; J00228; AAC82527.1; ALT_INIT.
CC PIR; A93433; GHU.
CC PDB; 1FC1; 15-JUL-92.
CC PDB; 1FC2; 15-JUL-92.
CC PDB; 1AU7; 12-NOV-97.
CC PDB; 1D5B; 09-FEB-00.
CC
CC DR

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FT NON TER 1 1 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 16 16
FT DISULFID 28 79
FT DISULFID 105 105 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 110 110 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 111 202
FT DISULFID 142 178
FT CARBOHYD 178 178 N-LINKED (GLCNAC. . .).
FT DISULFID 248 308
SQ SEQUENCE 329 AA; 36074 MW; 5D231B7164D1FBA9 CRC64;

Query Match 66.0%; Score 1158; DB 1; Length 329;
Best Local Similarity 67.3%; Pred. No. 8,7e-80;
Matches 224; Conservative 34; Mismatches 63; Indels 12; Gaps 4;

QY 3 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYRPEPTVSWNSGALTSGVHTFPAVLQSS 62
DB 2 ARTTAPSVFPLAASCVDTSGMWTLGCLVKGYFPEPTVWNSGALTSGVHTFPAVLQ-S 60
QY 63 GLYSLSVVTVFPSSSLGKTKYTCNVDPKPSNTKVDKRVESKYGP-----PCPCPAPEFL 117
DB 61 GLYSLSMTVPSS-----QKATCNVAHPASSTKVDKTVETPTZPBPCCTCPKCPPENL 116
QY 118 GGPSVFPLPPEPKKDTLMISRTPEVTCVVDVSDQEDPEVQFNWYVDGVEVNAKTKRREQ 177
DB 117 GGPSVFPLPPEPKKDTLMISLTPRTVCVVDVSDQEDPEVQFTWVDNKPVGNAETKPRVEQ 176
QY 178 FNSTYRVVSVLTVLHQDLWNGKEYCKVSKNGLPSSIEKTSKAKGQPREPQVYVTPPQS 237
DB 177 YNTFRVESVLPPIQHQLWLRGKEFKCKVYKALPAPIEKTSIKTGAPRMPDQVYVTPPQS 236
QY 238 EEMTKQVSLCLVKGFYPSDIAVEWESNGQP--ENNYKTPPVLDSDGSFFLYSRLTVD 295
DB 237 DELSKSKVSVTCLINFEFPADIHVEWASNRVFPVSEKYEKNTPTIEDADGSIFYLSKLTVD 296
QY 296 KSRWQEGNVFSCSVNMEALHNHYTKSLSLG 328
DB 297 KSNWQGVTVTCVNMHEALHNHYTKAISRSFG 329
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RESULT 6
GCB_RAT ID GCB_RAT STANDARD; PRT; 333 AA.
AC P20761;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig gamma-2B chain C region.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89232738; PubMed=3149946;
RA Bruggemann M.;
RT "Evolution of the rat immunoglobulin gamma heavy-chain gene family.";
RL Gene 74:473-482(1988).
CC -1- SIMILARITY: Contains 3 immunoglobulin-like domains.
DR PIR; PS0018; PS0018.
DR HSSP; P01842; 7FAB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00407; Igc1; 2.
DR PROSITE; PS00835; IG-LIKE; 3.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Repeat.
FT NON TER 1 1
FT DOMAIN 6 96 IG-LIKE 1.
FT DOMAIN 124 223 IG-LIKE 2.
FT DOMAIN 232 328 IG-LIKE 3.
FT
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```
FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 80
FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 115 115 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 147 207
FT DISULFID 253 311
SQ SEQUENCE 333 AA; 36497 MW; 55F8B64D48D460A6 CRC64;

Query Match 64.1%; Score 1124; DB 1; Length 333;
Best Local Similarity 62.8%; Pred. No. 3,1e-77;
Matches 211; Conservative 46; Mismatches 67; Indels 12; Gaps 3;

QY 3 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYRPEPTVSWNSGALTSGVHTFPAVLQSS 62
DB 1 AQTAPSVFPLAPGCGDTTSSTVTGLCLVKGYFPEPTVWNSGALTSDVHTFPAVLQ-S 59
QY 63 GLYSLSVVTVFPSSSLGKTKYTCNVDPKPSNTKVDKRVESKYG-----PPCPCPA 113
DB 60 GLYTITSSVT--SSTWPSQVTCNVHPASSTKVDKVERNGGIGHKCTCPTCHKCPV 117
QY 114 PEFLGGPSVFPLPPEPKKDTLMISRTPEVTCVVDVSDQEDPEVQFNWYVDGVEVNAKTKP 173
DB 118 PELLGGPSVFPLPPEPKKDTLLISQNAKVTCTVVDVSEEDPEVQFSWFWNNVEVHTAQTQP 177
QY 174 REEQNSTYRVSVLTVLHODLWNGKEYCKVSKNGLPSSIEKTSKAKGQPREPQVYVTL 233
DB 178 REEQNSTFRVVSALPIQHQLWLRGKEFKCKVYKALPAPIEKTSIKTGAPRMPDQVYVTP 237
QY 234 PPSQEMTKQVSLCLVKGFYPSDIAVEWESNGQPNYKTPPVLDSDGSFFLYSRLT 293
DB 238 GPPTQLTEQTVSLTCLTSGFLNDIGVETWSNGHIEKNYKNTPEVMDSDGSDGFFWYSKLN 297
QY 294 VDKSRWQEGNVFSCSVNMEALHNHYTKSLSLGK 329
DB 298 VERSRWDSRAPVCVSVNHEGLHNHNVTKAISRSFG 333
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RESULT 7
GCB_RAT ID GCB_RAT STANDARD; PRT; 326 AA.
AC P20759;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-1 chain C region.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89232738; PubMed=3149946;
RA Bruggemann M.;
RT "Evolution of the rat immunoglobulin gamma heavy-chain gene family.";
RL Gene 74:473-482(1988).
DR PIR; PS0017; PS0017.
DR HSSP; P01842; 7FAB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00407; Igc1; 2.
DR PROSITE; PS00835; IG-LIKE; 3.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
FT NON TER 1 1
FT DOMAIN 98 112 CH1.
FT DOMAIN 113 219 CH2.
FT DOMAIN 220 326 CH3.
FT DISULFID 27 82
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FT VARIAT 134 134 P -> L (IN OMM)
FT FTID=VAR 003891.
FT VARIAT 139 139 F -> Y (IN OMM)
FT FTID=VAR 003892.
FT VARIAT 182 182 T -> A (IN OMM)
FT FTID=VAR 003893.
FT VARIAT 227 227 S -> N (IN OMM)
FT FTID=VAR 003894.
FT VARIAT 227 227 MISSING (IN ZUC)
FT FTID=VAR 003895.
FT VARIAT 279 279 F -> Y (IN OMM)
FT FTID=VAR 003896.
SQ SEQUENCE 290 AA; 32331 MW; E6SCBC95705B2F46 CRC64;

Query Match 63.5%; Score 1113.5; DB 1; Length 290;
Best Local Similarity 73.8%; Pred. No. 1.6e-76;
Matches 211; Conservative 20; Mismatches 30; Indels 25; Gaps 2;

QY 66 SLSSVTVFSSSLGKTKVTCT-----NVDHKPSNTKVDKRVESK 103
Db :::::VTCTCTCRCPKPCSCDTPPCPCPEPKSCDTPPCPCPEPKSCD 64
8 TVSSSLKTP---LGTTHCTCRCPKPCSCDTPPCPCPEPKSCDTPPCPCPEPKSCD 64

QY 104 YGPPCPCAPBFLGSPVFLPPPKPKDTLMISRTPEVTCVVVDVSDDEVEQFNWYVDG 163
Db 65 TTPPCPCAPBFLGSPVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFKWYVDG 124
164 VEVHNAKTKPRQEQNSTYRVVSVLTVLHQDLNAGKEYCKVSKNGKLPSSIEKTIKSKAG 223
Db 125 VQVHNAKTKPRQEQNSTYRVVSVLTVLHQDLNAGKEYCKVSKNGKLPAPIEKTIKSKG 184
224 QPREQVTVLPSPQEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSD 283
Db 185 QPREQVTVLPSPQEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSD 244
284 GSFFLYSLKTVDKSRWQGNFSCSVWHEALHNHYTQKSLSLGLK 329
Db 245 GSFFLYSLKTVDKSRWQGNFSCSVWHEALHNHYTQKSLSLGLK 290

RESULT 9
GCC RAT ID GCC RAT STANDARD; PRT; 329 AA.
AC P20762;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-2C chain C region.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RX MEDLINE=88166903; PubMed=3127222;
RA Brueggemann M., Delmastro-Galfire P., Waldmann H., Calabi F.;
RT "Sequence of a rat immunoglobulin gamma 2c heavy chain constant
region cDNA: extensive homology to mouse gamma 3.";
RL Eur. J. Immunol. 18:317-319(1988).
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or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X07189; CAA30169.1; -
DR PIR; S00847; S00847.
DR HSSP; P01842; 7FAB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_C1.
DR InterPro; IPR003006; Ig_MHC.
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DR Pfam; PF00047; ig; 2.
DR SMART; SM00407; IGc1; 2.
DR PROSITE; PS00835; IG_LIKE; 3.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT KCON TER 1 97
FT DOMAIN 1 97 CHI.
FT DOMAIN 98 113 HINGE.
FT DOMAIN 114 222 CH2.
FT DOMAIN 223 329 CH3.
FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 82 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 111 111 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 113 113 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 143 203
FT DISULFID 249 307
SQ SEQUENCE 329 AA; 36571 MW; 5FCD7B7933850773 CRC64;

Query Match 63.2%; Score 1108; DB 1; Length 329;
Best Local Similarity 62.7%; Pred. No. 4.9e-76;
Matches 207; Conservative 50; Mismatches 69; Indels 4; Gaps 2;

QY 3 ASTKGPSVPLPAPCRSRSTSESTAALGCLVKDYFPPPTVSVNSGALTSGVHTFPAVLQSS 62
Db 1 ARTTAPSVYPLVFGSGTSGSLVTGLCLVKGYFPEPTVKWNSGALSSGVHTFPAVLQ-S 59
63 GLYSLSVVTVFSSSLGKTKVTCTNVDHKPSNTKVDKRVKVE---SKYGPCCPCPCPEFLGG 119
Db 60 GLYTSSVTVFSSVSSQTVCVAHPATKSNLKRLEPRPKPRPTDTCSCDNLGR 119
120 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSDDEVEQFNWYVDGVEVHNAKTKPRQEQFN 179
Db 120 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSEEDPDVQFQSWFVDNVRVFTAQTPHEEQIN 179
180 STYRVSVVLTVLHQDLNAGKEYCKVSKNGKLPSSIEKTIKSKAGOPRQPPVTVLPSPQEE 239
Db 180 GTRVSVVTLHIHQDQWMSGKFKCKVKNKNDLPSIEKTIKSKRGKARTPQVTVIIPPRQ 239
240 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSGFFLYSLKTVDKSRW 299
Db 240 MSKNKVSILTCMTVSFPASISVEWERNGELEQDYKNTLPLVLDSDSYFLYSLKSLVDTDSW 299
300 QEGNVFSCSVWHEALHNHYTQKSLSLGLK 329
Db 300 MRGDIYTCVSVHVALHNHHTQKLSRSPGK 329

RESULT 10
GCC RAT ID GCC MOUSE STANDARD; PRT; 324 AA.
AC P01868;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig gamma-1 chain C region secreted form.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RX MEDLINE=80045036; PubMed=115593;
RA Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,
RA Takahashi N., Mano Y.;
RT "Cloning and complete nucleotide sequence of mouse immunoglobulin
gamma 1 chain gene.";
RL Cell 18:559-568(1979).
RN [2]
RP SEQUENCE OF 76-324 FROM N.A. (MYELOMA PROTEIN MOPC 31C).
RX MEDLINE=80202559; PubMed=6769752;
RA Obata M., Yamawaki-Kataoka Y., Takahashi N., Kataoka T., Shimizu A.,
RA Mano Y., Seidman J.G., Peterlin B.M., Leder P., Honjo T.;
RT "Immunoglobulin gamma 1 heavy chain gene: structural gene sequences
```



RT cloned in a bacterial plasmid.";  
 RL Gene 9:87-97(1980).  
 RN [3]  
 RP SEQUENCE OF 70-322 FROM N.A. (MYELOMA PROTEIN MOPC 21).  
 RX MEDLINE=80012837; PubMed=113776;  
 RA Rogers J., Clarke P., Salsar W.;  
 RT "Sequence analysis of cloned cDNA encoding part of an immunoglobulin  
 heavy chain.";  
 RL Nucleic Acids Res. 6:3305-3321(1979).  
 RN [4]  
 RP SEQUENCE (MYELOMA PROTEIN MOPC 21).  
 RX MEDLINE=78242288; PubMed=98524;  
 RA Adetugbo K.;  
 RT "Evolution of immunoglobulin subclasses. Primary structure of a  
 murine myeloma gamma chain.";  
 RL J. Biol. Chem. 253:6068-6075(1978).  
 RN [5]  
 RP DISULFIDE BONDS (MOPC 21).  
 RX MEDLINE=73008889; PubMed=5073237;  
 RA Svasti J., Milstein C.;  
 RT "The disulphide bridges of a mouse immunoglobulin G1 protein.";  
 RL Biochem. J. 126:837-850(1972).  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event-Alternative splicing; Named isoforms=2;  
 CC Name=Secreted;  
 CC IsoId=P01868-1; Sequence=Displayed;  
 CC Note=May be the major isoform;  
 CC Name=Membrane-bound;  
 CC IsoId=P01869-1; Sequence=External;  
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 CC -----  
 DR EMBL; V00793; CAA24172.1; -;  
 DR EMBL; V00793; CAA24173.1; -;  
 DR EMBL; V00793; CAA24174.1; -;  
 DR EMBL; V00793; CAA24175.1; -;  
 DR EMBL; V00795; CAA24176.1; -;  
 DR PIR; A02159; GIMS.  
 DR PDB; 1IGC; 03-JUN-95.  
 DR GlycoSuiteDB; P01868; -;  
 DR MGD; MGI:96446; Igh-4;  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig\_c1.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR Pfam; PF00047; Ig; 3.  
 DR SMART; SM00407; Igcl; 2.  
 DR PROSITE; PS50835; IG LIKE; 3.  
 DR PROSITE; PS00290; IG\_MHC; 1.  
 DR Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;  
 KW Alternative splicing; 3D-structure.  
 FT NON\_TER 1  
 FT DOMAIN 1 97  
 FT CH1.  
 FT DOMAIN 98 110  
 FT HINGE.  
 FT DOMAIN 111 217  
 FT CH2.  
 FT DOMAIN 218 324  
 FT CH3.  
 FT DISULFID 27 82  
 FT DISULFID 102 102  
 FT DISULFID 104 104  
 FT DISULFID 107 107  
 FT DISULFID 109 109  
 FT DISULFID 109 109  
 FT DISULFID 138 198  
 FT CARSHVD 174 174  
 FT N-LINKED (GLCNAC. . .).  
 FT /FTID=CAR\_000055.  
 FT DISULFID 244 302  
 FT MOD\_RES 324 324  
 FT REMOVED POST-TRANSLATIONALLY.  
 FT CONFLICT 276 276  
 FT N -> D (IN REF. 3).

PT CONFLICT 278 278 N -> D (IN REF. 3).  
 SQ SEQUENCE 324 AA; 35704 MW; A338812F3D1F2C93 CRC64;  
 Query Match 63.1%; Score 1106.5; DB 1; Length 324;  
 Best Local Similarity 62.0%; Pred. No. 6.2e-76;  
 Matches 204; Conservative 55; Mismatches 63; Indels 7; Gaps 4;  
 QY 3 ASTKGSVPFLAPCSRSTSESTAALGCLVKDYFPEPTVTVSWNSGALTSGVHTFPAVLQSS 62  
 DB 1 AKTTPSVYPLAPGSAATNSMVTGLCLVKGYFPEPTVTVSWNSGSLSSGHTFPAVLQSD 60  
 QY 63 GLYSLSVVTVPSLSLGTTCNVVDHKPSNTKVDKVESK--YGPCCPSCPAPFLGGP 120  
 DB 61 -LYLSSSVTVPSPPSPSTVTCNVVHASSTKVDKIVPRCGCKPC-ICTVPEV---S 115  
 QY 121 SVLFPPPKPDTLMISRTPEVTCVVVDVSOEDPEVQFNWYVDGVEVHNAKTKPREPQFNS 180  
 DB 116 SVFIFPPKDKVTLITLTITPKVTCVVVDISKDDPEQFSNFDVDDVEVHTAQTQPREPQFNS 175  
 QY 181 TVRVSVLTVLDHQMGLNGKEYCKYKNKGLPSIEKTIKSKAKGQPREPOVYTLPPSQEEM 240  
 DB 176 TFRSVSELPIMHQDWLNGKEFKCRVNSAAPPAPIETIKTKRKPAPQVYTIPTPPEQM 235  
 QY 241 TKQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSRLTVDKSRMQ 300  
 DB 236 AKDKVSLTCVITDFPEDITVEMQWNGQPAENYKNTQPIMTNGSVFVYSLKNVQKSNWE 295  
 QY 301 EGNVFSCSVMHEALHNHYTQKSLSLGLK 329  
 DB 296 AGNTFTCSVLEGLHNHHTKSLSPGK 324  
 RESULT 11  
 GCAA\_MOUSE  
 ID GCAA\_MOUSE STANDARD; PRT; 330 AA.  
 AC P01863;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Ig gamma-2A chain C region, A allele.  
 OS Mus musculus (Mouse)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=81076554; PubMed=6777755;  
 RA Sikorav J.-L., Auffray C., Rougeon F.;  
 RT "Structure of the constant and 3' untranslated regions of the murine  
 Balb/c gamma 2a heavy chain messenger RNA.";  
 RL Nucleic Acids Res. 8:3143-3155(1980).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=81198976; PubMed=6262729;  
 RA Yamawaki-Kataoka Y., Miyata T., Honjo T.;  
 RT "The complete nucleotide sequence of mouse immunoglobulin gamma 2a gene  
 and evolution of heavy chain genes: further evidence for intervening  
 sequence-mediated domain transfer.";  
 RL Nucleic Acids Res. 9:1365-1381(1981).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=81223894; PubMed=6787604;  
 RA Olio R., Auffray C., Morchamps C., Rougeon F.;  
 RT "Comparison of mouse immunoglobulin gamma 2a and gamma 2b chain genes  
 suggests that exons can be exchanged between genes in a multigenic  
 family.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 78:2442-2446(1981).  
 RN [4]  
 RP MYELOMA PROTEIN MOPC 173.  
 RX MEDLINE=74175517; PubMed=4831970;  
 RA Bourgeois A., Fougereau M., Rocca-Serra J.;  
 RT "Determination of the primary structure of a mouse IgG2a  
 immunoglobulin: amino-acid sequence of the Fc fragment. Implications

for the evolution of immunoglobulin structure and function.";  
 Eur. J. Biochem. 43:423-435(1974).

```

RT  (5)
RN  DISULFIDE BONDS
RX  MEDLINE=73056887; PubMed=4565406;
RA  de Preval C., Fougereau M.;
RT  "Determination of the primary structure of a mouse gamma G2a
RL  immunoglobulin. Identification of the disulfide bridges."
RC  Eur. J. Biochem. 30:452-462(1972).
CC  -!- SIMILARITY: Contains 3 immunoglobulin-like domains.
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CC  between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC  entities requires a license agreement (See http://www.isb-sib.ch/
CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL; V00798; CAA24178.1; -.
DR  PIR; A02152; G2MSA.
DR  PDB; 1E4W; 12-JUL-01.
DR  PDB; 1E4X; 12-JUL-01.
DR  PDB; 1MNU; 06-MAY-99.
DR  InterPro; IPR007110; Ig-like.
DR  InterPro; IPR003597; Ig CL.
DR  InterPro; IPR003006; Ig_MHC.
DR  Pfam; PF00047; Ig; 2.
DR  SMART; SM00407; IgC1; 2.
DR  PROSITE; PS00835; IG LIKE; 3.
DR  PROSITE; PS00290; IG_MHC; 1.
KW  Immunoglobulin domain; Immunoglobulin C region; 3D-structure; Repeat.
FT  NON TER 1 1
FT  DOMAIN 1 98
FT  DOMAIN 121 220
FT  DOMAIN 229 325
FT  DISULFID 15 15
FT  DISULFID 27 82
FT  DISULFID 107 107
FT  DISULFID 110 110
FT  DISULFID 112 112
FT  DISULFID 144 208
FT  DISULFID 250 304
FT  MOD RES 330 330
SQ  SEQUENCE 330 AA; 36389 MW; B84361C5445A6864 CRC64;
Query Match 63.1%; Score 1106.5; DB 1; Length 330;
Best local Similarity 63.0%; Pred. No. 6.3e-76;
Matches 209; Conservative 47; Mismatches 69; Indels 7; Gaps 4;
QY 3 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 62
DB 1 AKTAPSVYPLAPVCGDTGSSVTLGCLVKGYFPEPVTLTWNSSGLSSGVHTFPAVLQSD 60
QY 63 GLYSLSVVVPPSSSLGKTKYTCNVDPKPSNTKVDKRVESKYGP---PCP--SCPAPFL 117
DB 61 -LYTLSSVTVTSSWPQSCITCNVAHPASSTKVDKKIEPR-GPTIKPCPKCPAPNLL 118
QY 118 GGPVSFLPPPKPDKTLMISRPETVTCVVVDYSDDEPQVFNWYDGVENNAKTKPREQ 177
DB 119 GGPVSFIFPPKTKDVLMLSLSPITCVVDVSEDPPQVLSFVNVEVHTAQCTHRED 178
QY 178 FNSTVRVSVLTZVLQDMLNKVEYCKVKSNKGLPSSIEKTIISKAKGPRPQVYTLPPSQ 237
DB 179 YNSTLRVVSALPIQHQQDWSGKEFKKVNKDLPAPIERTISKPKGSVRAPQVYVLPPE 238
QY 238 EEMTKNOVSLTCLVKGVPSPDIKAVESNGQPNKYKTPPVLDSDGSFFLYSLRTYDKS 297
DB 239 EEMTKKQVTLTCWVDFMPEDIIYEWNTNGKTELNYKTEPVLDSDGSFYFMISKLRVEKK 298
QY 298 RMOEGNVFSCSYMHEALHNHYTKSLSLGK 329
DB 299 NWVERNSYSCSVVHGLEHNNHHTKFSRTPGK 330

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RESULT 12
GCIM_MOUSE STANDARD; PRT; 393 AA.
ID GCIM_MOUSE
AC P01869;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig gamma-1 chain C region, membrane-bound form.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RX MEDLINE=80045036; PubMed=115593;
RA Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,
RA Takahashi N., Mano Y.;
RT "Cloning and complete nucleotide sequence of mouse immunoglobulin
RT gamma 1 chain gene."
RL Cell 18:559-568(1979).
RN [2]
RP SEQUENCE OF 323-393 FROM N.A.
RX MEDLINE=82197626; PubMed=6804950;
RA Tyler B.M., Cowman A.F., Gerondakis S.D., Adams J.M., Bernard O.;
RT "mRNA for surface immunoglobulin gamma chains encodes a highly
RT conserved transmembrane sequence and a 28-residue intracellular
RT domain."
RL Proc. Natl. Acad. Sci. U.S.A. 79:2008-2012(1982).
RN [3]
RP SEQUENCE OF 323-366 FROM N.A.
RX MEDLINE=82115295; PubMed=6799207;
RA Rogers J., Choi E., Souza L., Carter C., Word C.J., Kuehl M.,
RA Eisenberg D., Wall R.;
RT "Gene segments encoding transmembrane carboxyl termini of
RT immunoglobulin gamma chains."
RL Cell 26:19-27(1981).
RN [4]
RP SEQUENCE OF 1-44 FROM N.A.
RX MEDLINE=8222190; PubMed=6283537;
RA Yamawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;
RT "Nucleotide sequences of gene segments encoding membrane domains of
RT immunoglobulin gamma chains."
RL Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).
CC -!- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing, Named isoforms=2;
CC Name-Membrane-bound;
CC IsoID=P01869-1; Sequence=Displayed;
CC Name=Secreted;
CC IsoID=P01868-1; Sequence=External;
CC Note-May be the major isoform;
CC -----
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CC -----
DR EMBL; V00793; CAA24172.1; -.
DR EMBL; V00793; CAA24173.1; -.
DR PIR; B02159; GIMSW.
DR PDB; 15C8; 23-MAR-99.
DR PDB; 1A86; 18-MAR-98.
DR PDB; 1CL7; 12-JAN-00.
DR PDB; 1F11; 06-FEB-01.
DR PDB; 1F58; 29-DEC-99.
DR PDB; 1KCS; 24-JUL-02.
DR PDB; 1KCR; 11-MAY-02.
DR PDB; 25C8; 09-JUL-99.

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DR MGI:96446; Igh-4.  
DR InterPro; IPR007150; Ig-like.  
DR InterPro; IPR003597; Ig_c1.  
DR InterPro; IPR003006; Ig_MHC.  
DR Pfam; PF00047; Ig; 3.  
DR SMART; SM00407; Igc1; 2.  
DR PROSITE; PS00835; IG_LIKE; 3.  
DR PROSITE; PS00290; IG_MHC; 1.  
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;  
KW Alternative splicing; Transmembrane; 3D-structure.  
FT NON_TER 1  
FT DOMAIN 1 97 CH1.  
FT DOMAIN 98 110 HINGE.  
FT DOMAIN 111 217 CH2.  
FT DOMAIN 218 324 CH3.  
FT DISULFID 27 82  
FT DISULFID 102 102  
FT DISULFID 104 104 INTERCHAIN (WITH A LIGHT CHAIN).  
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).  
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).  
FT DISULFID 138 198  
FT CARBOHYD 174 174 N-LINKED (GLCNAC. . .).  
FT DISULFID 244 302  
FT TRANSMEM 340 337  
FT DOMAIN 358 393 POTENTIAL.  
SQ SEQUENCE 393 AA; 43386 MW; 4CC88343B7A1CE27 CRC64;  
  
Query Match 62.8%; Score 1101.5; DB 1; Length 393;  
Best Local Similarity 61.9%; Pred. No. 1.9e-75;  
Matches 203; Conservative 55; Mismatches 63; Indels 7; Gaps 4;  
  
QY 3 ASTKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPTVWSNMGALTSGVHTFPAVLQSS 62  
DB 1 AKTTPEPVPLAPGSAQAQNSMTLGLVKGYFPEPTVTVNSGSLSSGVHTFPAVLQSD 60  
  
QY 63 GLYSLSVVTVPSSSLGTYTCNVDPKPSNTKVDKRVESK--YGPFCPCPAPEFLGGP 120  
DB 61 -LYTSSSVTVPSRRPSETVTCNVAHPASSTKVDKIKVPRDCGKPC-ICTVPEV--S 115  
  
QY 121 SVFLPPPKPKDLMISRTPEVTCVVVDVSDPEQDFNMYVDGVEVHNKATKPREEQFNS 180  
DB 116 SVFIFFPKPKDVLITLPKVTCTVVDVSDKDPVEQFSFVDDVEVHTAQTQPREEQFNS 175  
  
QY 181 TVRVSVLTVLHODWLNKGYKCKVSNKGLPSSIEKTSKAGQPREPQVYTLPPSQHEM 240  
DB 176 TFRVSSELPIMHQDWLNKGYKCKVSNKGLPSSIEKTSKAGQPREPQVYTLPPSQHEM 235  
  
QY 241 TKNQVSLTCLVKGYFPSDIAVESNGOPENNYKTPPVLDSDGSEFPLYSLTVDKSRWQ 300  
DB 236 ADKVSILCMITDFFEDITVWQNGQPAENYKNTQPIIMNINGSYFVYSKLVNPKSNWE 295  
  
QY 301 EGNVFSVSMHEALNHYTQKSLSLG 328  
DB 296 AGNTFTCSVLHGLNHNHTEKSLSPG 323  
  
RESULT 13  
GCAM_MOUSE STANDARD; PRT; 399 AA.  
AC P01865;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 01-AUG-1991 (Rel. 19, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Ig gamma-2A chain C region, membrane-bound form.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=6222190; PubMed=6283537;  
RA Yamawaki-kataoka Y., Nakai S., Miyata T., Honjo T.;  
RT "Nucleotide sequences of gene segments encoding membrane domains of
```

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immunoglobulin gamma chains.";   
Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).  
CC -!- ALTERNATIVE PRODUCTS:  
CC Event-Alternative splicing; Named isoforms=2;  
CC Name-Membrane-bound;  
CC IsoId=P01865-1; Sequence=Displayed;  
CC Name=Secreted;  
CC IsoId=P01864-1; Sequence=External;  
CC Note=Probably the major isoform;  
CC -!- SIMILARITY: Contains 3 immunoglobulin-like domains.  
CC  
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CC  
CC EMBL; J00471; AAB59661.1; ALT_INIT.  
DR PIR; A02154; G2MSAM.  
DR PDB; 1KE5; 08-APR-98.  
DR PDB; 1YEE; 15-OCT-97.  
DR MGI:96443; Igh-1.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig_c1.  
DR InterPro; IPR003006; Ig_MHC.  
DR Pfam; PF00047; Ig; 2.  
DR SMART; SM00407; Igc1; 2.  
DR PROSITE; PS00835; IG_LIKE; 3.  
DR PROSITE; PS00290; IG_MHC; 1.  
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;  
KW Transmembrane; Alternative splicing; 3D-structure; Repeat.  
FT NON_TER 1 1  
FT DOMAIN 6 98 IG-LIKE 1.  
FT DOMAIN 121 220 IG-LIKE 2.  
FT DOMAIN 229 325 IG-LIKE 3.  
FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).  
FT DISULFID 27 82  
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).  
FT DISULFID 110 110 INTERCHAIN (WITH A HEAVY CHAIN).  
FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).  
FT DISULFID 144 204  
FT DISULFID 250 308  
FT TRANSMEM 346 363  
FT DOMAIN 364 399 POTENTIAL.  
FT CARBOHYD 180 180 CYTOPLASMIC (POTENTIAL).  
FT CARBOHYD 180 180 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 399 AA; 44020 MW; 4C38138BPAED3FE0 CRC64;  
  
Query Match 62.8%; Score 1101.5; DB 1; Length 399;  
Best Local Similarity 62.8%; Pred. No. 1.9e-75;  
Matches 208; Conservative 47; Mismatches 69; Indels 7; Gaps 4;  
  
QY 3 ASTKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPTVWSNMGALTSGVHTFPAVLQSS 62  
DB 1 AKTTAPSVVPLAPVCGDTTGSSTVGLVKGYFPEPTVTVNSGSLSSGVHTFPAVLQSD 60  
  
QY 63 GLYSLSVVTVPSSSLGTYTCNVDPKPSNTKVDKRVESKYP---PCP--SCPAPEL 117  
DB 61 -LYTSSSVTVTSSTWPSQITCNVAHPASSTKVDKIEPR-GPTIKPCPCCKCPAPNLL 118  
  
QY 118 GGPSVLEFPKPKDLMISRTPEVTCVVVDVSDPEQDFNMYVDGVEVHNKATKPREEQ 177  
DB 119 GGPSVFIFFPKIKDVLNLSLPIVTCVVVDVSDPEQDFNMYVDGVEVHNKATKPREEQ 178  
  
QY 178 FNSTYRVSVLTVLHODWLNKGYKCKVSNKGLPSSIEKTSKAGQPREPQVYTLPPSQ 237  
DB 179 YNSTLWVSALPIQHODWLNKGYKCKVSNKGLPSSIEKTSKAGQPREPQVYTLPPSQ 238  
  
QY 238 EEMTKNOVSLTCLVKGYFPSDIAVESNGQENNYKTPPVLDSDGSEFPLYSLTVDK 297  
DB 239 EEMTKNOVSLTCLVKGYFPSDIAVESNGQENNYKTPPVLDSDGSEFPLYSLTVDK 298
```

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QY 298 RWQEGNVFSCVMHEALHNNHYTKSLSLG 328
      |||:|||||:|||||:|||||:|||||:
Db 299 NWVERNSYSCSVWHEGLNHHHTKSFRTPG 329

RESULT 14
GCAB_MOUSE
ID GCAB_MOUSE STANDARD; PRT; 335 AA.
AC P01864;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 47, Last annotation update)
DE IG gamma-2A chain C region secreted form (B allele).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA MEDLINE=82037861; PubMed=6170065;
RX Schreier P.H., Bothwell A.L.M., Mueller-Hill B., Baltimore D.;
RT "Multiple differences between the nucleic acid sequences of the
  IGG2aa and IGG2ab alleles of the mouse.";
RL proc. Natl. Acad. Sci. U.S.A. 78:4495-4499(1981).
RN [2]
RP SEQUENCE.
RX MEDLINE=82037777; PubMed=6794027;
RA Dognin M.J., Lauwers M., Strosberg A.D.;
RT "Multiple amino acid substitutions between murine gamma 2a heavy
  chain Fc regions of Ig1a and Ig1b allotypic forms.";
RL proc. Natl. Acad. Sci. U.S.A. 78:4031-4035(1981).
CC -|- SURCELLULAR LOCATION: Secreted (Potential).
CC -|- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Secreted;
CC IsoId=P01864-1; Sequence=Displayed;
CC Note=Probably the major isoform;
CC Name=Membrane-bound;
CC IsoId=P01865-1; Sequence=External;
CC -|- MISCELLANEOUS: THE SEQUENCE DIFFERS FROM THAT OF THE A ALLELE,
CC FROM BALB/C MICE, AT 1% OF THE POSITIONS.
CC -|- SIMILARITY: Contains 3 immunoglobulin-like domains.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation
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CC -----
CC EMBL; J00479; -; NOT_ANNOTATED_CDS.
DR PIR; A02153; G2MSAB.
DR PDB; 1B0G; 23-MAR-99.
DR PDB; 1HH6; 26-JAN-01.
DR PDB; 1HH9; 12-JAN-01.
DR PDB; 1HI6; 08-FEB-01.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00407; IGC1; 2.
DR PROSITE; PS00835; IG_LIKE; 3.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Alternative splicing;
KW 3D-structure; Repeat.
FT NON_TER 1
FT DOMAIN 6 98 IG-LIKE 1.
FT DOMAIN 126 225 IG-LIKE 2.
FT DOMAIN 234 330 IG-LIKE 3.
FT SEQUENCE 335 AA; 36596 MW; FA3382792CBB1306 CRC64;
SQ

Query Match 62.7%; Score 1099; DB 1; Length 335;
Best Local Similarity 60.7%; Pred. No. 2.4e-75;
Matches 204; Conservative 53; Mismatches 69; Indels 10; Gaps 3;

QY 3 ASTKGPSVEPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 62
      |||:|||||:|||||:|||||:|||||:
Db 1 AKTTAPSVYPLVPVCGGTGSSVTLGCLVKGYFPEPTVLTWNSGSLSSGVHTFFALQ-S 59
      |||:|||||:|||||:|||||:|||||:
QY 63 GLYSLSVVTPSSSLGKTYYTQNVVDHKSNTKVDKRVESKY---GPPC-----PSCP 113
      |||:|||||:|||||:|||||:|||||:
Db 60 GLYTLSSSVTNTWPSQTITCNVAHPASSTKVDKIEPRVPTQNPCHPQRPVPCAA 119
      |||:|||||:|||||:|||||:|||||:
QY 114 REFLGSPSVLPPPKPKDTLMISRTPEVTCVVVDVSDPDQVQISWNVNNEVHTAQQT 173
      |||:|||||:|||||:|||||:|||||:
Db 120 PLLLGSPSVIFPPKIKDVLMSIPMTCCVVDDVSEDDPDQISWNVNNEVHTAQQT 179
      |||:|||||:|||||:|||||:|||||:
QY 174 REEQNSTYRVVSVLTVLDQWLGKSKCKVSKNGLPSSIEKTSKAKGQRPQVYTL 233
      |||:|||||:|||||:|||||:|||||:
Db 180 HREDYNSTLRVVSALPIQHDWMSCKEFCCKVNNRALPSPIEKTISKPRGVPRAQVYVL 239
      |||:|||||:|||||:|||||:|||||:
QY 234 PPSQEMTKNQVSLTCLVKGYFSPVDIAVWESNGQPENNYKTTPPVLDSDGSFYLSSLT 293
      |||:|||||:|||||:|||||:|||||:
Db 240 PPAPEMTKKFSLTGMTGLPDAIADWTSNGRTEQNTATVLDSDGSFYFWYKSR 299
      |||:|||||:|||||:|||||:|||||:
QY 294 VDKSRWQEGNVFSCVMHEALHNNHYTKSLSLG 329
      |||:|||||:|||||:|||||:|||||:
Db 300 VQKSTWERSLFPACSVVHEVHLNHLTTKTSRSLGK 335
      |||:|||||:|||||:|||||:|||||:

RESULT 15
GC3_MOUSE
ID GC3_MOUSE STANDARD; PRT; 329 AA.
AC P22436;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ig gamma-3 chain C region, secreted form.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85027161; PubMed=6092053;
RA Wels J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,
RA Tucker P.W., Blattner F.R.;
RT "Structural analysis of the murine IgG3 constant region gene.";
RL EMBO J. 3:2041-2046(1984).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; J00451; -; NOT_ANNOTATED_CDS.
DR PIR; B02156; G3MSC.
DR HSSP; P01857; 1FC1.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00407; IGC1; 2.
DR PROSITE; PS00835; IG_LIKE; 3.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW Transmembrane; Alternative splicing.
FT NON_TER 1
FT DOMAIN 98 113 CH1.
FT DOMAIN 114 223 HINGE.
FT SEQUENCE 329 AA; 36596 MW; FA3382792CBB1306 CRC64;
SQ

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FT DOMAIN 224 327 CH3
SQ SEQUENCE 329 AA; 36228 MW; F45827174182BAD6 CRC64;

Query Match 62.8%; Score 1098.5; DB 1; Length 329;
Best Local Similarity 61.8%; Pred. No. 2.5e-75;
Matches 204; Conservative 50; Mismatches 71; Indels 5; Gaps 2;

QY 4 STKGPSVEPLAPCSRSTSESTAALGCLVXDYPEPVTVSMNSGALTSGVHTTFAVLQSSG 63
Db :|||:||||: :|||:||||:||||:||||:||||:||||:||||:||||: 59
1 TTTAPSVYPLVPCSDTSSGVTLGCLVKGYPPEPVTVRWNYGALSSGVTVSSVLQ-SG 59

QY 64 LYSLSVTVTPSSSLGTYTCNVDHKPSNTKYDKRVESKY---GPPCPCPAPEFLGG 119
Db ||||:||||: :|||:||||: :|||:||||: :|||:||||: :|||:||||: 119
60 FYSLSLVTVPSSTWPSQTVICNVHPASKTELKRIEPIPKPSTPPGSSCPPGNILGG 119

QY 120 PSVLELPKPKDTLMISRTPEVTCVVVDYSDDEPVEQFNWYVDGVVHNAAKTPREBQFN 179
Db ||||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 179
120 PSVFIPEPKPKDALMISLTPKVTCCVVVDVSEDDPDVHVSFVNDKENVHTAMTQPREAQYN 179

QY 180 STYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAKGPREPQVYTLPPSOBE 239
Db ||||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 239
180 STRFVVSALPIQHODWNRGKEFKCKVYNNKALPAPIERTISKEPKGRAQTPQVYTIPEPREQ 239

QY 240 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFELYSLTVDKSRW 299
Db ||||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 299
240 MSKKKVSILTCLVNTFFSEAISEVWEERNGELEDQDYKNTPIILDSDGTFLYSLKLTVDTSW 299

QY 300 QEGNVPFCSVMHEALHNHYVTKSLSLGLK 329
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 329
300 LQGEIPTCSVMHEALHNHHTQKNLSRSPCK 329
```

Search completed: January 13, 2004, 12:39:29  
Job time : 14.3668 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 13, 2004, 12:20:44 ; Search time 58.9039 Seconds  
(without alignments)  
1441.318 Million cell updates/sec

Title: US-09-990-586-100  
Perfect score: 1754  
Sequence: 1 EFASIKGSPVFPPLACSRST.....MEALHNHYTKSLSLGK 329

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL.23.\*

- 1: sp\_archaea.\*
- 2: sp\_bacteria.\*
- 3: sp\_fungi.\*
- 4: sp\_human.\*
- 5: sp\_invertebrate.\*
- 6: sp\_mammal.\*
- 7: sp\_mhc.\*
- 8: sp\_organelle.\*
- 9: sp\_phage.\*
- 10: sp\_plant.\*
- 11: sp\_protein.\*
- 12: sp\_virus.\*
- 13: sp\_vertebrate.\*
- 14: sp\_unclassified.\*
- 15: sp\_rvirus.\*
- 16: sp\_bacteriap.\*
- 17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1743	99.4	473	4 Q8TC63	Q8tc63 homo sapien
2	1590.5	90.7	471	4 Q8TC77	Q8tc77 homo sapien
3	1578	90.0	521	4 Q8N4Y9	Q8n4y9 homo sapien
4	1570	89.5	509	4 Q8NF17	Q8nf17 homo sapien
5	1217	69.4	337	6 Q9SM34	Q9sm34 equus caball
6	1139.5	65.0	701	4 Q9PQ88	Q9pq88 homo sapien
7	1122.5	64.0	469	11 Q8R3V9	Q8r3v9 mus musculu
8	1119.5	63.8	463	11 Q99LC4	Q99lc4 mus musculu
9	1115.5	63.6	437	11 Q9R1A4	Q9r1a4 mus musculu
10	1112	63.4	473	11 Q9D8L4	Q9d8l4 mus musculu
11	1097.5	62.6	468	11 Q99L31	Q99l31 mus musculu
12	1087.5	62.6	473	11 Q99L25	Q99l25 mus musculu
13	1055.5	60.2	473	11 Q91Z05	Q91z05 mus musculu
14	1055.5	60.2	474	11 Q8R3H6	Q8r3h6 mus musculu
15	450	25.7	597	4 Q9BU10	Q9bu10 homo sapien
16	450	25.7	597	4 Q9BQB8	Q9bqb8 homo sapien

17	450	25.7	597	4	Q96BB9	Q96bb9 homo sapien
18	440	25.1	588	4	Q8WUX4	Q8wux4 homo sapien
19	440	25.1	613	4	Q96EY0	Q96ey0 homo sapien
20	440	25.1	613	4	Q8WUK1	Q8wuk1 homo sapien
21	440	25.1	614	4	Q96GA6	Q96ga6 homo sapien
22	440	25.1	618	4	Q96AA6	Q96aa6 homo sapien
23	417.5	23.8	613	11	Q8VCX7	Q8vcx7 mus musculu
24	409	23.3	278	11	Q921K1	Q921k1 mus musculu
25	402.5	22.9	375	4	Q9BSZ1	Q9bsz1 homo sapien
26	393	22.4	384	4	Q9UP60	Q9up60 homo sapien
27	393	22.4	493	4	Q8NCL6	Q8nc16 homo sapien
28	393	22.4	494	4	Q96K58	Q96k58 homo sapien
29	393	22.4	496	4	Q96KX8	Q96kx8 homo sapien
30	390	22.2	496	4	Q96DK0	Q96dk0 homo sapien
31	390	22.2	499	4	Q8NSK4	Q8nsk4 homo sapien
32	388	22.1	497	4	Q8WY24	Q8wy24 homo sapien
33	388	22.1	500	4	Q9BRV0	Q9brv0 homo sapien
34	383.5	21.9	416	4	Q9NPP6	Q9npp6 homo sapien
35	377.5	21.5	486	11	Q91207	Q91207 mus musculu
36	377.5	21.5	487	11	Q99KA4	Q99ka4 mus musculu
37	376.5	21.5	426	11	Q9DCD9	Q9dcd9 mus musculu
38	360	20.5	684	13	Q90544	Q90544 ginglymosto
39	358	20.4	481	11	Q91WT3	Q91wt3 mus musculu
40	358	20.4	481	11	Q91WT1	Q91wt1 mus musculu
41	358	20.4	482	11	Q91X92	Q91x92 mus musculu
42	358	20.4	482	11	Q8K172	Q8k172 mus musculu
43	358	20.4	484	11	Q8VEA0	Q8vea0 mus musculu
44	358	20.4	488	11	Q91WR1	Q91wr1 mus musculu
45	358	20.4	488	11	Q8XOF2	Q8xof2 mus musculu

#### ALIGNMENTS

#### RESULT 1

Q8TC63 ID Q8TC63 PRELIMINARY; PRT; 473 AA.  
AC Q8TC63;  
DT 01-JUN-2002 (T-EMBLrel. 21, Created)  
DT 01-JUN-2002 (T-EMBLrel. 21, Last sequence update)  
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N. A.  
RC TISSUE=Kidney;  
RA Strauberg R.;  
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
DR EXBL; BC025985; AAH25985.1; -.  
DR InterPro; IPR000923; BlueCu.1.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 4.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00196; COPPER\_BLUE; 1.  
DR PROSITE; PS00835; IG\_LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; 3.  
KW Hypothetical protein.  
SQ SEQUENCE 473 AA; 51986 MW; E29920B09BA369F5 CRC64;

Query Match 99.4%; Score 1743; DB 4; Length 473;  
Best Local Similarity 100.0%; Pred. No. 3.1e-150;  
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 ASIKGSPVFPPLACSRSTSESTAAALCLVKDYPPPEVTYSWNSGALTSQVHFPVQLQS 62  
Db 147 ASIKGSPVFPPLACSRSTSESTAAALCLVKDYPPPEVTYSWNSGALTSQVHFPVQLQS 206  
Qy 63 GLYSLGSWTVTPSSSLGTGTYTTCNVDPKPSNTKVDKRVESKYGPFCPCFAPEFLGGPSV 122

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Db 207 GLYSLSSVTVFPSSSLGKTKYTCNVNDHKPSNTKYDKVSKYGPCCSCPAPEFLGSPV 266
Qy 123 FLFPKPKDMLMISRTPEVTCVVVDVQEDPEVQFNWYVDGVEVHNATKTPREQFNSTY 182
Db 267 FLFPKPKDMLMISRTPEVTCVVVDVQEDPEVQFNWYVDGVEVHNATKTPREQFNSTY 326
Qy 183 RVSVSLTVLHODWLNKGYKCKVSNKGLPSSIEKTSKAGQPREPQVYTLPPSQEEMTK 242
Db 327 RVSVSLTVLHODWLNKGYKCKVSNKGLPSSIEKTSKAGQPREPQVYTLPPSQEEMTK 386
Qy 243 NOVSLTCLVKGYFSDIAVEVESNGQPENNYKTPPPVLDSDGSFPLYSLRTVDSKRWQEG 302
Db 387 NOVSLTCLVKGYFSDIAVEVESNGQPENNYKTPPPVLDSDGSFPLYSLRTVDSKRWQEG 446
Qy 303 NVFSCSVNHEALHNHYTKSLSLGGK 329
Db 447 NVFSCSVNHEALHNHYTKSLSLGGK 473

RESULT 2
Q8TC77 PRELIMINARY; PRT; 471 AA.
AC Q8TC77;
DT 01-JUN-2002 (TREMELrel. 21, Created)
DT 01-JUN-2002 (TREMELrel. 21, Last sequence update)
DT 01-MAR-2003 (TREMELrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC024289; AAH24289.1; -.
DR InterPro; IPR007110; IG_LIKE.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 4.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 2.
KW Hypothetical protein.
SQ SEQUENCE 471 AA; 51791 MW; 388F7F4CF588660E CRC64;

Query Match 90.7%; Score 1590.5; DB 4; Length 471;
Best Local Similarity 90.9%; Pred. No. 2.4e-136;
Matches 300; Conservative 12; Mismatches 15; Indels 3; Gaps 1;

Qy 3 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 62
Db 142 ASTKGPSVFPLAPSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 201
Qy 63 GLYSLSSVTVFPSSSLGKTKYTCNVNDHKPSNTKYDKVSKYGPCCSCPAPEFLGG 119
Db 202 GLYSLSSVTVFPSSSLGKTKYTCNVNHKPSNTKYDKVSKYGPCCSCPAPELLGG 261
Qy 120 PSVFLFPKPKDMLMISRTPEVTCVVVDVQEDPEVQFNWYVDGVEVHNATKPREQFN 179
Db 262 PSVFLFPKPKDMLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREQYN 321
Qy 180 STYRVSVSLTVLHODWLNKGYKCKVSNKGLPSSIEKTSKAGQPREPQVYTLPPSQEE 239
Db 322 STYRVSVSLTVLHODWLNKGYKCKVSNKGLPAPIEKTSKAGQPREPQVYTLPPSRDE 381
Qy 240 MTKNQVSLTCLVKGYFSDIAVEVESNGQPENNYKTPPPVLDSDGSFPLYSLRTVDSKRW 299
Db 382 LTKNQVSLTCLVKGYFSDIAVEVESNGQPENNYKTPPPVLDSDGSFPLYSLRTVDSKRW 441
Qy 300 QEGNVFSCSVNHEALHNHYTKSLSLGGK 329
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Db 442 QQGNVFCSVNHEALHNHYTKSLSLSPGK 471

RESULT 3
Q8N4Y9 PRELIMINARY; PRT; 521 AA.
AC Q8N4Y9;
DT 01-OCT-2002 (TREMELrel. 22, Created)
DT 01-OCT-2002 (TREMELrel. 22, Last sequence update)
DT 01-MAR-2003 (TREMELrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells from Tonsils;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC033178; AAH33178.1; -.
DR InterPro; IPR007110; IG_LIKE.
DR InterPro; IPR003597; IG_C1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 4.
DR SMART; SM00407; IG_C1; 3.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 2.
KW Hypothetical protein.
SQ SEQUENCE 521 AA; 57156 MW; 2AC7D22E72D6CAA2 CRC64;

Query Match 90.0%; Score 1578; DB 4; Length 521;
Best Local Similarity 79.8%; Pred. No. 3.8e-135;
Matches 301; Conservative 11; Mismatches 15; Indels 50; Gaps 1;

Qy 3 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 62
Db 145 ASTKGPSVFPLAPCSRSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 204
Qy 63 GLYSLSSVTVFPSSSLGKTKYTCNVNDHKPSNTKYDKVSKYGPCCSCPAPEFLGSPKPKDT 132
Db 205 GLYSLSSVTVFPSSSLGKTKYTCNVNHKPSNTKYDKVSKYGPCCSCPAPEFLGSPKPKDT 264
Qy 104 -----YGPCCSCPAPEFLGSPSVLFPKPKDT 132
Db 265 DTFPPCPKPKPKSCDTPPCPCPKPKSCDTPPCPCPAPELLGGPSVFLFPKPKDT 324
Qy 133 LMISRTPEVTCVVVDVQEDPEVQFNWYVDGVEVHNATKPREQFNSTYRVSVSLTVLH 192
Db 325 LMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNATKPREQFNSTYRVSVSLTVLH 384
Qy 193 QDWLNKGYKCKVSNKGLPSSIEKTSKAGQPREPQVYTLPPSQEEMTKNQVSLTCLVK 252
Db 385 QDWLNKGYKCKVSNKGLPAPIEKTSKAGQPREPQVYTLPPSQEEMTKNQVSLTCLVK 444
Qy 253 GYPYSDIAVEVESNGQPENNYKTPPPVLDSDGSFPLYSLRTVDSKRWQEGNVFSCSVNHE 312
Db 445 GFYPSDIAVEVESNGQPENNYKTPPPVLDSDGSFPLYSLRTVDSKRWQEGNVFSCSVNHE 504
Qy 313 ALHNHYTKSLSLGGK 329
Db 505 ALHNHYTKSLSLGGK 521

RESULT 4
Q8NF17 PRELIMINARY; PRT; 509 AA.
AC Q8NF17;
DT 01-OCT-2002 (TREMELrel. 22, Created)
DT 01-OCT-2002 (TREMELrel. 22, Last sequence update)
```

DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)  
DE FLJ00385 protein (Fragment).  
GN FLJ00385.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Spleen.  
RA Jikuya H., Takano J., Kikuro R., Nagase T., Ohara O.;  
RT "The nucleotide sequence of a long cDNA clone isolated from human spleen."  
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AK090464; BAC03445.1; -  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003597; IG-cl.  
DR InterPro; IPR003006; IG\_MHC.  
DR Pfam; PF00047; IG\_3.  
DR SMART; SM00407; IGcl; 3.  
DR PROSITE; PS00835; IG LIKE; 3.  
DR PROSITE; PS00290; IG\_MHC; 2.  
FT NON TER 1  
SQ SEQUENCE 509 AA; 56111 MW; 089498D8076E5863C CRC64;  
  
Query Match 79.5%; Score 1570; DB 4; Length 509;  
Best Local Similarity 79.9%; Pred. No. 2e-134;  
Matches 299; Conservative 11; Mismatches 14; Indels 50; Gaps 1;  
  
QY 3 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSNWNSGALTSGVHTFPAVLQSS 62  
DB 64 ASTKGPSVFPLAPCSRSTSGTALGCLVKDYFPEPTVSNWNSGALTSGVHTFPAVLQSS 123  
  
QY 63 GLYSLSVVTVFSSSLGKTTCNVYDHPKSNKVDKRVESK----- 103  
DB 124 GLYSLSVVTVFSSSLGKTTCNVYDHPKSNKVDKRVELTPLGDTTHTCPCPEPKSC 183  
  
QY 104 -----YGPCCSCPAPEFLGGPSVFLPPPKPDT 132  
DB 184 DTPPCPCPEPKSCDTPPPCPCPEPKSCDTPPPCPCPAPELLGGPSVFLPPPKPDT 243  
  
QY 133 LMISRTPEVTCVVVDVSDVEDPEVQFNWYVDGVEVHNAKTKPREQFNSTYRVWSVLTVLH 192  
DB 244 LMISRTPEVTCVVVDVSDVEDPEVQFNWYVDGVEVHNAKTKPREQFNSTYRVWSVLTVLH 303  
  
QY 193 QDWLNGKEYKCKVSNKGLPSSIEKTIISKAKGPREPQVYTIIPQSEEMTKNQVSLTCLVK 252  
DB 304 QDWLNGKEYKCKVSNKGLPAPLIEKTIISKAKGPREPQVYTIIPQSEEMTKNQVSLTCLVK 363  
  
QY 253 GFPYSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSLRTVDSKRWQEGNVFSCSVNHE 312  
DB 364 GFPYSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSLRTVDSKRWQEGNVFSCSVNHE 423  
  
QY 313 ALHNYTKQSLSL 326  
DB 424 ALHNYTKQSLSL 437  
  
RESULT 5  
Q95M34 PRELIMINARY; PRT; 337 AA.  
ID AC Q95M34  
AC Q95M34; (TReMBLrel. 19, Created)  
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)  
DT 01-DEC-2001 (TReMBLrel. 23, Last annotation update)  
DE Immunoglobulin gamma 1 heavy chain constant region (Fragment).  
GN IGHC1.  
OS Equus caballus (Horse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.  
OX NCBI\_TaxID=9796;  
RN [1]  
RP SEQUENCE FROM N.A.

RA Wagner B.;  
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98383416; PubMed=9717671;  
RA Wagner B., Overesch G., Sheoran A., Holmes M., Richards C.,  
RA Leibold W., Radbruch A.;  
RT "Organization of the equine immunoglobulin heavy chain constant region genes. III. Alignment of c-mu, c-gamma, c-epsilon and c-alpha genes."  
RL Immunobiology 199;105-119(1998).  
DR EMBL; AJ300675; CAC44624.1; -  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003597; IG-cl.  
DR Pfam; PF00047; IG\_2.  
DR SMART; SM00407; IGcl; 2.  
DR PROSITE; PS00835; IG LIKE; 3.  
DR PROSITE; PS00290; IG\_MHC; 2.  
FT NON TER 1  
SQ SEQUENCE 337 AA; 37438 MW; A60BF2B01DEFD1F6 CRC64;  
  
Query Match 69.4%; Score 1217; DB 6; Length 337;  
Best Local Similarity 66.3%; Pred. No. 1.6e-102;  
Matches 226; Conservative 46; Mismatches 51; Indels 18; Gaps 3;  
  
QY 3 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSNWNSGALTSGVHTFPAVLQSS 62  
DB 1 ASTAPKVPALAPGCGTSDSTVALGCLVSGYFPEPKVSNWNSGALTSGVHTFPAVLQSS 60  
  
QY 63 GLYSLSVVTVFSSSLGKTTCNVYDHPKSNKVDKRVESK-----SKYGPCCPS 110  
DB 61 GFYSLSSVMVTPASTWTSETYICNVVHAASNFVKDKRIEPIPDNHQKVKCDMSK---CPK 116  
  
QY 111 CPAPEFLGGPSVFLPPPKPDTLMISRTPEVTCVVVDVSDVEDPEVQFNWYVDGVEVHNAK 170  
DB 117 CPAPEFLGGPSVFLPPPKPDTLMISRTPEVTCVVVDVSDVEDPEVQFNWYVDGVEVHNAK 176  
  
QY 171 TKPREQFNSTYRVWSVLTVLHQQDWLNGKEYKCKVSNKGLPSSIEKTIISKAKGPREPQV 230  
DB 177 TRPKPEQFNSTYRVWSVLTVLHQQDWLNGKEYKCKVSNKGLPSSIEKTIISKAKGPREPQV 236  
  
QY 231 YLTPPQSEEMTKNQVSLTCLVKGFPSDTAVWESNGQP--ENNYKTTPPVLDSDGSFYL 288  
DB 237 YLAPHPDLSKSKSVTCLVKDFYPPEINIEQWNGQPELETKYSTTQAQDSDGSYFL 296  
  
QY 289 YSLTVDKSRWQEGNVFSCSVNHEALHNYTKQSLSLSLGK 329  
DB 297 YSLVDNRWQCGITFTCGVWHEALHNYTKQVSKNFGK 337  
  
RESULT 6  
Q96P08 PRELIMINARY; PRT; 701 AA.  
ID AC Q96P08  
AC Q96P08; (TReMBLrel. 19, Created)  
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)  
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)  
DE Factor VII active site mutant immunofugate.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21477448; PubMed=11593034;  
RA Hu Z., Garen A.;  
RT "Targeting tissue factor on tumor vascular endothelial cells and tumor cells for immunotherapy in mouse models of prostatic cancer."  
RL Proc Natl. Acad. Sci. U.S.A. 98:12180-12185(2001).  
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.  
DR EMBL; AF272774; AAK58686.1; -  
DR HSP; P00761; IAN1.  
DR InterPro; IPR000152; Asx\_hydroxyl.



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DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR000742; EGF 2.
DR InterPro: IPR001881; EGF_Ca.
DR InterPro: IPR001438; EGF_III.
DR InterPro: IPR006209; EGF-like.
DR InterPro: IPR002383; GLA blood.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003597; Ig c1.
DR InterPro: IPR001306; Ig MHC.
DR InterPro: IPR001254; Ser. protease Try.
DR InterPro: IPR000294; vit_k_dep_GLA.
DR Pfam: PF00008; EGF_2.
DR Pfam: PF00047; Ig; 2.
DR Pfam: PF00089; trypsin; 1.
DR PRINTS: PRO0722; CHYMOTRYPSIN.
DR PRINTS: PRO0010; EGFLOOD.
DR PRINTS: PRO0001; GLABLOOD.
DR SMART: SM00179; EGF_CA; 1.
DR SMART: SM00069; GLA; 1.
DR SMART: SM00020; Tryp_SPC; 1.
DR PROSITE: PS00010; ASX HYDROXYL; 1.
DR PROSITE: PS00022; EGF_1; 1.
DR PROSITE: PS01186; EGF_2; 1.
DR PROSITE: PS01187; EGF_CA; 1.
DR PROSITE: PS00011; GLU CARBOXYLATION; 1.
DR PROSITE: PS00835; IG LIKE; 2.
DR PROSITE: PS00290; IG MHC; 1.
DR PROSITE: PS00240; TRYPSIN_DOM; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; 1.
DR PROSITE: PS00135; TRYPSIN_SER; 1.
DR EGF-like domain; Hydrolase; Protease; Serine protease.
KW EGF-like domain; Hydrolase; Protease; Serine protease.
SQ SEQUENCE 701 AA; 77826 MW; 9456C6B42CC992F CRC64;

Query Match 65.0%; Score 1139.5; DB 4; Length 701;
Best Local Similarity 73.0%; Pred. No. 5,1e-95;
Matches 219; Conservative 17; Mismatches 33; Indels 31; Gaps 3;

QY 41 VSNWGSALTSG-----VHTFPAVLQSSGLYSSVVTPSSSLGKTTCNVDH 89
DB 422 VSWGQCATVGHFVYTRVSQVIEWLQKLMSEPRFGVLLRAPFGSA---EPKSCDTH 478

QY 90 KPSNTKVDKRVESKYGPPCPAPFELGSPSVFLFPPKPKDTLMISRTPEVTCVVDVS 149
DB 479 -----TCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVS 521

QY 150 QEDPEVQFNWYDGVENVNAKTPREBQFNSTYRVSVLTVLHQDLNKGKEYKCKVSKNG 209
DB 522 HEDPEVKFNWYDGVENVNAKTPREBQFNSTYRVSVLTVLHQDLNKGKEYKCKVSKNKA 581

QY 210 LPSSTIEKTSKAGQGPPEQVYTLPPSOBEMTKQVSLTCLVKGFPSPDIAVEVESNGQP 269
DB 582 LPAPEKTSKAGQGPPEQVYTLPPSRDELTKQVSLTCLVKGFPSPDIAVEVESNGQP 641

QY 270 ENNYKTPPVLDSGDSFFLYSLRTVYDKRWEGNWFVSCVMHEALHNNHYTKSLSLGGK 329
DB 642 ENNYKTPPVLDSGDSFFLYSLRTVYDKRWQGNWFVSCVMHEALHNNHYTKSLSLSPGK 701

RESULT 7
Q8R3V9 ID Q8R3V9 PRELIMINARY; PRT; 469 AA.
AC Q8R3V9;
DT 01-JUN-2002 (TREMELrel. 21, Created)
DT 01-JUN-2002 (TREMELrel. 21, Last sequence update)
DT 01-WAR-2003 (TREMELrel. 23, Last annotation update)
DE Hypothetical 52.0 kDa protein.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]

SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR ENBL; BC024405; AAH24405.1; -.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_v.
DR Pfam: PF00047; Ig; 4.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 469 AA; 51976 MW; 534793F155D08457 CRC64;

Query Match 64.0%; Score 1122.5; DB 11; Length 469;
Best Local Similarity 62.9%; Pred. No. 1e-93;
Matches 207; Conservative 53; Mismatches 62; Indels 7; Gaps 4;

QY 3 ASTKGPSVPEPLAPCSRSTSESTAALGCLVKDYFPPSVTVSNWNSGALTSVHTFPAVLQSS 62
DB 146 AKTTPPSVYPLAPGSAQAQNSMTVGLCLVKGYFPEPVTVWNSGSLSSGVHTFPAVLQSD 205

QY 63 GLYSLSVVTVPSSSISLTGKTYTCNVDHKPSNTKVDKRVESK--YGPSPCPAPFELGSP 120
DB 206 -LYTLSSSVTVPSSTWPSQTVCNVAHPASSTKVDKIVPRDCGCKPC-ICTVPEV--S 260

QY 121 SVFLPPPKPKDTLMISRTPEVTCVVDVSQEDPEVQFNWYDGVENVNAKTPREBQFN 180
DB 261 SVFIPEPKPKDTLITLTKVTCVVDVDSKDDPEVQFQFVDFVDDVHTAQTAKPREBQFN 320

QY 181 TYRVSVLTVLHQDLNKGKEYKCKVSNKGLPISIEKTSKAGQGPPEQVYTLPPSQEEM 240
DB 321 TFRSVSELPFIMHQDLNKGKEYKCKRVNSAFAFPAPEKTSKTKGRPKAQQVYTIIPKQEQM 380

QY 241 TNQVSLTCLVKGFPSPDIAVEVESNGQPENNYKTPPVLDSGDSFFLYSLRTVYDKSRWQ 300
DB 381 AKDKVSLTCLVTDFFPEDITVEQWNGQPAENYKNTQPTIMDTDGSFYFVSKLVNQSKE 440

QY 301 EGNVFCSCVMHEALHNNHYTKSLSLGGK 329
DB 441 AGNTFTCSVLHGLNHNHTEKSLSHSPGK 469

RESULT 8
Q99LC4 ID Q99LC4 PRELIMINARY; PRT; 463 AA.
AC Q99LC4;
DT 01-JUN-2001 (TREMELrel. 17, Created)
DT 01-JUN-2001 (TREMELrel. 17, Last sequence update)
DT 01-MAR-2003 (TREMELrel. 23, Last annotation update)
DE Similar to RIKEN cdna 1810060009 gene.
GN IGH-4.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]

SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR ENBL; BC003435; AAH03435.1; -.
DR HSSP; P01842; 7FAB.
DR MGD; MGI:96446; Igh-4.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_v.
DR Pfam: PF00047; Ig; 4.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 1.
KW PROSITE; PS00290; IG_MHC; 1.
SQ SEQUENCE 463 AA; 51007 MW; EAA674C6BEC30783 CRC64;

Query Match 63.8%; Score 1119.5; DB 11; Length 463;
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Best Local Similarity 62.6%; Pred. No. 1.9e-93;
Matches 206; Conservative 54; Mismatches 62; Indels 7; Gaps 4;

QY 3 ASTKGPSVPLAPCSRSTSESTAALGCLVKDYFPEPVTVWNQSGALTSGVHTFPAVLQSS 62
Db 140 AKTTPSVVPLAPGAAQNSMTVIGLVKGYFPEPVTVWNQSGLSGVHTFPAVLQSD 199
QY 63 GLYSLSVVTVFSSSLGTYTCNVDHKPSNTKVDKRVESK--YGPCCPSCPAPFELGGP 120
Db 200 -LYTLSSVTVFSSWTPSETVTCNVAHPASSTKVDKIVPRDCGKPC-ICTVPEV---S 254
QY 121 SVFLPPPKDPTLMISRTPEVTCVVVDVSOEDPEVQFNWYVDGVVHNKATKPREEQFNS 180
Db 255 SVFIFFPKPKDPTLITLTPKVTCTVVVDISKDDDEVQFNFVDDVEVHTACTQPREEQFNS 314
QY 181 TYRVSVLVTLVHODWLNKGEYKCKVNSKGLPSPSIEKTSISKAKQPREPQVYTLPPSQEEM 240
Db 315 TFRSVSELPIMHQDWLNKGEYKCKVNSAAPPAPAEIEKTSISKGRPKAPQVYTLPPKPEQM 374
QY 241 TKNOVSLTCLVKGFPSPDIADVESNGQPNENYKTTTPVLDSDGSPFLYSRLTVDKSRWQ 300
Db 375 AKDKVSLTCMTITDFPEDITVEMQNGQPAENYKNTQPIMDTDGSPFLYSRLTVDKSRWQ 434
QY 301 EGNVFCSCVMEALHNHYTKSLSLGK 329
Db 435 AGNTFTCSVLHGLHNHTEKLSHSPGK 463

RESULT 9
QY 9R1A4 PRELIMINARY; PRT; 437 AA.
ID Q9R1A4
AC Q9R1A4
DT 01-WAY-2000 (TrEMBLrel. 13, Created)
DT 01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-WAY-2003 (TrEMBLrel. 23, Last annotation update)
DE Gammai heavy chain of Mab7 (Fragment).
GN IGH-4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
RT "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
RT antibody (Mab 7, its light and heavy chains) and construction of a
RT single chain antibody (scFv)".
RL Submitted (WAY-1999) to the EMBL/GenBank/DDBJ databases.
DR EMBL; A152372; AAD40243.1; -.
DR FSSP; P01842; 7FAB.
DR MGD; MGI:96446; Igh-4.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 4.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PSS0835; IG-LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 1.
FT NON_TER 1
FT NON_TER 437
SQ SEQUENCE 437 AA; 48142 MW; 5C3A7BB3E7D697C CRC64;

Query Match 63.6%; Score 1115.5; DB 11; Length 437;
Best Local Similarity 62.3%; Pred. No. 4.1e-93;
Matches 205; Conservative 55; Mismatches 62; Indels 7; Gaps 4;

QY 3 ASTKGPSVPLAPCSRSTSESTAALGCLVKDYFPEPVTVWNQSGALTSGVHTFPAVLQSS 62
Db 114 AKTTPSVVPLAPGAAQNSMTVIGLVKGYFPEPVTVWNQSGLSGVHTFPAVLQSD 173
QY 63 GLYSLSVVTVFSSSLGTYTCNVDHKPSNTKVDKRVESK--YGPCCPSCPAPFELGGP 120
Db 174 -LYTLSSVTVFSSWTPSETVTCNVAHPASSTKVDKIVPRDCGKPC-ICTVPEV---S 228

Best Local Similarity 62.6%; Pred. No. 1.9e-93;
Matches 206; Conservative 54; Mismatches 62; Indels 7; Gaps 4;

QY 121 SVFLPPPKDPTLMISRTPEVTCVVVDVSOEDPEVQFNWYVDGVVHNKATKPREEQFNS 180
Db 229 SVFIFFPKPKDPTLITLTPKVTCTVVVDISKDDDEVQFNFVDDVEVHTACTQPREEQFNS 288
QY 181 TYRVSVLVTLVHODWLNKGEYKCKVNSKGLPSPSIEKTSISKAKQPREPQVYTLPPSQEEM 240
Db 289 TFRSVSELPIMHQDWLNKGEYKCKVNSAAPPAPAEIEKTSISKGRPKAPQVYTLPPKPEQM 348
QY 241 TKNOVSLTCLVKGFPSPDIADVESNGQPNENYKTTTPVLDSDGSPFLYSRLTVDKSRWQ 300
Db 349 AKDKVSLTCMTITDFPEDITVEMQNGQPAENYKNTQPIMDTDGSPFLYSRLTVDKSRWQ 408
QY 301 EGNVFCSCVMEALHNHYTKSLSLGK 329
Db 409 AGNTFTCSVLHGLHNHTEKLSHSPGK 437

RESULT 10
QY Q9D8L4 PRELIMINARY; PRT; 473 AA.
ID Q9D8L4
AC Q9D8L4
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE 1810060009Rik protein.
GN IGH-1 OR 1810060009RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=C57BL/6J; TISSUE=Pancreas;
RA MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Giasi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Resole G., Quackenbush J.,
RA Schiraldi L.M., Staudl F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S.,
RA Hayaishizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK007918; BAB29349.1; -.
DR FSSP; P01842; 7FAB.
DR MGD; MGI:96443; Igh-1.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 4.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PSS0835; IG-LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 1.
SQ SEQUENCE 473 AA; 51699 MW; 9DED57A514475FBB CRC64;

Query Match 63.4%; Score 1112; DB 11; Length 473;
Best Local Similarity 61.3%; Pred. No. 9.5e-93;
Matches 206; Conservative 53; Mismatches 67; Indels 10; Gaps 3;

QY 3 ASTKGPSVPLAPCSRSTSESTAALGCLVKDYFPEPVTVWNQSGALTSGVHTFPAVLQSS 62
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Db 139 AKTAPSVYPLAPVCGGTTGSSVTGLCLVKGYPPEPVTLTWNSSLSGGVHTPPALQ-S 197
Qy 63 GLYSLSVVTPSSSLGTTTCNVVDHFKPSNTKDKRVESKYG-----PP---CPSCPA 113
Db 198 GLYTLSSSVTVTSNTQPTTCNVVNAHPASSTKVDKIEPRVPTQNPCKPLKECPCAA 257
Qy 114 PEFLLGGSVFLPPPKPKDITLMSRTPETCVVVDVSDDEPVEQFNWYVDGVVHNAKTKP 173
Db 258 PDLLGGSPSVFFPPKIKDVLMSLSPMVTCVVVDSEDDPDVQISWFWVNVVHTAQTT 317
Qy 174 REEQNSTYRVSVLTVLHODWLNKGYKCKVSNKGLPSSIEKTIISAKGQPREPOVYTL 233
Db 318 HREDYNTSLRVVSALPIQHDWMSGKFEKCKVNNRALSPIETKISKRGFVRAPQYVL 377
Qy 234 PPSQEMTKNOVSLTCLVKGFPSPDIAVWESNGQPNKYKTPPVLDSGSPFLYSLRT 293
Db 378 PPPAEMTKKPSLTCTMTGFLPARIAVDWTSNGRTEQYKNTATVLDSGSPFYMSKLR 437
Qy 294 VDKRWQGNVFCSCVMHEALHNHYTKQSLSLGK 329
Db 438 VOKSTWERSGLFACSVVHGLHNHLLTTKTSRSLGK 473

RESULT 11
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AC Q99L31;
DT 01-JUN-2001 (T-EMBLrel. 17, Created)
DT 01-JUN-2001 (T-EMBLrel. 17, Last sequence update)
DE 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
DE Similar to RIKEN CDNA 1810060009 gene.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003878; AA039878.1; -.
DR HSSP; P01842; 7FAB.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; IG_3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 1.
DR PROSITE; PS00290; IG_MHC; 1.
SQ SEQUENCE 468 AA; 51661 MW; 96352328B3332ADB CRC64;

Query Match 62.6%; Score 1097.5; DB 11; Length 468;
Best Local Similarity 62.7%; Pred. No. 2e-91;
Matches 208; Conservative 47; Mismatches 70; Indels 7; Gaps 4;

Qy 3 ASTKGSVPFLAPCSRSTSESTAALGCLVKDYFPPVTVSMNSGALTSGVHTFPAVLQSS 62
Db 139 AKTAPSVYPLAPVCGGTTGSSVTGLCLVKGYPPEPVTLTWNSSLSGGVHTFPAVLQSD 198
Qy 63 GLYSLSVVTPSSSLGTTTCNVVDHFKPSNTKDKRVESKYGP---PCP--SCPAPEFL 117
Db 199 -LYTLSSSVTVTSSTWPSQITCNVAHPASSTKVDKIEPR-GPTIKCPCKCPAPNLL 256
Qy 118 GGPSVFLFPKPKDITLMSRTPETCVVVDVSDDEPVEQFNWYVDGVVHNAKTKPREEQ 177
Db 257 GGPSVFIFFPKIKDVLMSLSPMVTCVVVDSEDDPDVQISWFWVNVVHTAQTTTHRED 316
Qy 178 FNSTYRVSVLTVLHODWLNKGYKCKVSNKGLPSSIEKTIISAKGQPREPOVYTLPPSQ 237
Db 317 YNSTLRVVSALPIQHDWMSGKFEKCKVNNKALPAPIERTISKPGSVRAPQVYVLPPE 376
Qy 238 EEMTKNQVSLTCLAVKGFPSPDIAVWESNGQPNKYKTPPVLDSGSPFLYSLRTVDKS 297
Db 377 EEMTKNQVTLTCNVTDMPEDIVVETWNNKGLTSLYKNTPEVLDSDGSPFYMSKLRVKK 436

Query Match 62.6%; Score 1097.5; DB 11; Length 468;
Best Local Similarity 62.7%; Pred. No. 2e-91;
Matches 208; Conservative 47; Mismatches 70; Indels 7; Gaps 4;

Qy 3 ASTKGSVPFLAPCSRSTSESTAALGCLVKDYFPPVTVSMNSGALTSGVHTFPAVLQSS 62
Db 144 AKTAPSVYPLAPVCGGTTGSSVTGLCLVKGYPPEPVTLTWNSSLSGGVHTFPAVLQSD 203
Qy 63 GLYSLSVVTPSSSLGTTTCNVVDHFKPSNTKDKRVESKYGP---PCP--SCPAPEFL 117
Db 204 -LYTLSSSVTVTSSTWPSQITCNVAHPASSTKVDKIEPR-GPTIKCPCKCPAPNLL 261
Qy 118 GGPSVFLFPKPKDITLMSRTPETCVVVDVSDDEPVEQFNWYVDGVVHNAKTKPREEQ 177
Db 262 GGPSVFIFFPKIKDVLMSLSPMVTCVVVDSEDDPDVQISWFWVNVVHTAQTTTHRED 321
Qy 178 FNSTYRVSVLTVLHODWLNKGYKCKVSNKGLPSSIEKTIISAKGQPREPOVYTLPPSQ 237
Db 322 YNSTLRVVSALPIQHDWMSGKFEKCKVNNKALPAPIERTISKPGSVRAPQVYVLPPE 381
Qy 238 EEMTKNQVSLTCLAVKGFPSPDIAVWESNGQPNKYKTPPVLDSGSPFLYSLRTVDKS 297
Db 382 EEMTKNQVTLTCNVTDMPEDIVVETWNNKGLTSLYKNTPEVLDSDGSPFYMSKLRVKK 441
Qy 298 RWQEGNVFCSCVMHEALHNHYTKQSLSLGK 329
Db 442 NWVERNSYSCSVVHGLHNHHTTKSPSRTPGK 473

RESULT 13
Q91205 PRELIMINARY; PRT; 473 AA.
AC Q91205;
DT 01-DEC-2001 (T-EMBLrel. 19, Created)
DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
DE Hypothetical 51.9 kDa protein.
GN AU049491.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
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Qy 298 RWQEGNVFCSCVMHEALHNHYTKQSLSLGK 329
Db 437 NWVERNSYSCSVVHGLHNHHTTKSPSRTPGK 468

RESULT 12
Q99L25 PRELIMINARY; PRT; 473 AA.
AC Q99L25;
DT 01-JUN-2001 (T-EMBLrel. 17, Created)
DT 01-JUN-2001 (T-EMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
DE Similar to RIKEN CDNA 1810060009 gene.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003888; AA03888.1; -.
DR HSSP; P01842; 7FAB.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG_3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 1.
DR PROSITE; PS00290; IG_MHC; 1.
SQ SEQUENCE 473 AA; 52449 MW; BE9889B7986DA155 CRC64;

Query Match 62.6%; Score 1097.5; DB 11; Length 473;
Best Local Similarity 62.7%; Pred. No. 2e-91;
Matches 208; Conservative 47; Mismatches 70; Indels 7; Gaps 4;

Qy 3 ASTKGSVPFLAPCSRSTSESTAALGCLVKDYFPPVTVSMNSGALTSGVHTFPAVLQSS 62
Db 144 AKTAPSVYPLAPVCGGTTGSSVTGLCLVKGYPPEPVTLTWNSSLSGGVHTFPAVLQSD 203
Qy 63 GLYSLSVVTPSSSLGTTTCNVVDHFKPSNTKDKRVESKYGP---PCP--SCPAPEFL 117
Db 204 -LYTLSSSVTVTSSTWPSQITCNVAHPASSTKVDKIEPR-GPTIKCPCKCPAPNLL 261
Qy 118 GGPSVFLFPKPKDITLMSRTPETCVVVDVSDDEPVEQFNWYVDGVVHNAKTKPREEQ 177
Db 262 GGPSVFIFFPKIKDVLMSLSPMVTCVVVDSEDDPDVQISWFWVNVVHTAQTTTHRED 321
Qy 178 FNSTYRVSVLTVLHODWLNKGYKCKVSNKGLPSSIEKTIISAKGQPREPOVYTLPPSQ 237
Db 322 YNSTLRVVSALPIQHDWMSGKFEKCKVNNKALPAPIERTISKPGSVRAPQVYVLPPE 381
Qy 238 EEMTKNQVSLTCLAVKGFPSPDIAVWESNGQPNKYKTPPVLDSGSPFLYSLRTVDKS 297
Db 382 EEMTKNQVTLTCNVTDMPEDIVVETWNNKGLTSLYKNTPEVLDSDGSPFYMSKLRVKK 441
Qy 298 RWQEGNVFCSCVMHEALHNHYTKQSLSLGK 329
Db 442 NWVERNSYSCSVVHGLHNHHTTKSPSRTPGK 473

RESULT 13
Q91205 PRELIMINARY; PRT; 473 AA.
AC Q91205;
DT 01-DEC-2001 (T-EMBLrel. 19, Created)
DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
DE Hypothetical 51.9 kDa protein.
GN AU049491.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
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OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Strausberg R.;  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC010327; AAH10327.1; -.  
 DR MGD; MGI:2144967; AU044919.  
 DR InterPro; IPR000345; CytC\_heme\_bind.  
 DR InterPro; IPR007110; Ig-Like.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF00447; Ig; 3.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS00190; CYTOCHROME\_C; 1.  
 DR PROSITE; PS00835; IG\_LIKE; 4.  
 DR PROSITE; PS00290; IG\_MHC; 1.  
 KW Hypothetical protein\_  
 SQ SEQUENCE 473 AA; 51946 MW; CF625F008932AF12 CRC64;

Query Match 60.2%; Score 1055.5; DB 11; Length 473;  
 Best Local Similarity 59.5%; Pred. NO. 1.3e-87;  
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 Db 138 AKTTPEVYPLAPGCGDTGSSVTGLCLVKGYFPPESVTVWNSGSLSSVHTFPALLQ-S 196  
 QY 63 GLYSLSVVTVPSSSLGTTKTYTCNVDHKPSNTKVDKRVESKYGP-----PCP-----SC 111  
 Db 197 GLYTSSSVTVPSSTWPSQTVCVAHPASSTTVDKLEPS-GPISTINPCPKCKECHKC 255  
 QY 112 PAPEFLGGPSVFLPPKPKDTLMISRTPEVTCVVDVDSQEDPEVQFNWYVDGVEVHNAKT 171  
 Db 256 PARNLEGGPSVFIFPPNIKDVLMSLTPTKVTCTVVDVSEDDPDVQISWFWNNVEVHTAQT 315  
 QY 172 KPREEQFNSTYRVSVLTVLHQDWLNGKEYCKVSKNGLPSIEKTIKAKGQPREPQVY 231  
 Db 316 QTHREDYNSTIRVVSALPPIQHCDWMSGKEFKCKVNNKDLPSPIERTISKIGLVRAPOVY 375  
 QY 232 TLPPSQEEMTKQVSLTCLVKGYFPPSDIAVESNGQPNENYKTTTPVLDSDGSPFFLYSR 291  
 Db 376 ILPPPAEQSKRDVSLTCLVGFNPGDISVETNSNGTEENYKDTAPVLDSDGSFYFIYSK 435  
 QY 292 LTVDKSRWQEGNVFSCVMHEALHNNHYTKSLSLGK 329  
 Db 436 LDIKTSKWEKTSFSCNVRHEGLKNYLYKKTISRSPGK 473

RESULT 14  
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 AC Q8R3H6  
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Hypothetical protein.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Strausberg R.;  
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC025447; AAH25447.1; -.  
 DR InterPro; IPR000345; CytC\_heme\_bind.  
 DR InterPro; IPR007110; Ig-Like.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF00447; Ig; 3.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS00190; CYTOCHROME\_C; 1.

DR PROSITE; PS00835; IG\_LIKE; 4.  
 DR PROSITE; PS00290; IG\_MHC; 1.  
 KW Hypothetical protein\_  
 SQ SEQUENCE 474 AA; 51748 MW; 8608B57C6CD2874A CRC64;  
 Query Match 60.2%; Score 1055.5; DB 11; Length 474;  
 Best Local Similarity 59.5%; Pred. NO. 1.3e-87;  
 Matches 201; Conservative 51; Mismatches 73; Indels 13; Gaps 4;  
 QY 3 ASTKGPSVPLAPCSRSTSESTAALGCLVKDYFPPVTVSWNSGALTSGVHTFPAVLQSS 62  
 Db 139 AKTTPEVYPLAPGCGDTGSSVTGLCLVKGYFPPESVTVWNSGSLSSVHTFPALLQ-S 197  
 QY 63 GLYSLSVVTVPSSSLGTTKTYTCNVDHKPSNTKVDKRVESKYGP-----PCP-----SC 111  
 Db 198 GLYTSSSVTVPSSTWPSQTVCVAHPASSTTVDKLEPS-GPISTINPCPKCKECHKC 256  
 QY 112 PAPEFLGGPSVFLPPKPKDTLMISRTPEVTCVVDVDSQEDPEVQFNWYVDGVEVHNAKT 171  
 Db 257 PARNLEGGPSVFIFPPNIKDVLMSLTPTKVTCTVVDVSEDDPDVQISWFWNNVEVHTAQT 316  
 QY 172 KPREEQFNSTYRVSVLTVLHQDWLNGKEYCKVSKNGLPSIEKTIKAKGQPREPQVY 231  
 Db 317 QTHREDYNSTIRVVSALPPIQHCDWMSGKEFKCKVNNKDLPSPIERTISKIGLVRAPOVY 376  
 QY 232 TLPPSQEEMTKQVSLTCLVKGYFPPSDIAVESNGQPNENYKTTTPVLDSDGSPFFLYSR 291  
 Db 377 ILPPPAEQSKRDVSLTCLVGFNPGDISVETNSNGTEENYKDTAPVLDSDGSFYFIYSK 436  
 QY 292 LTVDKSRWQEGNVFSCVMHEALHNNHYTKSLSLGK 329  
 Db 437 LDIKTSKWEKTSFSCNVRHEGLKNYLYKKTISRSPGK 474

RESULT 15  
 Q9BU10 PRELIMINARY; PRT; 597 AA.  
 AC Q9BU10  
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC Tissue=Lymph;  
 RA Strausberg R.;  
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC002963; AAH02963.1; -.  
 DR HSSP; P01825; 7PAB.  
 DR InterPro; IPR007110; Ig-Like.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF00447; Ig; 5.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS00835; IG\_LIKE; 5.  
 DR PROSITE; PS00290; IG\_MHC; 3.  
 KW Hypothetical protein\_  
 SQ SEQUENCE 597 AA; 65274 MW; 2DAFA8FB7E055851 CRC64;

Query Match 25.7%; Score 450; DB 4; Length 597;  
 Best Local Similarity 26.9%; Pred. NO. 2.6e-32;  
 Matches 118; Conservative 71; Mismatches 132; Indels 118; Gaps 17;  
 QY 4 STKGPSVPLAPCSRSTSESTAALGCLVKDYFPPVTVSW--NSGALTSGVHTFPAVLQ 60  
 Db 146 SASAPLFLVLCNSPSTSSVAVCCLAQDLPSITFSWKYKNSDSSISRGFFSVLR 205  
 QY 61 SSGLYSLSSVTVPSSSL--GTKTY--TCNVHKNPSNTKVDKRV----- 100

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Db 206 -GGKYAATSQVLLPSKDMQGTDEHVCKVCH-PNGNK-EKNVPLPVIABLPPKVSFVP 262
QY 101 --ESKYGPSPS---CPAPEL-----GGPS---- 121
Db 263 PRDGFNGNPRKSLICQATGSPRQIQVSWLREKQVSGVTTDOVAEAKESGPTTKV 322
QY 122 -----VFLPPPKPKDTLMIS 136
Db 323 TSTLTIKESDMLSQSMFTCRVDHRGLTFQNASMCPVDDQTAIRVFAIPPS-FASIFLT 381
QY 137 RPEVTCVVVDVQEDPEVFQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVHLHODWL 196
Db 382 KSTKTCUVTDLTTTYD-SVTISWTRQNGEAVKTHNISESHPNATFSAVGEASICEDDWN 440
QY 197 NGKEYKCKVSNKGLPSSIEKTIKAKQP-REPQVYTLPPSQEEMT-KNOVSLTCLVKGF 254
Db 441 SGERFTCTVHTDLPSPPLKQIISRPKGVALHRPDVYLLPPAREQLNLRGATITCLVTGF 500
QY 255 YPSDIWVESNGQP--ENNYKTTTPVLD--SDGSFPLYSELTYDKSRWQEGNVFSCSYM 310
Db 501 SPADVFMQMRGQPLSPEKYTSAPMPEPQAGRYFAHSILTVSEEWNTGETYTTCVA 560
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Db 561 HEALPNRVTERIVDKSTCK 579
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Job time : 59.9039 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 13, 2004, 12:18:44 ; Search time 76.7188 Seconds  
(without alignments)  
680.681 Million cell updates/sec

Title: US-09-990-586-100

Perfect score: 1754

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1743	99.4	327	18 AAW37346	Immunoglobulin C-g
2	1743	99.4	327	23 AAM47859	Human Ig-G4 heavy
3	1743	99.4	327	24 AAE32630	Human immunoglobul
4	1743	99.4	327	24 AAE32918	Human immunoglobul
5	1743	99.4	329	20 AAW70801	Amino acid sequenc
6	1743	99.4	329	21 AAY32190	Human IGG1 C-gamma
7	1743	99.4	443	18 AAW13564	Humanised anti-I-s
8	1743	99.4	444	20 AAY31672	Human IGG4 chain C
9	1743	99.4	463	18 AAW14935	2A2 Human IGG4 exp

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10 1743 99.4 463 18 AAW14932
11 1743 99.4 464 18 AAW14941
12 1743 99.4 464 18 AAW14938
13 1743 99.4 467 16 AAR80617
14 1743 99.4 467 18 AAW14925
15 1743 99.4 468 13 AAR28808
16 1738 99.1 450 24 ABP96294
17 1736 99.0 467 18 AAW14926
18 1731 98.7 467 18 AAW14927
19 1725 98.3 422 20 AAY29771
20 1725 98.3 533 20 AAY29773
21 1720 98.1 646 20 AAY29775
22 1716 97.9 447 18 AAW10232
23 1716 97.8 462 22 AAB72234
24 1710 97.5 462 22 AAB72229
25 1649.5 94.0 462 18 AAW14933
26 1649.5 94.0 462 18 AAW14934
27 1649.5 94.0 463 18 AAW14939
28 1649.5 94.0 463 18 AAW14940
29 1649.5 94.0 472 23 ABP51695
30 1611.5 91.9 530 13 AAR25783
31 1611.5 91.9 530 21 AAY85080
32 1611.5 91.9 530 22 AAB80884
33 1611.5 91.9 530 22 AAB67323
34 1611.5 91.9 530 24 ABG71123
35 1607.5 91.6 442 22 AAB72230
36 1607.5 91.6 461 22 AAB72236
37 1605.5 91.5 326 23 ABG77148
38 1605.5 91.5 326 23 ABG30462
39 1605.5 91.5 326 23 AAM47857
40 1605.5 91.5 326 23 AAE32628
41 1605.5 91.5 326 24 AAE32916
42 1605.5 91.5 326 24 AAE32916
43 1605.5 91.5 443 20 AAY31670
44 1605.5 91.5 451 21 AAY93734
45 1605.5 91.5 462 21 AAB26884

```

#### ALIGNMENTS

```

RESULT 1
AAW37346
ID AAW37346 standard; Protein; 327 AA.
XX
XX AAW37346;
XX AC
XX
XX
DT 11-MAY-1998 (first entry)
XX
DE Immunoglobulin C-gamma-4 region.
XX
XX Vaccine; B-cell malignancy; lymphoma; leukaemia; tumour;
KW gene amplification; immunotherapy; therapy; immunoglobulin;
KW C-gamma-4; constant region.
XX
XX Homo sapiens.
XX
XX WO9741244-A1.
XX
XX 06-NOV-1997.
XX
XX 25-APR-1997; 97WO-US07039.
XX
XX 06-DEC-1996; 96US-0761277.
XX 01-MAY-1996; 96US-0644664.
XX (GENI-) GENITOPE CORP.
XX Denney DW;
XX WPI; 1997-549743/50.
XX N-PSDB; AAT97189.
XX

```

```

Murine anti-porcine
3F4 Human IGG4 exp
Murine anti-porcine
Anti-human IL-4 hu
Human gamma-4 heavy
pre-FA8 humanised
4A5-3.1.1-B4 antib
Human gamma-4E hea
Human gamma-4E hea
P-selectin ligand
P-selectin ligand
P-selectin ligand
TP8-SG9 CDR-grafte
Humanised 323/A3 (
Humanised 323/A3 (
2A2 (Chimeric) hum
2A2 (Chimeric) hum
3F4 (Chimeric) hum
3F4 (Chimeric) hum
SG1-1-TPO heavy ch
CD4-IGG2 chimeric
CD4-IGG2 chimeric
Human CD4-IGG2 chi
CD4-IGG2 chimeric
CD4-IGG2 chimeric
CD4-immunoglobulin
Humanised 323/A3 (
Humanised 323/A3 (
Human immunoglobul
Anti-IGF-1R consta
Human anti-CD40 mo
Human Ig-G2 heavy
Human immunoglobul
Human immunoglobul
Human IGG2 chain C
The heavy chain of
Human immunoglobul

```

PT Multivalent vaccine to treat B cell lymphoma or leukaemia -  
 PT comprises at least 2 different recombinant variable regions of  
 PT immunoglobulin molecules derived from B cell lymphoma cells

PS Example 10; Page 126-127; 177pp; English.

XX This protein comprises an immunoglobulin (Ig) C-gamma-4 region.  
 CC The invention provides a method for the production of tumour-  
 CC specific Ig derived from a B-cell lymphoma patient. In the novel  
 CC method, expression plasmids containing the patient's VH region(s)  
 CC joined to either a C-gamma-3 (see AAT97189) or C-gamma-4 (see AAT97189)  
 CC sequence and expression plasmids containing the patient's VL  
 CC region(s) joined to either a C-kappa (see AAT97190) or C-lambda-2  
 CC (see AAT97191) sequence are cotransfected along with a selectable and  
 CC amplifiable marker into a cell line (e.g. BMS147.G1.4), and  
 CC transfected cells are then subjected to selection and amplification.  
 CC The method permits the production of a multivalent vaccine which  
 CC reflects the degree of somatic variation found within the patient's  
 CC tumour. These novel multivalent vaccines provide superior vaccines  
 CC for the treatment of B-cell lymphoma.

XX SQ Sequence 327 AA;

Query Match 99.4%; Score 1743; DB 18; Length 327;  
 Best Local Similarity 100.0%; Pred. No. 2.1e-126;  
 Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ASTKGPSVFLPAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 62  
 DB 1 ASTKGPSVFLPAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60  
 QY 63 GLYSLSSVTVTPSSSLGKTYTCNVDRKPSNTKYDKRVESKYGPPCPAPFLGSPV 122  
 DB 61 GLYSLSSVTVTPSSSLGKTYTCNVDRKPSNTKYDKRVESKYGPPCPAPFLGSPV 120  
 QY 123 FLPPKPKDTLMISRTPEVTCVVDVDSQEDPEVQFNWYDGVVHNATKPREQFNSTY 182  
 DB 121 FLPPKPKDTLMISRTPEVTCVVDVDSQEDPEVQFNWYDGVVHNATKPREQFNSTY 180  
 QY 183 RVSVSLTVLHODWLNKGEYKCKVSNKGLPSISIEKTSKAKGQPREPQVYTLPPSQEEMTK 242  
 DB 181 RVSVSLTVLHODWLNKGEYKCKVSNKGLPSISIEKTSKAKGQPREPQVYTLPPSQEEMTK 240  
 QY 243 NVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEG 302  
 DB 241 NVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEG 300  
 QY 303 NVFSCSVNMEALHNYHTQKLSLSLGLK 329  
 DB 301 NVFSCSVNMEALHNYHTQKLSLSLGLK 327

RESULT 2

ID AAM47859  
 ID AAM47859 standard; Protein; 327 AA.

XX AC AAM47859;

XX DT 22-FEB-2002 (first entry)

XX DE Human Ig-G4 heavy chain constant region amino acid sequence.

XX KW Human; immunoadhesin; intercellular adhesion molecule; ICAM-1;  
 KW human rhinovirus; immunoglobulin heavy chain; J chain; HRV; common cold;  
 KW transgenic plant.

XX OS Homo sapiens.

XX PN WO200183529-A2.

XX PD 08-NOV-2001.

XX PF 28-APR-2001; 2001WO-US13932.

XX 28-APR-2000; 2000US-200298P.  
 XX (PLAN-) PLANET BIOTECHNOLOGY INC.  
 XX Larrick JW, Wycoff KL;

XX WPI; 2002-041481/05.

XX N-PSDB; ABA05268.

XX Immunoadhesin for treating human rhinovirus infection comprises  
 PT chimeric intercellular adhesion molecule-1, and optionally a J chain  
 PT and secretory component in association -  
 XX Disclosure; Fig 7; 138pp; English.

XX The invention relates to an immunoadhesin comprising:

CC (a) a chimeric intercellular adhesion molecule (ICAM)-1 comprising a  
 CC rhinovirus receptor protein linked to at least a portion of an  
 CC immunoglobulin heavy chain; and  
 CC (b) optionally a J chain and secretory component associated with the  
 CC chimeric ICAM-1 molecule. The immunoadhesin has plant-specific  
 CC glycosylation and virucide activity. The immunoadhesin is useful for  
 CC reducing infection by human rhinovirus (HRV) and hence the initiation or  
 CC spread of the common cold by HRV. The immunoadhesin binds to HRV and  
 CC reduces its infectivity, competing with cell surface ICAM-1 for binding  
 CC sites, interfering with virus entry or uncoating and directing premature  
 CC release of viral RNA and formation of empty capsids. Expression of the  
 CC immunoadhesin in plants would be tetrameric, rather than dimeric.  
 CC Immunoadhesin having multiple binding sites have a higher effective  
 CC affinity for the virus, thereby increasing the effectiveness of the  
 CC immunoadhesin. Association of secretory component and immunoglobulin J  
 CC chain increases the stability of the immunoadhesin in the mucosal  
 CC environment. Production is significantly less expensive in plants than in  
 CC animal cell culture and production in plants is safer for human use,  
 CC since plants are not known to harbor any animal viruses. The present  
 CC sequence is that of a human immunoglobulin protein sequence, useful to  
 CC the invention.

XX SQ Sequence 327 AA;

Query Match 99.4%; Score 1743; DB 23; Length 327;  
 Best Local Similarity 100.0%; Pred. No. 2.1e-126;  
 Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ASTKGPSVFLPAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 62  
 DB 1 ASTKGPSVFLPAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60  
 QY 63 GLYSLSSVTVTPSSSLGKTYTCNVDRKPSNTKYDKRVESKYGPPCPAPFLGSPV 122  
 DB 61 GLYSLSSVTVTPSSSLGKTYTCNVDRKPSNTKYDKRVESKYGPPCPAPFLGSPV 120  
 QY 123 FLPPKPKDTLMISRTPEVTCVVDVDSQEDPEVQFNWYDGVVHNATKPREQFNSTY 182  
 DB 121 FLPPKPKDTLMISRTPEVTCVVDVDSQEDPEVQFNWYDGVVHNATKPREQFNSTY 180  
 QY 183 RVSVSLTVLHODWLNKGEYKCKVSNKGLPSISIEKTSKAKGQPREPQVYTLPPSQEEMTK 242  
 DB 181 RVSVSLTVLHODWLNKGEYKCKVSNKGLPSISIEKTSKAKGQPREPQVYTLPPSQEEMTK 240  
 QY 243 NVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEG 302  
 DB 241 NVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEG 300  
 QY 303 NVFSCSVNMEALHNYHTQKLSLSLGLK 329  
 DB 301 NVFSCSVNMEALHNYHTQKLSLSLGLK 327

RESULT 3

AAB32630  
 ID AAB32630 standard; Protein; 327 AA.

XX AAE32630;  
AC 24-MAR-2003 (first entry)  
DT Human immunoglobulin G4 (IgG4) heavy chain Fc region.  
DE Human; immunogenic; therapy; immunoglobulin G4; IgG4.  
XX Homo sapiens.  
OS WO200279415-A2.  
XX 10-OCT-2002.  
PD 29-MAR-2002; 2002WO-US09650.  
XX 30-MAR-2001; 2001US-280625P.  
PR (LEXI-) LEXIGEN PHARM CORP.  
XX Gillies SD;  
PI WPI; 2003-111794/10.  
XX Reducing the immunogenicity of a fusion protein by changing an amino  
PT acid within the junction region spanning a fusion junction of a fusion  
PT protein to reduce the ability of the candidate T-cell epitope to  
PT interact with a T-cell receptor -  
XX Disclosure; Page 53; 67pp; English.

XX The present invention relates to a method of reducing the immunogenicity  
CC of a fusion protein. The method involves identifying a candidate T-cell  
CC epitope within a junction region spanning a fusion junction of a fusion  
CC protein and changing an amino acid within the junction region to reduce  
CC the ability of the candidate T-cell epitope to interact with a T-cell  
CC receptor. The method is useful for reducing the immunogenicity of fusion  
CC proteins for use in therapy. The present sequence is human immunoglobulin  
CC G4 (IgG4) heavy chain Fc region. This sequence is used to illustrate the  
CC method of the invention.

SQ Sequence 327 AA;

Query Match 99.4%; Score 1743; DB 24; Length 327;

Best Local Similarity 100.0%; Pred. No. 2.1e-126;

Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ASTKGSVPFLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 62  
DB 1 ASTKGSVPFLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60  
QY 63 GLYSLSVVTVFSSSLGTYTCNVNDHKPSNTKVDKRVESKYGPPCPSCPAPEFLGGPSV 122  
DB 61 GLYSLSVVTVFSSSLGTYTCNVNDHKPSNTKVDKRVESKYGPPCPSCPAPEFLGGPSV 120  
QY 123 FLFPPKPDMLSRPTEVTCVVDVSDQEDPEVQFNWYDGVGVHNAKTKPREQFNSTY 182  
DB 121 FLFPPKPDMLSRPTEVTCVVDVSDQEDPEVQFNWYDGVGVHNAKTKPREQFNSTY 180  
QY 183 RVSVLTVLHQDLNKGKEYCKVSKNGLPSSIEKTIISKAKGQPREPQVYTLPPSQEEMTK 242  
DB 181 RVSVLTVLHQDLNKGKEYCKVSKNGLPSSIEKTIISKAKGQPREPQVYTLPPSQEEMTK 240  
QY 243 NOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSLRTVDSRWQEG 302  
DB 241 NOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSLRTVDSRWQEG 300  
QY 303 NVFSCSWMEALHNYHTQKSLSLSLK 329  
DB 301 NVFSCSWMEALHNYHTQKSLSLSLK 327

RESULT 4  
AAE32918  
ID AAE32918 standard; Protein; 327 AA.  
XX AAE32918;  
AC 24-MAR-2003 (first entry)  
DT Human immunoglobulin G4 (IgG4) heavy chain Fc region.  
DE Human; immunogenic; therapy; human; immunoglobulin G4; IgG4.  
XX T-cell; immunogenic; therapy; human; immunoglobulin G4; IgG4.  
XX Homo sapiens.  
OS WO200279232-A2.  
XX 10-OCT-2002.  
PD 30-MAR-2002; 2002WO-US09815.  
XX 30-MAR-2001; 2001US-280625P.  
PR (LEXI-) LEXIGEN PHARM CORP.  
XX Gillies SD;  
PI WPI; 2003-103259/09.

XX Reducing the immunogenicity of a fusion protein comprises changing an  
PT amino acid within the junction region to reduce the ability of the  
PT candidate T-cell epitope identified within the junction spanning to  
PT interact with T-cell receptor -  
XX Disclosure; Page 53-54; 68pp; English.

XX The invention relates to a method for reducing the immunogenicity of a  
CC fusion protein which involves identifying a candidate T-cell epitope  
CC within a junction spanning a fusion junction of a fusion protein, and  
CC changing an amino acid within the junction region to reduce the ability  
CC of the candidate T-cell epitope to interact with a T-cell receptor. The  
CC method is useful for reducing the immunogenicity of a fusion protein.  
CC It is useful for analysing, changing or modifying one or more amino  
CC acids in the junction region of a fusion protein to identify a T-cell  
CC epitope and reduce its ability to interact with a T-cell receptor. The  
CC less immunogenic fusion proteins are useful in providing therapeutic  
CC treatment. The present sequence is human immunoglobulin G4 (IgG4) heavy  
CC chain Fc region used to illustrate the method of the invention.

SQ Sequence 327 AA;

Query Match 99.4%; Score 1743; DB 24; Length 327;

Best Local Similarity 100.0%; Pred. No. 2.1e-126;

Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ASTKGSVPFLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 62  
DB 1 ASTKGSVPFLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60  
QY 63 GLYSLSVVTVFSSSLGTYTCNVNDHKPSNTKVDKRVESKYGPPCPSCPAPEFLGGPSV 122  
DB 61 GLYSLSVVTVFSSSLGTYTCNVNDHKPSNTKVDKRVESKYGPPCPSCPAPEFLGGPSV 120  
QY 123 FLFPPKPDMLSRPTEVTCVVDVSDQEDPEVQFNWYDGVGVHNAKTKPREQFNSTY 182  
DB 121 FLFPPKPDMLSRPTEVTCVVDVSDQEDPEVQFNWYDGVGVHNAKTKPREQFNSTY 180  
QY 183 RVSVLTVLHQDLNKGKEYCKVSKNGLPSSIEKTIISKAKGQPREPQVYTLPPSQEEMTK 242  
DB 181 RVSVLTVLHQDLNKGKEYCKVSKNGLPSSIEKTIISKAKGQPREPQVYTLPPSQEEMTK 240  
QY 243 NOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSLRTVDSRWQEG 302  
DB 241 NOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSLRTVDSRWQEG 300



QY 303 NVFSCVMHEALHNYTKSLSLGK 329  
 DB 301 NVFSCVMHEALHNYTKSLSLGK 327

RESULT 5  
 ID AAW70801  
 XX AAW70801 standard; protein; 329 AA.  
 AC AAW70801;  
 DT 03-FEB-1999 (first entry)  
 XX  
 DE Amino acid sequence of C-gamma-4.  
 KW gp130; cytokine antagonist; interleukin; gamma-interferon;  
 KW granulocyte macrophage colony-stimulating factor; J peptide;  
 KW transforming growth factor-beta.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Protein 2..329  
 FT /note= "C-gamma-4"  
 XX  
 PN US8644099-A.  
 XX  
 PD 01-DEC-1998.  
 XX  
 PF 27-NOV-1995; 95US-0563105.  
 XX  
 PR 27-NOV-1995; 95US-0563105.  
 PR 20-OCT-1993; 93US-0140222.  
 XX  
 PA (REG- ) REGENERON PHARM INC.  
 XX  
 PI Economides A, Stahl N, Yancopoulos GD;  
 XX WPI; 1999-044669/04.  
 XX  
 DR Cytokine antagonists - comprising extracellular domains of  
 PT specificity-determining and signal-transducing components of  
 PT cytokine receptor  
 XX  
 PS Example 4; Fig 12; 46pp; English.  
 XX  
 CC The present sequence represents the amino acid sequence of  
 CC C-gamma-4. The protein is used in the course of the invention.  
 CC The specification describes cytokine antagonists comprising only the  
 CC extracellular domain of the specificity-determining component of  
 CC the cytokine receptor and the extracellular domain of a  
 CC signal-transducing component of the cytokine receptor. The cytokine  
 CC is an interleukin (IL-1, IL-2, IL-3, IL-4, IL-5 or IL-15),  
 CC granulocyte macrophage colony-stimulating factor (GM-CSF),  
 CC gamma-interferon or transforming growth factor-beta (TGF-beta). The  
 CC antagonist is capable of binding the cytokine to form a nonfunctional  
 CC complex. The compounds have therapeutic activity as cytokine antagonists  
 CC and can also be used in assays for identifying novel agonists and  
 CC antagonists of cytokines.  
 XX  
 SQ Sequence 329 AA;

Query Match 99.4%; Score 1743; DB 20; Length 329;  
 Best Local Similarity 100.0%; Pred. No. 2.le-126;  
 Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ASTKPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPTVSNVSGALTSVGVTHFPVAVLQSS 62  
 DB 3 ASTKPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPTVSNVSGALTSVGVTHFPVAVLQSS 62  
 QY 63 GLYSLSVVTVPSSSLGTTKTYTCNVNDHKPSNTKVDKRVESKYGPPCPSCPAPEFLGGPSV 122

DB 63 GLYSLSVVTVPSSSLGTTKTYTCNVNDHKPSNTKVDKRVESKYGPPCPSCPAPEFLGGPSV 122  
 QY 123 FLFPKPKDITLMISRTPEVTCVWVDVSOEDPEVQFNMTVDGVEVHNATKPREEQFNSTY 182  
 DB 123 FLFPKPKDITLMISRTPEVTCVWVDVSOEDPEVQFNMTVDGVEVHNATKPREEQFNSTY 182  
 QY 183 RVSVLTVLHODWLNKGEYKCKVSNKGLPSSIEKTIKAKGQPREPQVYITLPPSQEENTK 242  
 DB 183 RVSVLTVLHODWLNKGEYKCKVSNKGLPSSIEKTIKAKGQPREPQVYITLPPSQEENTK 242  
 QY 243 NOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLXSRLLVTDKSRWQEG 302  
 DB 243 NOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLXSRLLVTDKSRWQEG 302  
 QY 303 NVFSCVMHEALHNYTKSLSLGK 329  
 DB 303 NVFSCVMHEALHNYTKSLSLGK 329

RESULT 6  
 ID AAY92190 standard; protein; 329 AA.  
 XX  
 AC AAY92190;  
 DT 01-AUG-2000 (first entry)  
 XX  
 DE Human IgG1 C-gamma-4 domain.  
 XX  
 KW gp130-C-gamma-1; cytokine; antagonist; CNTF; receptor; fusion protein;  
 KW cytostatic; immunomodulator; osteopathic.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..2  
 FT /note= "ser-Gly bridge"  
 FT Protein 3..329  
 FT /label= C-gamma-4  
 XX  
 PN WO200018932-A2.  
 XX  
 PD 06-APR-2000.  
 XX  
 PF 22-SEP-1999; 99WO-US22045.  
 XX  
 PR 25-SEP-1998; 98US-0101858.  
 PR 19-MAY-1999; 99US-0313942.  
 XX  
 PA (REG- ) REGENERON PHARM INC.  
 XX  
 PI Stahl N, Yancopoulos GD;  
 XX WPI; 2000-293165/25.  
 XX  
 DR Isolated nucleic acid molecule for treating cytokine-related diseases  
 PT or disorders encodes a fusion polypeptide capable of binding a cytokine  
 PT to form a nonfunctional complex  
 XX  
 PS Example 4; Fig 12; 152pp; English.  
 XX  
 CC The invention concerns production of antagonists to any cytokine that  
 CC utilizes an alpha specificity determining component, which when combined  
 CC with the cytokine, binds to a first beta signal transducing component to  
 CC form a non-functional intermediate which then binds to a second beta  
 CC signal transducing component causing beta-receptor dimerization, the  
 CC soluble alpha specificity determining component of the receptor  
 CC (sr-alpha) and the extracellular domain of the first beta signal  
 CC transducing component of the cytokine receptor (beta-1) are combined to  
 CC form heterodimers (sr-alpha.beta-1) that act as antagonist to the  
 CC cytokine by binding the cytokine to form a non-functional complex. The  
 CC receptor components are shared by cytokines such as the CNTF (ciliary

CC neurotrophic factor) family of cytokines. The invention provides the  
 CC basis for the development of IL-6 antagonists, as they show that if, in  
 CC the presence of a ligand, a non-functional intermediate complex,  
 CC consisting of the ligand, its alpha receptor and its beta-1 receptor  
 CC component, can be formed, it will effectively block the action of the  
 CC ligand. Effective antagonists of IL-6 or CNTF consist of heterodimers  
 CC of the extracellular domains of the alpha specificity determining  
 CC components of their receptors and the extracellular domain of gp130.  
 CC The resultant heterodimers, function as high-affinity traps, rendering  
 CC the cytokine inaccessible to form a signal transducing complex with the  
 CC native membrane-bound forms of their receptor. The nucleic acids and  
 CC polypeptides are useful for treating cytokine-related diseases or  
 CC disorders such as osteoporosis and primary and secondary effects of  
 CC cancer including multiple myeloma or cachexia.  
 XX  
 SQ Sequence 329 AA;  
 Query Match 99.4%; Score 1743; DB 21; Length 329;  
 Best Local Similarity 100.0%; Pred. No. 2.1e-126;  
 Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSNVNSGALTSGVHTFPAVLQSS 62  
 Db 3 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSNVNSGALTSGVHTFPAVLQSS 62  
 QY 63 GLYSLSVVTVFSSSLGKTYTCNVDRKPSNTKVDKRVESKYGPPCPSCAPEFLGGPSV 122  
 Db 63 GLYSLSVVTVFSSSLGKTYTCNVDRKPSNTKVDKRVESKYGPPCPSCAPEFLGGPSV 122  
 QY 123 FLFPPKPKDTLMISRTPEVTCVVDVDSQEDPEVQFNWYVDGVEVHNATKPREQFNSTY 182  
 Db 123 FLFPPKPKDTLMISRTPEVTCVVDVDSQEDPEVQFNWYVDGVEVHNATKPREQFNSTY 182  
 QY 183 RVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAKGQPREPOVYTLPPSQEEMTK 242  
 Db 183 RVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAKGQPREPOVYTLPPSQEEMTK 242  
 QY 243 NOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSRLTVDKSRWQEG 302  
 Db 243 NOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSRLTVDKSRWQEG 302  
 QY 303 NVFSCSVMEALHNHYTQKSLSLGLK 329  
 Db 303 NVFSCSVMEALHNHYTQKSLSLGLK 329  
 RESULT 7  
 ID AAW13564  
 XX AAW13564 standard; Protein; 443 AA.  
 AC AAW13564;  
 DT 03-JUN-1997 (first entry)  
 XX Humanised anti-L-selectin antibody HuDreg 55 heavy chain.  
 DE  
 XX L-selectin; humanised antibody; HuDreg 55; acute organ damage;  
 KW organ failure; poly-trauma; haemorrhagic-traumatic shock.  
 XX Chimeric Mus sp.;  
 OS Chimeric Homo sapiens.  
 XX  
 PN WC9706822-A1.  
 XX  
 XX 27-FEB-1997.  
 XX  
 XX 14-AUG-1996; 96WO-US13152.  
 PF  
 PR 27-DEC-1995; 95US-0578953.  
 PR 17-AUG-1995; 95EP-0112895.  
 PR 19-SEP-1995; 95EP-0114696.  
 XX  
 XX (BOE ) BOEHRINGER MANNHEIM GMBH.

PA (PROT-) PROTEIN DESIGN LABS INC.  
 XX  
 PI Co M, Haselbeck A, Martin U, Schumacher G;  
 XX  
 XX WPI; 1997-165036/15.  
 DR N-PSDB; AAT61281.  
 XX  
 PT Using anti-selectin antibody to prevent acute organ damage and  
 PT multiple organ failure - during extracorporeal circulation or  
 PT following polytrauma, e. g. haemorrhagic-traumatic shock  
 XX  
 PS Disclosure; Page 34-36; 52pp; English.  
 XX  
 CC Humanised anti-L-selectin antibody HuDreg 55 comprises 2 heavy  
 CC chains each having the sequence given in AAW13564 and 2 light chains  
 CC each having the sequence given in AAW13563. These are encoded by the  
 CC cDNA clones given in AAT61281 and AAT61280. HuDreg 55 can be used to  
 CC prevent multiple organ failure associated with polytrauma and for  
 CC the prevention of acute organ damage associated with extracorporeal  
 CC blood circulation. The antibody inhibits interaction between the  
 CC carbohydrate-recognising domain of the selectin and the  
 CC corresponding cell surface receptor.  
 XX  
 SQ Sequence 443 AA;  
 Query Match 99.4%; Score 1743; DB 18; Length 443;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-126;  
 Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSNVNSGALTSGVHTFPAVLQSS 62  
 Db 117 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSNVNSGALTSGVHTFPAVLQSS 176  
 QY 63 GLYSLSVVTVFSSSLGKTYTCNVDRKPSNTKVDKRVESKYGPPCPSCAPEFLGGPSV 122  
 Db 177 GLYSLSVVTVFSSSLGKTYTCNVDRKPSNTKVDKRVESKYGPPCPSCAPEFLGGPSV 236  
 QY 123 FLFPPKPKDTLMISRTPEVTCVVDVDSQEDPEVQFNWYVDGVEVHNATKPREQFNSTY 182  
 Db 237 FLFPPKPKDTLMISRTPEVTCVVDVDSQEDPEVQFNWYVDGVEVHNATKPREQFNSTY 296  
 QY 183 RVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAKGQPREPOVYTLPPSQEEMTK 242  
 Db 297 RVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAKGQPREPOVYTLPPSQEEMTK 356  
 QY 243 NOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSRLTVDKSRWQEG 302  
 Db 357 NOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSRLTVDKSRWQEG 416  
 QY 303 NVFSCSVMEALHNHYTQKSLSLGLK 329  
 Db 417 NVFSCSVMEALHNHYTQKSLSLGLK 443  
 RESULT 8  
 ID AAW131672  
 XX AAW131672 standard; Protein; 444 AA.  
 AC AAW131672;  
 DT 09-NOV-1999 (first entry)  
 XX Human Igg4 chain C.  
 DE  
 XX Igg4; C-gamma-4; antibody; fusion protein; circulating half-life;  
 KW human; drug delivery.  
 XX Homo sapiens.  
 XX  
 XX Key Location/Qualifiers  
 FT Misc-difference 1..117 "the identity of these residues is not  
 FT specified"

XX WO9943713-A1.  
 XX 02-SEP-1999.  
 XX 24-FEB-1999; 99WO-US03966.  
 XX 25-FEB-1998; 98US-0075887.  
 XX (LEXI-) LEXIGEN PHARM CORP.  
 XX Gillies SD, Lan Y, Lo K, Wesolowski J;  
 XX WPI; 1999-527594/44.  
 XX New antibody-based fusion proteins, used for the delivery of e.g. a  
 XX cytokine, ligand-binding protein or protein toxin to target cells in  
 XX vivo  
 XX Disclosure; Page 35-36; 41pp; English.  
 XX The present sequence represents the constant region of human IgG  
 XX isotype 4 (IgG4, C-gamma-4). C-gamma-1 (see AAY31669) and C-gamma-3  
 XX (see AY31672) bind Fc receptors with high affinity whereas C-gamma-4  
 XX has 10-fold lower binding affinity and C-gamma-2 (see AY31670) does  
 XX not bind to Fc receptor gamma-1. The invention provides methods  
 XX for the genetic construction and expression of antibody-based  
 XX fusion proteins with enhanced circulating half-lives. The  
 XX fusion proteins lack the ability to bind to immunoglobulin Fc  
 XX receptors, either as a consequence of the antibody isotype used  
 XX for protein construction, i.e. a C-gamma-2 constant region (Fc)  
 XX or a C-gamma-4 Fc receptor, or through directed mutagenesis of  
 XX antibody isotypes that normally bind Fc receptors, i.e. C-gamma-1  
 XX or C-gamma-3. The methods can be used for to increase the  
 XX circulating half-life of a non-immunoglobulin (Ig) protein such as  
 XX a cytokine, e.g. tumour necrosis factor (TNF), an interleukin or a  
 XX lymphokine such as a lymphotoxin or a colony stimulating factor, a  
 XX ligand-binding protein, e.g. CD4, CTLA-4, TNF receptor or an  
 XX interleukin receptor, or a protein toxin (claimed). The fusion  
 XX proteins are used to deliver selectively the second non-Ig protein  
 XX to a target cell in vivo so that the second non-Ig protein can  
 XX exert a localised biological effect.  
 XX Sequence 444 AA;  
 XX Query Match 99.4%; Score 1743; DB 20; Length 444;  
 XX Best Local Similarity 100.0%; Pred. No. 3.1e-126; Indels 0; Gaps 0;  
 XX Matches 327; Conservative 0; Mismatches 0;  
 QY 3 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 62  
 DB 118 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 177  
 QY 63 GLYSLSVVTVPPSSSLGKTKYTCNVDHKPSNTKVDKRVESKYGPPCPSCPAPEFLGSPV 122  
 DB 178 GLYSLSVVTVPPSSSLGKTKYTCNVDHKPSNTKVDKRVESKYGPPCPSCPAPEFLGSPV 237  
 QY 123 FLFPKPDKDTLMISRTPEVTCVVDVDSQEDPEVQFNWYVDGVEVHNAKTPREEQFNSTY 182  
 DB 238 FLFPKPDKDTLMISRTPEVTCVVDVDSQEDPEVQFNWYVDGVEVHNAKTPREEQFNSTY 297  
 QY 183 RVSVLTVLHODWLNKGEYKCKVSNKGLPSSIEKTIISKAKGQPREPOVYITLPPSQEEMTK 242  
 DB 298 RVSVLTVLHODWLNKGEYKCKVSNKGLPSSIEKTIISKAKGQPREPOVYITLPPSQEEMTK 357  
 QY 243 NOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSGDSGFFLYSLRTVDSKRWQEG 302  
 DB 358 NOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSGDSGFFLYSLRTVDSKRWQEG 417  
 QY 303 NVFCSVNHAEALHNHYTQKSLSLIGK 329  
 DB 418 NVFCSVNHAEALHNHYTQKSLSLIGK 444

RESULT 9  
 AAW14935  
 ID AAW14935 standard; Protein; 463 AA.  
 XX AC AAW14935;  
 XX 16-JUN-1997 (first entry)  
 XX 2A2 Human IgG4 expression plasmid insert product (heavy chain).  
 XX Xenotransplantation; graft rejection; cell interaction; pig;  
 XX vascular cell adhesion molecule; VCAM; monoclonal antibody;  
 XX chimeric antibody; diagnosis.  
 XX Mus sp.  
 XX WO9711971-A1.  
 XX 03-APR-1997.  
 XX 27-SEP-1996; 96WO-US15575.  
 XX 26-SEP-1996; 96US-0004489.  
 XX 28-SEP-1995; 95US-0004489.  
 XX (ALEX-) ALEXION PHARM INC.  
 XX Evans MJ, Matis LA, Mueller EE, Mueller JP, Rollins S;  
 XX Rother RP;  
 XX WPI; 1997-212855/19.  
 XX N-PSDB; AAT62933.  
 XX Antibodies binding to porcine but not human cell interaction  
 XX proteins - useful to treat and assay for rejection of xenografted  
 XX porcine organs, tissues or cells  
 XX Disclosure; Page 48-50; 105pp; English.  
 XX Heavy chain (AAW14935) and light chain (AAW14936) sequences  
 XX correspond to murine anti-porcine soluble vascular cell adhesion  
 XX molecule (VCAM) monoclonal antibody 2A2 (see also AAW14931-32). They  
 XX are encoded by a 2A2 human IgG4 expression plasmid insert (see  
 XX also AAT62933). A chimeric antibody specific for porcine VCAM can be  
 XX produced in transfected host cells. It is useful for diagnosing  
 XX human rejection of porcine xenotransplants and for improving  
 XX xenotransplantation of porcine cells, tissues and organs into human  
 XX recipients.  
 XX Sequence 463 AA;  
 XX Query Match 99.4%; Score 1743; DB 18; Length 463;  
 XX Best Local Similarity 100.0%; Pred. No. 3.2e-126; Indels 0; Gaps 0;  
 XX Matches 327; Conservative 0; Mismatches 0;  
 QY 3 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 62  
 DB 137 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 196  
 QY 63 GLYSLSVVTVPPSSSLGKTKYTCNVDHKPSNTKVDKRVESKYGPPCPSCPAPEFLGSPV 122  
 DB 197 GLYSLSVVTVPPSSSLGKTKYTCNVDHKPSNTKVDKRVESKYGPPCPSCPAPEFLGSPV 256  
 QY 123 FLFPKPDKDTLMISRTPEVTCVVDVDSQEDPEVQFNWYVDGVEVHNAKTPREEQFNSTY 182  
 DB 257 FLFPKPDKDTLMISRTPEVTCVVDVDSQEDPEVQFNWYVDGVEVHNAKTPREEQFNSTY 316  
 QY 183 RVSVLTVLHODWLNKGEYKCKVSNKGLPSSIEKTIISKAKGQPREPOVYITLPPSQEEMTK 242  
 DB 317 RVSVLTVLHODWLNKGEYKCKVSNKGLPSSIEKTIISKAKGQPREPOVYITLPPSQEEMTK 376  
 QY 243 NOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSGDSGFFLYSLRTVDSKRWQEG 302

Db 377 NQVSLTCLVKGYPSPDIWVESNGQPNENYKTTPEVLDSGSPFLYSRLTVDKSRWQEG 436  
 QY 303 NVFSCSVMEALHNHYTKLSLSLKG 329  
 Db 437 NVFSCSVMEALHNHYTKLSLSLKG 463

RESULT 10  
 AAW14932  
 ID AAW14932 standard; Protein; 463 AA.  
 XX  
 AC AAW14932;  
 XX  
 DT 16-JUN-1997 (first entry)  
 XX  
 DE Murine anti-porcine VCAM 2A2 heavy chain.  
 KW Xenotransplantation; graft rejection; cell interaction; pig;  
 KW vascular cell adhesion molecule; VCAM; monoclonal antibody;  
 KW chimeric antibody; diagnosis.  
 XX  
 OS Mus sp.  
 XX  
 FH Key Location/Qualifiers  
 FT Region 50..54  
 FT /label= CDR1  
 FT Region 59..85  
 FT /label= CDR2  
 FT Region 118..125  
 FT /label= CDR3

WO9711971-A1.  
 XX  
 PD 03-APR-1997.  
 XX  
 PF 27-SEP-1996; 96WO-US15575.  
 XX  
 PR 26-SEP-1996; 96US-0004489.  
 PR 28-SEP-1995; 95US-0004489.  
 XX  
 PA (ALEX-) ALEXION PHARM INC.  
 XX  
 PI Evans MJ, Matis LA, Mueller EE, Mueller JP, Rollins S;  
 PI Rother RP;  
 XX  
 DR WPI: 1997-212855/19.  
 DR N-PSDB; AAT62930.  
 XX  
 PT Antibodies binding to porcine but not human cell interaction  
 PT proteins - useful to treat and assay for rejection of xenografted  
 PT porcine organs, tissues or cells  
 XX  
 PS Disclosure; Page 40-42; 105pp; English.  
 XX  
 CC Heavy chain (AAW14932) and light chain (AAW14931) sequences are  
 CC provided for the murine anti-porcine soluble vascular cell adhesion  
 CC molecule (VCAM) monoclonal antibody (Mab) 2A2. Hybridoma 2A2 was  
 CC produced by standard techniques using recombinant, soluble porcine  
 CC VCAM as immunogen. Chimeric antibodies can be produced by cloning  
 CC Mab 2A2 and 3F4 (see also AAW14937-38) variable regions into  
 CC expression plasmid pAPEX-3P modified to contain the human gamma4  
 CC constant region in place of the human gamma1 CI region. Sequences  
 CC are provided for 2A2 (chimeric) human G2/G4 cDNA (AAW14933), a 2A2  
 CC human G2/G4 expression plasmid insert product (AAW14934), and 2A2  
 CC human IgG4 expression plasmid insert products (AAW14935-36). The  
 CC chimeric antibodies are specific for porcine VCAM. They are useful  
 CC for diagnosing human rejection of porcine xenotransplants and for  
 CC improving xenotransplantation of porcine cells, tissues and organs  
 CC into human recipients.  
 XX  
 SQ Sequence 463 AA;

Query Match 99.4%; Score 1743; DB 18; Length 463;  
 Best Local Similarity 100.0%; Pred. No. 3.2e-126;  
 Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ASTKGPSVPLAPCSRSTSESTAALGCLVKDYFPEPVTWNSGALTSVHTFPAVLQSS 62  
 Db 137 ASTKGPSVPLAPCSRSTSESTAALGCLVKDYFPEPVTWNSGALTSVHTFPAVLQSS 196  
 QY 63 GLYSLSSVTVFSSSLGTITTCNVDPKPSNTKVDKRVESKYGPPCPAPPEFLGQPSV 122  
 Db 197 GLYSLSSVTVFSSSLGTITTCNVDPKPSNTKVDKRVESKYGPPCPAPPEFLGQPSV 256  
 QY 123 FLPPPKDPTLMISRTPETVCVVDVDSQEDPEVQFNWYVDGVHNAKTKPRREQFNSTY 182  
 Db 257 FLPPPKDPTLMISRTPETVCVVDVDSQEDPEVQFNWYVDGVHNAKTKPRREQFNSTY 316  
 QY 183 RVSVSLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTTISKAKGQPREPQVYVTLPPSQEEMTK 242  
 Db 317 RVSVSLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTTISKAKGQPREPQVYVTLPPSQEEMTK 376  
 QY 243 NQVSLTCLVKGYPSPDIWVESNGQPNENYKTTPEVLDSGSPFLYSRLTVDKSRWQEG 302  
 Db 377 NQVSLTCLVKGYPSPDIWVESNGQPNENYKTTPEVLDSGSPFLYSRLTVDKSRWQEG 436  
 QY 303 NVFSCSVMEALHNHYTKLSLSLKG 329  
 Db 437 NVFSCSVMEALHNHYTKLSLSLKG 463

RESULT 11  
 AAW14941  
 ID AAW14941 standard; Protein; 464 AA.  
 XX  
 AC AAW14941;  
 XX  
 DT 16-JUN-1997 (first entry)  
 XX  
 DE 3F4 Human IgG4 expression plasmid insert product (heavy chain).  
 KW Xenotransplantation; graft rejection; cell interaction; pig;  
 KW vascular cell adhesion molecule; VCAM; monoclonal antibody;  
 KW chimeric antibody; diagnosis.  
 XX  
 OS Mus sp.  
 XX  
 PN WO9711971-A1.  
 XX  
 PD 03-APR-1997.  
 XX  
 PF 27-SEP-1996; 96WO-US15575.  
 XX  
 PR 26-SEP-1996; 96US-0004489.  
 PR 28-SEP-1995; 95US-0004489.  
 XX  
 PA (ALEX-) ALEXION PHARM INC.  
 XX  
 PI Evans MJ, Matis LA, Mueller EE, Mueller JP, Rollins S;  
 PI Rother RP;  
 XX  
 DR WPI: 1997-212855/19.  
 DR N-PSDB; AAT62938.  
 XX  
 PT Antibodies binding to porcine but not human cell interaction  
 PT proteins - useful to treat and assay for rejection of xenografted  
 PT porcine organs, tissues or cells  
 XX  
 PS Disclosure; Page 62-64; 105pp; English.  
 XX  
 CC Heavy chain (AAW14941) and light chain (AAW14942) sequences  
 CC correspond to murine anti-porcine soluble vascular cell adhesion  
 CC molecule (VCAM) monoclonal antibody 3F4 (see also AAW14937-38). They  
 CC are encoded by a 3F4 human IgG4 expression plasmid insert (see  
 CC also AAT62938). A chimeric antibody specific for porcine VCAM can be

CC produced in transfected host cells. It is useful for diagnosing  
 CC human rejection of porcine xenotransplants and for improving  
 CC xenotransplantation of porcine cells, tissues and organs into human  
 CC recipients.  
 XX Sequence 464 AA;  
 SQ

Query Match 99.4%; Score 1743; DB 18; Length 464;  
 Best Local Similarity 100.0%; Pred. No. 3.2e-126;  
 Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ASTKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 62  
 DB 138 ASTKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 197  
 QY 63 GLYSLSSVTVTPSSSLGKTTCNVDPKPTKVDKRVESKYGPPCPCPAPEFLGGPSV 122  
 DB 198 GLYSLSSVTVTPSSSLGKTTCNVDPKPTKVDKRVESKYGPPCPCPAPEFLGGPSV 257  
 QY 123 FLFPKPKDMLISRTPEVTCVVDVDSQEDPEVQFNWYDGVGVHNAKTPREEQFNSTY 182  
 DB 258 FLFPKPKDMLISRTPEVTCVVDVDSQEDPEVQFNWYDGVGVHNAKTPREEQFNSTY 317  
 QY 183 RVSVLTVLHQDLNKGKEYCKVSNKGLPSSIEKTIISKAKGQPREPQVYTLPPSQEEMTK 242  
 DB 318 RVSVLTVLHQDLNKGKEYCKVSNKGLPSSIEKTIISKAKGQPREPQVYTLPPSQEEMTK 377  
 QY 243 NOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSLRTVDSRWQEG 302  
 DB 378 NOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSLRTVDSRWQEG 437

RESULT 12  
 AA014938  
 ID AA014938 standard; Protein; 464 AA.  
 XX  
 AC AA014938;  
 XX  
 DT 16-JUN-1997 (first entry)  
 XX  
 DE Murine anti-porcine VCAM 3F4 heavy chain.  
 XX  
 KW Xenotransplantation; graft rejection; cell interaction; pig;  
 KW vascular cell adhesion molecule; VCAM; monoclonal antibody;  
 KW chimeric antibody; diagnosis.  
 XX  
 OS Mus sp.  
 XX  
 FH Key Location/Qualifiers  
 FT Region 50..54  
 FT /label= CDR1  
 FT Region 69..85  
 FT /label= CDR2  
 FT Region 118..126  
 FT /label= CDR3  
 XX  
 PN WO97111971-A1.  
 XX  
 PD 03-APR-1997.  
 XX  
 PF 27-SEP-1996; 96WO-US15575.  
 XX  
 PR 26-SEP-1996; 96US-0004489.  
 PR 28-SEP-1995; 95US-0004489.  
 XX  
 PA (ALEX-) ALEXION PHARM INC.  
 XX  
 PI Evans MJ, Matis LA, Mueller EE, Mueller JP, Rollins S;  
 PI Rother RP;

XX WPI; 1997-212855/19.  
 DR N-PSDB; AAT62935.  
 XX  
 PT Antibodies binding to porcine but not human cell interaction  
 PT proteins - useful to treat and assay for rejection of xenografted  
 PT porcine organs, tissues or cells  
 XX  
 PS Disclosure; Page 53-55; 105pp; English.  
 XX  
 CC Heavy chain (AAW14938) and light chain (AAW14937) sequences are  
 CC provided for the murine anti-porcine soluble vascular cell adhesion  
 CC molecule (VCAM) monoclonal antibody (MAB) 3F4. Hybridoma 3F4 was  
 CC produced by standard techniques using recombinant, soluble porcine  
 CC VCAM as immunogen. Chimeric antibodies can be produced by cloning  
 CC MAB 3F4 and 2A2 (see also AAW14931-32) variable regions into  
 CC expression plasmid PAPEX-3P modified to contain the human gamma4  
 CC constant region in place of the human gamma1 C1 region. Sequences  
 CC are provided for 3F4 (chimeric) human G2/G4 cDNA (AAW14939), a 3F4  
 CC human G2/G4 expression plasmid insert products (AAW14940), and 3F4  
 CC human IgG4 expression plasmid insert products (AAW14941-42). The  
 CC chimeric antibodies are specific for porcine VCAM. They are useful  
 CC for diagnosing human rejection of porcine xenotransplants and for  
 CC improving xenotransplantation of porcine cells, tissues and organs  
 CC into human recipients.  
 XX  
 CC Sequence 464 AA;  
 SQ

Query Match 99.4%; Score 1743; DB 18; Length 464;  
 Best Local Similarity 100.0%; Pred. No. 3.2e-126;  
 Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ASTKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 62  
 DB 138 ASTKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 197  
 QY 63 GLYSLSSVTVTPSSSLGKTTCNVDPKPTKVDKRVESKYGPPCPCPAPEFLGGPSV 122  
 DB 198 GLYSLSSVTVTPSSSLGKTTCNVDPKPTKVDKRVESKYGPPCPCPAPEFLGGPSV 257  
 QY 123 FLFPKPKDMLISRTPEVTCVVDVDSQEDPEVQFNWYDGVGVHNAKTPREEQFNSTY 182  
 DB 258 FLFPKPKDMLISRTPEVTCVVDVDSQEDPEVQFNWYDGVGVHNAKTPREEQFNSTY 317  
 QY 183 RVSVLTVLHQDLNKGKEYCKVSNKGLPSSIEKTIISKAKGQPREPQVYTLPPSQEEMTK 242  
 DB 318 RVSVLTVLHQDLNKGKEYCKVSNKGLPSSIEKTIISKAKGQPREPQVYTLPPSQEEMTK 377  
 QY 243 NOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSLRTVDSRWQEG 302  
 DB 378 NOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSLRTVDSRWQEG 437

RESULT 13  
 AAR80617  
 ID AAR80617 standard; Protein; 467 AA.  
 XX  
 AC AAR80617;  
 XX  
 DT 19-APR-1996 (first entry)  
 XX  
 DE Anti-human IL-4 humanised MAB h25D2-9 mature heavy chain.  
 XX  
 KW Anti-human interleukin-4; IL-4; humanised; purification;  
 KW treatment; IL-4 diseases; immunoassay; heavy chain; h25D2-9;  
 KW antibody.  
 XX  
 OS Homo sapiens.  
 XX



RESULT 15  
 AAR28808  
 ID AAR28808 standard; Protein; 468 AA.  
 XX AC AAR28808;  
 XX DT 25-MAR-2003 (updated)  
 XX DT 02-APR-1993 (first entry)  
 XX DE pre-5A8 humanised heavy chain.  
 XX KW Vector; pMDR1002; NotI; HindIII; pMDR1001; pSAB132; pBAG101; E. coli;  
 KW JA221(Ig); ampicillin; resistance; immunoglobulin; signal sequence;  
 KW humanised; 5A8; heavy chain; variable; region; HV; IGH4; constant;  
 KW HC; antibody; homolog; CD4; gp120; cell surface glycoprotein; CD4+;  
 KW lymphocytes; helper; inducer; HIV; syncytia; formation.  
 XX OS Synthetic.  
 XX Location/Qualifiers  
 FH Key 1..19  
 FT Peptide /note= "Immunoglobulin signal peptide"  
 FT Region 20..141  
 FT /note= "Humanised 5A8 HV"  
 FT Region 142..468  
 FT /note= "Human IGH4 HC"  
 XX WO9209305-A1.  
 XX 11-JUN-1992.  
 XX 27-NOV-1991; 91WO-US08843.  
 XX 27-NOV-1990; 90US-0618542.  
 XX (BIOJ) BIOGEN INC.  
 XX Burkly LC, Chisholm PL, Rosa JJ, Rosa MD, Thomas DW;  
 XX WPI; 1992-398399/48.  
 XX N-PSDB; AAQ30910.  
 XX New anti-CD4 antibody homologues - which bind CD4, do not block  
 PT binding of HIV gp120 to CD4 but block HIV-induced syncytia  
 PT formation between CD4+ cells  
 XX Disclosure; Page 155-56; 205pp; English.  
 XX This sequence is encoded by the insert of the vector pMDR1002. Three  
 CC fragments were used in the construction of pMDR1002; a 443 bp NotI/  
 CC HindIII fragment of pMDR1001 (see AAQ30905), the 7913 bp NotI linearised  
 CC pSAB132 (see AAQ30906) and a 2109 bp NotI/HindIII fragment of pBAG101  
 CC (see AAQ30909). These fragments were ligated together and the ligation  
 CC mixture was used to transform E. coli JA221(Ig) to ampicillin  
 CC resistance. This sequence represents the immunoglobulin signal  
 CC sequence, amino acids (AA) 1-122 of the humanised 5A8 heavy chain  
 CC variable region (HV) and AA114-AA478 of the human IGH4 heavy chain,  
 CC ie. the constant region (HC). This polypeptide is an antibody homolog  
 CC which was shown to bind to CD4 but did not block the binding of gp120  
 CC to CD4. CD4 is a cell surface glycoprotein of CD4+ lymphocytes  
 CC (helper/inducer cells). The homolog blocked HIV-induced syncytia  
 CC formation. This homolog can be used in the detection, prophylaxis  
 CC and treatment of diseases caused by infective agents whose primary  
 CC targets are CD4+ cells.  
 CC (Updated on 25-MAR-2003 to correct PN field.)  
 XX Sequence 468 AA;

Query Match 99.4%; Score 1743; DB 13; Length 468;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-126;  
 Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	3	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS	62
DB	142	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS	201
QY	63	GLYSLSVVTVFPSSSLGKTTCNVDPKPSNTKVDKRVESKYGPCCPCPAPEFLGGPSV	122
DB	202	GLYSLSVVTVFPSSSLGKTTCNVDPKPSNTKVDKRVESKYGPCCPCPAPEFLGGPSV	261
QY	123	FLFPPKPKDTLMISRTPEVTCVVVDVSDQEDPEVFQFNWYVDGVEVHNAKTKPREEQFNSTY	182
DB	262	FLFPPKPKDTLMISRTPEVTCVVVDVSDQEDPEVFQFNWYVDGVEVHNAKTKPREEQFNSTY	321
QY	183	RVSVLTITLVHQDWLNQGYKCKVSNKGLPSSIEKTIISKAKQPRPQVYITLPPSQEEMTK	242
DB	322	RVSVLTITLVHQDWLNQGYKCKVSNKGLPSSIEKTIISKAKQPRPQVYITLPPSQEEMTK	381
QY	243	NOVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSRLTVDKSRWQEG	302
DB	382	NOVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSRLTVDKSRWQEG	441
QY	303	NVFSCSVMEALHNNHYTOKSLSLGK	329
DB	442	NVFSCSVMEALHNNHYTOKSLSLGK	468

Search completed: January 13, 2004, 12:38:29  
 Job time : 78.7188 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 13, 2004, 12:43:20 ; Search time 52.5825 Seconds  
(without alignments)  
1260.812 Million cell updates/sec

Title: US-09-990-586-100

Perfect score: 1754

Sequence: 1 EFASFKGPSVFLPACSRST.....MHEALHNYTKSLSLGK 329

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747907 segs, 201509753 residues

Total number of hits satisfying chosen parameters: 747907

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.\*

- 1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US05\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/2/pubpaa/FCUS\_PUBCOMB.pep.\*
- 7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*
- 8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep.\*
- 9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep.\*
- 10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep.\*
- 13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep.\*
- 14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*
- 17: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*
- 18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1754	100.0	329	11	US-09-990-586-100
2	1754	100.0	329	12	US-10-310-113-169
3	1754	100.0	329	12	US-10-230-880-100
4	1743	99.4	327	10	US-09-925-664-47
5	1743	99.4	327	12	US-10-112-582-4
6	1743	99.4	327	12	US-10-310-719-7
7	1743	99.4	327	14	US-10-047-542-26
8	1743	99.4	329	10	US-09-935-868-12
9	1743	99.4	329	12	US-10-282-162-12
10	1743	99.4	329	15	US-10-287-035-12
11	1743	99.4	443	9	US-09-917-410-4
12	1743	99.4	444	11	US-09-256-156-4
13	1743	99.4	448	9	US-09-917-410-6
14	1743	99.4	465	12	US-10-401-344-2
15	1743	99.4	467	15	US-10-211-357-8

16	1738	99.1	467	12	US-10-428-408A-30
17	1736	99.0	467	15	US-10-211-357-10
18	1731	98.7	467	15	US-10-211-357-12
19	1649.5	94.0	472	12	US-10-307-724-67
20	1649.5	94.0	472	15	US-10-006-593-67
21	1638.5	93.4	580	12	US-10-310-719-37
22	1611.5	91.9	530	8	US-08-485-163-5
23	1611.5	91.9	530	9	US-09-766-995-4
24	1605.5	91.5	326	12	US-10-112-582-2
25	1605.5	91.5	326	12	US-10-310-719-9
26	1605.5	91.5	326	14	US-10-047-542-22
27	1605.5	91.5	433	11	US-09-256-156-2
28	1605.5	91.5	451	15	US-10-153-382-17
29	1605.5	91.5	463	15	US-10-153-382-3
30	1605.5	91.5	463	15	US-10-153-382-13
31	1605.5	91.5	464	15	US-10-153-382-9
32	1605.5	91.5	470	10	US-09-859-053-28
33	1605.5	91.5	470	10	US-09-859-053-32
34	1605.5	91.5	470	10	US-09-859-053-35
35	1604.5	91.5	468	15	US-10-071-485-67
36	1604.5	91.5	711	15	US-10-071-485-90
37	1601.5	91.3	332	11	US-09-990-586-98
38	1601.5	91.3	332	12	US-10-310-113-167
39	1601.5	91.3	332	12	US-10-230-880-98
40	1599.5	91.2	330	12	US-10-366-709-52
41	1599.5	91.2	450	9	US-09-796-848A-37
42	1599.5	91.2	450	9	US-09-796-848A-39
43	1599.5	91.2	450	9	US-09-796-848A-41
44	1599.5	91.2	450	9	US-09-796-848A-43
45	1599.5	91.2	450	9	US-09-796-848A-45

ALIGNMENTS

RESULT 1

US-09-990-586-100  
; Sequence 100, Application US/09990586  
; Publication No. US20030109680A1  
; GENERAL INFORMATION:  
; APPLICANT: JIAO, JIN-AN  
; APPLICANT: WONG, HING C.  
; TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD COAGULATION AND METHODS  
; TITLE OF INVENTION: OF USE THEREOF  
; FILE REFERENCE: 71758/46943-CIP2  
; CURRENT APPLICATION NUMBER: US/09/990,586  
; CURRENT FILING DATE: 2001-11-21  
; PRIOR APPLICATION NUMBER: 09/293,854  
; PRIOR FILING DATE: 1999-04-16  
; NUMBER OF SEQ ID NOS: 102  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 100  
; LENGTH: 329  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-990-586-100

Query Match		100.0%;	Score 1754;	DB 11;	Length 329;
Best Local Similarity		100.0%;	Pred. No. 1.7e-140;		
Matches 329,		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	EFASFKGPSVFLPACSRSTSESTAALGCLVKDIFPEPTVSNWNSGALTSGVHTFPAVLQ	60		
Db	1	EFASFKGPSVFLPACSRSTSESTAALGCLVKDIFPEPTVSNWNSGALTSGVHTFPAVLQ	60		
Qy	61	SSGLYSSLVVTVPPSSSLGKTKYTCNVDKHPSNTKVDKRVESKYGPPCSPCAPEFLGGP	120		
Db	61	SSGLYSSLVVTVPPSSSLGKTKYTCNVDKHPSNTKVDKRVESKYGPPCSPCAPEFLGGP	120		
Qy	121	SVFLFPKPKDITLMISRTPEVTCVVDVSDDEVDVFNWVDGVFVHNATKTRREQFNS	180		
Db	121	SVFLFPKPKDITLMISRTPEVTCVVDVSDDEVDVFNWVDGVFVHNATKTRREQFNS	180		



QY 181 TYRVSVLTLVHQDWLNGKEYCKYKSNKGLPSSIEKTSKAGQPREPQVYTLPPSQEEM 240  
Db 181 TYRVSVLTLVHQDWLNGKEYCKYKSNKGLPSSIEKTSKAGQPREPQVYTLPPSQEEM 240  
QY 241 TKQVSLTCLVKGFPSPDIWESNGQPPENNYKTPPVLDSDGSGFFLYSLRSLTVDKSRWQ 300  
Db 241 TKQVSLTCLVKGFPSPDIWESNGQPPENNYKTPPVLDSDGSGFFLYSLRSLTVDKSRWQ 300  
QY 301 EGNVFCSCVMHEALHNNHYTKSLSLSLGK 329  
Db 301 EGNVFCSCVMHEALHNNHYTKSLSLSLGK 329

## RESULT 2

US-10-310-113-169  
; Sequence 169, Application US/10310113  
; Publication No. US20030176664A1  
; GENERAL INFORMATION:  
; APPLICANT: JIAO, JIN-AN  
; APPLICANT: WONG, HING C.  
; APPLICANT: NIEVES, ESPERANZA LILIANA  
; APPLICANT: MOSQUERA, LUIS A.  
; TITLE OF INVENTION: USE OF ANTI-TISSUE FACTOR ANTIBODIES FOR TREATING  
; FILE REFERENCE: 58122(71758)  
; CURRENT APPLICATION NUMBER: US/10/310,113  
; PRIOR FILING DATE: 2002-12-04  
; PRIOR APPLICATION NUMBER: 09/990,586  
; PRIOR FILING DATE: 2001-11-21  
; PRIOR APPLICATION NUMBER: 60/343,306  
; PRIOR FILING DATE: 2001-10-29  
; PRIOR APPLICATION NUMBER: 09/293,854  
; PRIOR FILING DATE: 1999-04-16  
; PRIOR APPLICATION NUMBER: 08/914,806  
; PRIOR FILING DATE: 1997-03-10  
; NUMBER OF SEQ ID NOS: 169  
; SOFTWARE: Patent in Ver. 2.1  
; SEQ ID NO 169  
; LENGTH: 329  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-310-113-169

Query Match 100.0%; Score 1754; DB 12; Length 329;  
Best Local Similarity 100.0%; Pred. No. 1.7e-140;  
Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 EFASITKGPSVFPLAPCSRSTSTSTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 60  
Db 1 EFASITKGPSVFPLAPCSRSTSTSTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 60  
QY 61 SSGLYSLSSVTVPPSSSLGTTKTYTCNVDPKPTNTKVDKRVESKYGPPCPAPAEFLGGP 120  
Db 61 SSGLYSLSSVTVPPSSSLGTTKTYTCNVDPKPTNTKVDKRVESKYGPPCPAPAEFLGGP 120  
QY 121 SVFLFPPKPKDTLMISRTPEVTCVVDVSDQEPVEVFQFNWYDGVVHNATKPREEQFNS 180  
Db 121 SVFLFPPKPKDTLMISRTPEVTCVVDVSDQEPVEVFQFNWYDGVVHNATKPREEQFNS 180  
QY 181 TYRVSVLTLVHQDWLNGKEYCKYKSNKGLPSSIEKTSKAGQPREPQVYTLPPSQEEM 240  
Db 181 TYRVSVLTLVHQDWLNGKEYCKYKSNKGLPSSIEKTSKAGQPREPQVYTLPPSQEEM 240  
QY 241 TKQVSLTCLVKGFPSPDIWESNGQPPENNYKTPPVLDSDGSGFFLYSLRSLTVDKSRWQ 300  
Db 241 TKQVSLTCLVKGFPSPDIWESNGQPPENNYKTPPVLDSDGSGFFLYSLRSLTVDKSRWQ 300  
QY 301 EGNVFCSCVMHEALHNNHYTKSLSLSLGK 329  
Db 301 EGNVFCSCVMHEALHNNHYTKSLSLSLGK 329

## RESULT 3

US-10-230-880-100  
; Sequence 100, Application US/10230880  
; Publication No. US20030190705A1  
; GENERAL INFORMATION:  
; APPLICANT: WONG, HING C.  
; APPLICANT: STINSON, JEFFREY L.  
; APPLICANT: MOSQUERA, LUIS A.  
; TITLE OF INVENTION: METHOD OF HUMANIZING IMMUNE SYSTEM MOLECULES  
; FILE REFERENCE: 71758/58066  
; CURRENT APPLICATION NUMBER: US/10/230,880  
; CURRENT FILING DATE: 2002-12-23  
; PRIOR APPLICATION NUMBER: 09/990,586  
; PRIOR FILING DATE: 2001-11-21  
; PRIOR APPLICATION NUMBER: 60/343,306  
; PRIOR FILING DATE: 2001-10-29  
; PRIOR APPLICATION NUMBER: 09/293,854  
; PRIOR FILING DATE: 1999-04-16  
; NUMBER OF SEQ ID NOS: 174  
; SOFTWARE: Patent in Ver. 2.1  
; SEQ ID NO 100  
; LENGTH: 329  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-230-880-100

Query Match 100.0%; Score 1754; DB 12; Length 329;  
Best Local Similarity 100.0%; Pred. No. 1.7e-140;  
Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 EFASITKGPSVFPLAPCSRSTSTSTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 60  
Db 1 EFASITKGPSVFPLAPCSRSTSTSTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 60  
QY 61 SSGLYSLSSVTVPPSSSLGTTKTYTCNVDPKPTNTKVDKRVESKYGPPCPAPAEFLGGP 120  
Db 61 SSGLYSLSSVTVPPSSSLGTTKTYTCNVDPKPTNTKVDKRVESKYGPPCPAPAEFLGGP 120  
QY 121 SVFLFPPKPKDTLMISRTPEVTCVVDVSDQEPVEVFQFNWYDGVVHNATKPREEQFNS 180  
Db 121 SVFLFPPKPKDTLMISRTPEVTCVVDVSDQEPVEVFQFNWYDGVVHNATKPREEQFNS 180  
QY 181 TYRVSVLTLVHQDWLNGKEYCKYKSNKGLPSSIEKTSKAGQPREPQVYTLPPSQEEM 240  
Db 181 TYRVSVLTLVHQDWLNGKEYCKYKSNKGLPSSIEKTSKAGQPREPQVYTLPPSQEEM 240  
QY 241 TKQVSLTCLVKGFPSPDIWESNGQPPENNYKTPPVLDSDGSGFFLYSLRSLTVDKSRWQ 300  
Db 241 TKQVSLTCLVKGFPSPDIWESNGQPPENNYKTPPVLDSDGSGFFLYSLRSLTVDKSRWQ 300  
QY 301 EGNVFCSCVMHEALHNNHYTKSLSLSLGK 329  
Db 301 EGNVFCSCVMHEALHNNHYTKSLSLSLGK 329

RESULT 4  
US-09-925-664-47  
; Sequence 47, Application US/09925664  
; Patent No. US20020160006A1  
; GENERAL INFORMATION:  
; APPLICANT: Denney, Jr., Dan W.  
; TITLE OF INVENTION: Methods of Treating Lymphoma and Leukemia  
; FILE REFERENCE: GENTOPR-08499  
; CURRENT APPLICATION NUMBER: US/09/925,664  
; CURRENT FILING DATE: 2001-08-09  
; PRIOR APPLICATION NUMBER: 09/370,453  
; PRIOR FILING DATE: 1999-08-09  
; PRIOR APPLICATION NUMBER: 08/644,664  
; PRIOR FILING DATE: 1996-05-01  
; PRIOR APPLICATION NUMBER: 08/761,277  
; PRIOR FILING DATE: 1996-12-06  
; NUMBER OF SEQ ID NOS: 80  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 47

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; LENGTH: 327
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-664-47

Query Match          99.4%; Score 1743; DB 10; Length 327;
Best Local Similarity 100.0%; Pred. No. 1.4e-139; Indels 0; Gaps 0;
Matches 327; Conservative 0; Mismatches 0;

QY 3 ASTKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 62
Db 1 ASTKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60

QY 63 GLYSLSVVTVPSSSLGTTKTYTCNVDPKSNKVDKRVESKYGPPCPAPFELGGPSV 122
Db 61 GLYSLSVVTVPSSSLGTTKTYTCNVDPKSNKVDKRVESKYGPPCPAPFELGGPSV 120

QY 123 FLPPPKPDTLMISRTPEVTCVVVDVSDPEVQFNWYVDGVEVHNATKPREEQFNSTY 182
Db 121 FLPPPKPDTLMISRTPEVTCVVVDVSDPEVQFNWYVDGVEVHNATKPREEQFNSTY 180

QY 183 RVSVSLTVLHQDLWNGKEYCKVSNKGLPSSIEKTIISKAKQPRPQVYTLPPSQEEMTK 242
Db 181 RVSVSLTVLHQDLWNGKEYCKVSNKGLPSSIEKTIISKAKQPRPQVYTLPPSQEEMTK 240

QY 243 NOVSLTCLVKGYFPPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSRLTVDKSRWQEG 302
Db 241 NOVSLTCLVKGYFPPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSRLTVDKSRWQEG 300

QY 303 NVFSCSVMEALHNHYTQKSLSLGLK 329
Db 301 NVFSCSVMEALHNHYTQKSLSLGLK 327

RESULT 5
US-10-112-582-4
; Sequence 4, Application US/10112582
; Publication No. US20030166877A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; TITLE OF INVENTION: Reducing the Immunogenicity of Fusion Proteins
; FILE REFERENCE: LEX-017
; CURRENT APPLICATION NUMBER: US/10/112,582
; CURRENT FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: US 60/280,625
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 4
; LENGTH: 327
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; OTHER INFORMATION: Ig gamma-4 chain C region
US-10-112-582-4

Query Match          99.4%; Score 1743; DB 12; Length 327;
Best Local Similarity 100.0%; Pred. No. 1.4e-139; Indels 0; Gaps 0;
Matches 327; Conservative 0; Mismatches 0;

QY 3 ASTKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 62
Db 1 ASTKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60

QY 63 GLYSLSVVTVPSSSLGTTKTYTCNVDPKSNKVDKRVESKYGPPCPAPFELGGPSV 122
Db 61 GLYSLSVVTVPSSSLGTTKTYTCNVDPKSNKVDKRVESKYGPPCPAPFELGGPSV 120

QY 123 FLPPPKPDTLMISRTPEVTCVVVDVSDPEVQFNWYVDGVEVHNATKPREEQFNSTY 182
Db 121 FLPPPKPDTLMISRTPEVTCVVVDVSDPEVQFNWYVDGVEVHNATKPREEQFNSTY 180
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183 RVSVSLTVLHQDLWNGKEYCKVSNKGLPSSIEKTIISKAKQPRPQVYTLPPSQEEMTK 242
181 RVSVSLTVLHQDLWNGKEYCKVSNKGLPSSIEKTIISKAKQPRPQVYTLPPSQEEMTK 240
243 NOVSLTCLVKGYFPPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSRLTVDKSRWQEG 302
241 NOVSLTCLVKGYFPPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSRLTVDKSRWQEG 300
303 NVFSCSVMEALHNHYTQKSLSLGLK 329
301 NVFSCSVMEALHNHYTQKSLSLGLK 327

RESULT 6
US-10-310-719-7
; Sequence 7, Application US/10310719
; Publication No. US20030166163A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; TITLE OF INVENTION: Immunocytokines With Modulated Selectivity
; FILE REFERENCE: LEX-020
; CURRENT APPLICATION NUMBER: US/10/310,719
; CURRENT FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: 60/337,113
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/371,966
; PRIOR FILING DATE: 2002-04-12
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 7
; LENGTH: 327
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc
; LOCATION: (1)..(327)
; OTHER INFORMATION: Human gamma 4 constant region
US-10-310-719-7

Query Match          99.4%; Score 1743; DB 12; Length 327;
Best Local Similarity 100.0%; Pred. No. 1.4e-139; Indels 0; Gaps 0;
Matches 327; Conservative 0; Mismatches 0;

QY 3 ASTKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 62
Db 1 ASTKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60

QY 63 GLYSLSVVTVPSSSLGTTKTYTCNVDPKSNKVDKRVESKYGPPCPAPFELGGPSV 122
Db 61 GLYSLSVVTVPSSSLGTTKTYTCNVDPKSNKVDKRVESKYGPPCPAPFELGGPSV 120

QY 123 FLPPPKPDTLMISRTPEVTCVVVDVSDPEVQFNWYVDGVEVHNATKPREEQFNSTY 182
Db 121 FLPPPKPDTLMISRTPEVTCVVVDVSDPEVQFNWYVDGVEVHNATKPREEQFNSTY 180

QY 183 RVSVSLTVLHQDLWNGKEYCKVSNKGLPSSIEKTIISKAKQPRPQVYTLPPSQEEMTK 242
Db 181 RVSVSLTVLHQDLWNGKEYCKVSNKGLPSSIEKTIISKAKQPRPQVYTLPPSQEEMTK 240

QY 243 NOVSLTCLVKGYFPPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSRLTVDKSRWQEG 302
Db 241 NOVSLTCLVKGYFPPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSRLTVDKSRWQEG 300

QY 303 NVFSCSVMEALHNHYTQKSLSLGLK 329
Db 301 NVFSCSVMEALHNHYTQKSLSLGLK 327

RESULT 7
US-10-047-542-26
; Sequence 26, Application US/10047542
; Publication No. US20020168367A1
; GENERAL INFORMATION:
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APPLICANT: LARRICK, JAMES W.  
APPLICANT: WYCOFF, KEITH L.  
TITLE OF INVENTION: NOVEL IMMUNOADHESINS FOR TREATING AND PREVENTING VIRAL  
FILE REFERENCE: 030905.0004.C1P1  
CURRENT APPLICATION NUMBER: US/10/047,542  
CURRENT FILING DATE: 2001-10-26  
PRIOR APPLICATION NUMBER: PCT/US01/13932  
PRIOR FILING DATE: 2001-04-28  
PRIOR APPLICATION NUMBER: 60/200,298  
PRIOR FILING DATE: 2000-04-28  
NUMBER OF SEQ ID NOS: 101  
SOFTWARE: Patent In Ver. 2.1  
SEQ ID NO 26  
LENGTH: 327  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-047-542-26

Query Match 99.4%; Score 1743; DB 14; Length 327;  
Best Local Similarity 100.0%; Pred. No. 1.4e-139;  
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ASTKGPSVFLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 62  
DB 1 ASTKGPSVFLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60  
QY 63 GLYSLSVVTVFSSSLGKTKYTCNVDRKPSNTKVDKRVESKYGPPCPCPAPEFLGGPSV 122  
DB 61 GLYSLSVVTVFSSSLGKTKYTCNVDRKPSNTKVDKRVESKYGPPCPCPAPEFLGGPSV 120  
QY 123 FLFPPKPKDTLMISRTPEVTCVVVDVSDQEDPEVFQFNWYVDGVEVHNAKTKPREEQFNSTY 182  
DB 121 FLFPPKPKDTLMISRTPEVTCVVVDVSDQEDPEVFQFNWYVDGVEVHNAKTKPREEQFNSTY 180  
QY 183 RVSVLTVLHODWLNKGEYKCKVSNKGLPSSIEKTIISKAKGQPREPQVYTLPPSQEEMTK 242  
DB 181 RVSVLTVLHODWLNKGEYKCKVSNKGLPSSIEKTIISKAKGQPREPQVYTLPPSQEEMTK 240  
QY 243 NOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSLRTVDKSRWQEG 302  
DB 241 NOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSLRTVDKSRWQEG 300  
QY 303 NVFSCSVMEALHNNHYTKQSLSLGK 329  
DB 301 NVFSCSVMEALHNNHYTKQSLSLGK 327

RESULT 8  
US-09-935-868-12  
Sequence 12, Application US/09935868  
Patent No. US2002016490A1  
GENERAL INFORMATION:  
APPLICANT: Regeneron Pharmaceuticals, Inc  
TITLE OF INVENTION: Receptor Based Antagonists, and Methods of Making and Using  
FILE REFERENCE: REG 203D  
CURRENT APPLICATION NUMBER: US/09/935,868  
CURRENT FILING DATE: 2002-04-11  
PRIOR APPLICATION NUMBER: PCT/US99/22045  
PRIOR FILING DATE: 1999-09-22  
NUMBER OF SEQ ID NOS: 52  
SOFTWARE: Patent In version 3.0  
SEQ ID NO 12  
LENGTH: 329  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-935-868-12

Query Match 99.4%; Score 1743; DB 10; Length 329;  
Best Local Similarity 100.0%; Pred. No. 1.4e-139;  
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ASTKGPSVFLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 62

DB 3 ASTKGPSVFLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 62  
QY 63 GLYSLSVVTVFSSSLGKTKYTCNVDRKPSNTKVDKRVESKYGPPCPCPAPEFLGGPSV 122  
DB 63 GLYSLSVVTVFSSSLGKTKYTCNVDRKPSNTKVDKRVESKYGPPCPCPAPEFLGGPSV 122  
QY 123 FLFPPKPKDTLMISRTPEVTCVVVDVSDQEDPEVFQFNWYVDGVEVHNAKTKPREEQFNSTY 182  
DB 123 FLFPPKPKDTLMISRTPEVTCVVVDVSDQEDPEVFQFNWYVDGVEVHNAKTKPREEQFNSTY 182  
QY 183 RVSVLTVLHODWLNKGEYKCKVSNKGLPSSIEKTIISKAKGQPREPQVYTLPPSQEEMTK 242  
DB 183 RVSVLTVLHODWLNKGEYKCKVSNKGLPSSIEKTIISKAKGQPREPQVYTLPPSQEEMTK 242  
QY 243 NOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSLRTVDKSRWQEG 302  
DB 243 NOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSLRTVDKSRWQEG 302  
QY 303 NVFSCSVMEALHNNHYTKQSLSLGK 329  
DB 303 NVFSCSVMEALHNNHYTKQSLSLGK 329

RESULT 9  
US-10-282-162-12  
Sequence 12, Application US/10282162  
Publication No. US20030143697A1  
GENERAL INFORMATION:  
APPLICANT: REGENERON PHARMACEUTICALS, INC.  
TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING  
FILE REFERENCE: REG 203-B-US  
CURRENT APPLICATION NUMBER: US/10/282,162  
CURRENT FILING DATE: 2002-10-28  
PRIOR APPLICATION NUMBER: 09/787,835  
PRIOR FILING DATE: 1999-09-22  
PRIOR APPLICATION NUMBER: PCT/US99/22045  
PRIOR FILING DATE: 1999-09-22  
NUMBER OF SEQ ID NOS: 56  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 12  
LENGTH: 329  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-282-162-12

Query Match 99.4%; Score 1743; DB 12; Length 329;  
Best Local Similarity 100.0%; Pred. No. 1.4e-139;  
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ASTKGPSVFLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 62  
DB 3 ASTKGPSVFLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 62  
QY 63 GLYSLSVVTVFSSSLGKTKYTCNVDRKPSNTKVDKRVESKYGPPCPCPAPEFLGGPSV 122  
DB 63 GLYSLSVVTVFSSSLGKTKYTCNVDRKPSNTKVDKRVESKYGPPCPCPAPEFLGGPSV 122  
QY 123 FLFPPKPKDTLMISRTPEVTCVVVDVSDQEDPEVFQFNWYVDGVEVHNAKTKPREEQFNSTY 182  
DB 123 FLFPPKPKDTLMISRTPEVTCVVVDVSDQEDPEVFQFNWYVDGVEVHNAKTKPREEQFNSTY 182  
QY 183 RVSVLTVLHODWLNKGEYKCKVSNKGLPSSIEKTIISKAKGQPREPQVYTLPPSQEEMTK 242  
DB 183 RVSVLTVLHODWLNKGEYKCKVSNKGLPSSIEKTIISKAKGQPREPQVYTLPPSQEEMTK 242  
QY 243 NOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSLRTVDKSRWQEG 302  
DB 243 NOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSLRTVDKSRWQEG 302  
QY 303 NVFSCSVMEALHNNHYTKQSLSLGK 329

Db 303 NVFSCVMHEALHNHYTQKSLSLGK 329

RESULT 10

US-10-287-035-12

Sequence 12, Application US/10287035

Publication No. US20030104567A1

GENERAL INFORMATION:

APPLICANT: Neil Stahl and George D. Yancopoulos

TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING

TITLE OF INVENTION: AND USING

FILE REFERENCE: REG 203DA

CURRENT APPLICATION NUMBER: US/10/287,035

CURRENT FILING DATE: 2002-11-01

PRIOR APPLICATION NUMBER: USSN 09/935,868

PRIOR FILING DATE: 2001-08-23

PRIOR APPLICATION NUMBER: USSN 09/787,835

PRIOR FILING DATE: 2001-03-22

PRIOR APPLICATION NUMBER: USSN 09/313,942

PRIOR FILING DATE: 1998-05-19

PRIOR APPLICATION NUMBER: 09/313,942

PRIOR FILING DATE: 1999-05-19

PRIOR APPLICATION NUMBER: 60/101,858

PRIOR FILING DATE: 1998-09-25

NUMBER OF SEQ ID NOS: 60

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 12

LENGTH: 329

TYPE: PRT

ORGANISM: Homo sapiens

US-10-287-035-12

Query Match 99.4%; Score 1743; DB 15; Length 329;

Best Local Similarity 100.0%; Pred. No. 1.4e-139;

Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ASTKGPSVPLAPCSRSTSESTAALGCLVKDYFPEPTVWSNLSGALTSGVHTFPAVLQSS 62

Db 3 ASTKGPSVPLAPCSRSTSESTAALGCLVKDYFPEPTVWSNLSGALTSGVHTFPAVLQSS 62

QY 63 GLYSLSVVTVFSSSLGKTYTCNVNDHKPSNTKVDKRVESKYGPPCPSCPAPEFLGGPSV 122

Db 63 GLYSLSVVTVFSSSLGKTYTCNVNDHKPSNTKVDKRVESKYGPPCPSCPAPEFLGGPSV 122

QY 123 FLFPPKPKDTLMISRTPEVTCVVDVSDQEDPEVQFNWYVDGVEVHNATKPREEQFNSTY 182

Db 123 FLFPPKPKDTLMISRTPEVTCVVDVSDQEDPEVQFNWYVDGVEVHNATKPREEQFNSTY 182

QY 183 RVSVLTVLHQDLNKGKEYCKVSNKGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMTK 242

Db 183 RVSVLTVLHQDLNKGKEYCKVSNKGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMTK 242

QY 243 NVSLTCLVKGFPYSDIAVWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEG 302

Db 243 NVSLTCLVKGFPYSDIAVWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEG 302

QY 303 NVFSCVMHEALHNHYTQKSLSLGK 329

Db 303 NVFSCVMHEALHNHYTQKSLSLGK 329

RESULT 11

US-09-917-410-4

Sequence 4, Application US/09917410

Patent No. US20020098183A1

GENERAL INFORMATION:

APPLICANT: MARTIN, Ulrich; HASELBECK, Anton; SCHUMACHER, Guenther; CO, Man S.

TITLE OF INVENTION: ANTI-L-SELECTIN ANTIBODIES FOR PREVENTION OF MULTIPLE ORGAN FAILURE AFTER POLYTRAUMA AND FOR PREVENTION OF ACUTE ORGAN DAMAGE AFTER EXTRACORPOREAL BLOOD CIRCULATION

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: Felte & Lynch

STREET: 805 Third Avenue

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10022

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Computer Disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII, WordPerfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/917,410

FILING DATE: 26-Jul-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/578,953

FILING DATE: <Unknown>

APPLICATION NUMBER: EP 95 114 969.9

FILING DATE: 19-Sep-95

ATTORNEY/AGENT INFORMATION:

NAME: Hanson, No. US20020098183A1man D.

REGISTRATION NUMBER: 30,946

REFERENCE/DOCKET NUMBER: BOER 1059-PFF/NDH/SLH

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 688-9200

TELEFAX: (212) 838-3884

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 443

TYPE: amino acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-09-917-410-4

Query Match 99.4%; Score 1743; DB 9; Length 443;

Best Local Similarity 100.0%; Pred. No. 2.1e-139;

Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ASTKGPSVPLAPCSRSTSESTAALGCLVKDYFPEPTVWSNLSGALTSGVHTFPAVLQSS 62

Db 117 ASTKGPSVPLAPCSRSTSESTAALGCLVKDYFPEPTVWSNLSGALTSGVHTFPAVLQSS 176

QY 63 GLYSLSVVTVFSSSLGKTYTCNVNDHKPSNTKVDKRVESKYGPPCPSCPAPEFLGGPSV 122

Db 177 GLYSLSVVTVFSSSLGKTYTCNVNDHKPSNTKVDKRVESKYGPPCPSCPAPEFLGGPSV 236

QY 123 FLFPPKPKDTLMISRTPEVTCVVDVSDQEDPEVQFNWYVDGVEVHNATKPREEQFNSTY 182

Db 237 FLFPPKPKDTLMISRTPEVTCVVDVSDQEDPEVQFNWYVDGVEVHNATKPREEQFNSTY 296

QY 183 RVSVLTVLHQDLNKGKEYCKVSNKGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMTK 242

Db 297 RVSVLTVLHQDLNKGKEYCKVSNKGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMTK 356

QY 243 NVSLTCLVKGFPYSDIAVWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEG 302

Db 357 NVSLTCLVKGFPYSDIAVWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEG 416

QY 303 NVFSCVMHEALHNHYTQKSLSLGK 329

Db 417 NVFSCVMHEALHNHYTQKSLSLGK 443

RESULT 12

US-09-256-156-4

Sequence 4, Application US/09256156A

Publication No. US20030105294A1

GENERAL INFORMATION:

APPLICANT: GILLIES, Stephen D

```

; APPLICANT: LO, Kin-Ming
; APPLICANT: LAN, Yan
; APPLICANT: WESOLOWSKI, John
; TITLE OF INVENTION: Enhancing the Circulating Half-life of Antibody-based
; TITLE OF INVENTION: Fusion Proteins
; FILE REFERENCE: LEX-003
; CURRENT APPLICATION NUMBER: US/09/256,156A
; CURRENT FILING DATE: 1999-02-24
; EARLIER APPLICATION NUMBER: US 60/075,887
; EARLIER FILING DATE: 1998-02-25
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 4
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: IGG-4 CHAIN C REGION
; NAME/KEY: VARIANT
; LOCATION: (1)..(117)
; OTHER INFORMATION: The Xaa at positions 1 to 117 are non-conserved
; OTHER INFORMATION: amino acids
US-09-256-156-4

Query Match          99.4%; Score 1743; DB 11; Length 444;
Best Local Similarity 100.0%; Pred. No. 2.1e-139; Indels 0; Gaps 0;
Matches 327; Conservative 0; Mismatches 0;

QY 3 ASTKPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 62
DB 118 ASTKPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 177
QY 63 GLYSLSVVTPSSSLGKTKYTCNVDPKPSNTKVDKRVESKYGPPCPSCAPEFLGGPSV 122
DB 178 GLYSLSVVTPSSSLGKTKYTCNVDPKPSNTKVDKRVESKYGPPCPSCAPEFLGGPSV 237
QY 123 FLFPKPDKDTLMISRTPEVTCVVDVSDQEDPEVQFNWYVDGVEVHNATKPREEQFNSTY 182
DB 238 FLFPKPDKDTLMISRTPEVTCVVDVSDQEDPEVQFNWYVDGVEVHNATKPREEQFNSTY 297
QY 183 RVVSVLTVLHQDLNGKEYCKVSNKGLPSSIEKTIISKAKQPREPQVYTLPPSQEEMTK 242
DB 298 RVVSVLTVLHQDLNGKEYCKVSNKGLPSSIEKTIISKAKQPREPQVYTLPPSQEEMTK 357
QY 243 NOVSLTCLVKGYPSPDI AVEWESNGQPENNYKTTTPVLDSDGSPFLYSRLTVDKSRWQEG 302
DB 358 NOVSLTCLVKGYPSPDI AVEWESNGQPENNYKTTTPVLDSDGSPFLYSRLTVDKSRWQEG 417
QY 303 NVFSCSVMEALHNHYTQKSLSLGLK 329
DB 418 NVFSCSVMEALHNHYTQKSLSLGLK 444

RESULT 13
US-09-917-410-6
; Sequence 6, Application US/09917410
; Patent No. US20020098183A1
; GENERAL INFORMATION:
; APPLICANT: MARTIN, Ulrich; HASELBECK, Anton; SCHUMACHER, Guenther;
; CO. Man S.
; TITLE OF INVENTION: ANTI-L-SELECTIN ANTIBODIES FOR PREVENTION OF
; MULTIPLE ORGAN FAILURE AFTER POLYTRAUMA AND FOR
; PREVENTION OF ACUTE ORGAN DAMAGE AFTER
; EXTRACORPOREAL BLOOD CIRCULATION
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10022

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Computer Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII, WordPerfect 5.1
; CURRENT APPLICATION DATA: US/09/917,410
; APPLICATION NUMBER: 30,946
; FILING DATE: 26-Jul-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/578,953
; FILING DATE: <Unknown>
; APPLICATION NUMBER: EP 95 114 969.9
; FILING DATE: 13-Sep-95
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. US20020098183A1man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: BOER 1059-PFF/NDH/SLH
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 448 amino acid residues
; TYPE: amino acid
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-917-410-6

Query Match          99.4%; Score 1743; DB 9; Length 448;
Best Local Similarity 100.0%; Pred. No. 2.2e-139; Indels 0; Gaps 0;
Matches 327; Conservative 0; Mismatches 0;

QY 3 ASTKPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 62
DB 122 ASTKPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 181
QY 63 GLYSLSVVTPSSSLGKTKYTCNVDPKPSNTKVDKRVESKYGPPCPSCAPEFLGGPSV 122
DB 182 GLYSLSVVTPSSSLGKTKYTCNVDPKPSNTKVDKRVESKYGPPCPSCAPEFLGGPSV 241
QY 123 FLFPKPDKDTLMISRTPEVTCVVDVSDQEDPEVQFNWYVDGVEVHNATKPREEQFNSTY 182
DB 242 FLFPKPDKDTLMISRTPEVTCVVDVSDQEDPEVQFNWYVDGVEVHNATKPREEQFNSTY 301
QY 183 RVVSVLTVLHQDLNGKEYCKVSNKGLPSSIEKTIISKAKQPREPQVYTLPPSQEEMTK 242
DB 302 RVVSVLTVLHQDLNGKEYCKVSNKGLPSSIEKTIISKAKQPREPQVYTLPPSQEEMTK 361
QY 243 NOVSLTCLVKGYPSPDI AVEWESNGQPENNYKTTTPVLDSDGSPFLYSRLTVDKSRWQEG 302
DB 362 NOVSLTCLVKGYPSPDI AVEWESNGQPENNYKTTTPVLDSDGSPFLYSRLTVDKSRWQEG 421
QY 303 NVFSCSVMEALHNHYTQKSLSLGLK 329
DB 422 NVFSCSVMEALHNHYTQKSLSLGLK 448

RESULT 14
US-10-401-344-2
; Sequence 2, Application US/10401344
; Publication No. US20030194404A1
; GENERAL INFORMATION:
; APPLICANT: Schering Corporation and Abgenix, Inc.
; APPLICANT: Greenfeder, Scott
; APPLICANT: Corvalan, Jose
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO INTERLEUKIN-5 AND METHODS AND COM
; FILE REFERENCE: L101564W1
; CURRENT APPLICATION NUMBER: US/10/401,344
; CURRENT FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patent in version 3.1

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SEQ ID NO 2  
LENGTH: 465  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: SIGNAL  
LOCATION: (1)..(19)  
OTHER INFORMATION:  
FEATURE:  
NAME/KEY: Variable Region  
LOCATION: (20)..(138)  
OTHER INFORMATION:  
FEATURE:  
NAME/KEY: CH1 Region  
LOCATION: (139)..(236)  
OTHER INFORMATION:  
FEATURE:  
NAME/KEY: Hinge Region  
LOCATION: (237)..(248)  
OTHER INFORMATION:  
FEATURE:  
NAME/KEY: CH2 Region  
LOCATION: (249)..(358)  
OTHER INFORMATION:  
FEATURE:  
NAME/KEY: CH3 Region  
LOCATION: (359)..(465)  
OTHER INFORMATION:  
US-10-401-344-2

Query Match 99.4%; Score 1743; DB 12; Length 465;  
Best Local Similarity 100.0%; Pred. No. 2.3e-139;  
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3 ASTKGSVPFLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 62  
DB 139 ASTKGSVPFLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 198  
QY 63 GLYSLSSVTVTPSSSLGKTYYTCNVDPKPSNTKVDKRVESKYGPPCPSPCPAEPFLGGPSV 122  
DB 199 GLYSLSSVTVTPSSSLGKTYYTCNVDPKPSNTKVDKRVESKYGPPCPSPCPAEPFLGGPSV 258  
QY 123 FLPPPKPDTLMISRPEVTCVVDVSQEDPEVFQFNWYDGVGVHNAKTKPRREEQFNSTY 182  
DB 259 FLPPPKPDTLMISRPEVTCVVDVSQEDPEVFQFNWYDGVGVHNAKTKPRREEQFNSTY 318  
QY 183 RVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAKGQPREPQVYTLPPSQEEMTK 242  
DB 319 RVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAKGQPREPQVYTLPPSQEEMTK 378  
QY 243 NQVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSRLTVDKSRWQEG 302  
DB 379 NQVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSRLTVDKSRWQEG 438  
QY 303 NVFSCSVWHEALHNHYTQKSLSLGLK 329  
DB 439 NVFSCSVWHEALHNHYTQKSLSLGLK 465

RESULT 15  
US-10-211-357-8  
Sequence 8, Application US/10211357  
Publication No. US2003007275A1  
GENERAL INFORMATION:  
APPLICANT: Hanna, Nabil  
Newman, Roland A.  
Reff, Mitchell E.  
TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human  
Therapy  
NUMBER OF SEQUENCES: 59  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
STREET: 699 Prince Street

CITY: Alexandria  
STATE: VA  
COUNTRY: USA  
ZIP: 22314-3187  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/211,357  
FILING DATE: 05-Aug-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/612,914A  
FILING DATE: 10-Jul-2000  
APPLICATION NUMBER: US 08/523,894  
FILING DATE: 08-SEP-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Teskin, Robin L.  
REGISTRATION NUMBER: 35,030  
REFERENCE/DOCKET NUMBER: 012712-165  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-836-6620  
TELEFAX: 703-836-2021  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 467 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 8:  
US-10-211-357-8

Query Match 99.4%; Score 1743; DB 15; Length 467;  
Best Local Similarity 100.0%; Pred. No. 2.3e-139;  
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3 ASTKGSVPFLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 62  
DB 141 ASTKGSVPFLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 200  
QY 63 GLYSLSSVTVTPSSSLGKTYYTCNVDPKPSNTKVDKRVESKYGPPCPSPCPAEPFLGGPSV 122  
DB 201 GLYSLSSVTVTPSSSLGKTYYTCNVDPKPSNTKVDKRVESKYGPPCPSPCPAEPFLGGPSV 260  
QY 123 FLPPPKPDTLMISRPEVTCVVDVSQEDPEVFQFNWYDGVGVHNAKTKPRREEQFNSTY 182  
DB 261 FLPPPKPDTLMISRPEVTCVVDVSQEDPEVFQFNWYDGVGVHNAKTKPRREEQFNSTY 320  
QY 183 RVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAKGQPREPQVYTLPPSQEEMTK 242  
DB 321 RVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAKGQPREPQVYTLPPSQEEMTK 380  
QY 243 NQVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSRLTVDKSRWQEG 302  
DB 381 NQVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSRLTVDKSRWQEG 440  
QY 303 NVFSCSVWHEALHNHYTQKSLSLGLK 329  
DB 441 NVFSCSVWHEALHNHYTQKSLSLGLK 467

Search completed: January 13, 2004, 13:13:47  
Job time : 53.5825 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 13, 2004, 12:33:50 ; Search time 28.4463 Seconds  
(without alignments)  
489.353 Million cell updates/sec

Title: US-09-990-586-100  
Perfect score: 1754  
Sequence: 1 EFASKGSPVFLAPCSRST.....MHEALHNYTKSLSLGK 329

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.\*

- 1: /cgn2\_6/ptodata/1/1aa/5A.COMB.pdp.\*
- 2: /cgn2\_6/ptodata/1/1aa/5B.COMB.pdp.\*
- 3: /cgn2\_6/ptodata/1/1aa/6A.COMB.pdp.\*
- 4: /cgn2\_6/ptodata/1/1aa/6B.COMB.pdp.\*
- 5: /cgn2\_6/ptodata/1/1aa/PTUS.COMB.pdp.\*
- 6: /cgn2\_6/ptodata/1/1aa/Backfiles.pdp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1743	99.4	327	2	US-08-761-277A-47
2	1743	99.4	329	4	US-09-313-942-12
3	1743	99.4	443	5	PCT-US96-13152-4
4	1743	99.4	467	1	US-08-704-744-81
5	1743	99.4	467	3	US-08-523-894-8
6	1736	99.0	467	3	US-08-523-894-10
7	1731	98.7	467	3	US-08-523-894-12
8	1726.5	98.4	467	2	US-07-916-098A-45
9	1611.5	91.9	530	3	US-08-477-460B-4
10	1611.5	91.9	530	3	US-08-379-516-4
11	1611.5	91.9	530	3	US-09-329-916-4
12	1611.5	91.9	530	3	US-08-485-372A-4
13	1611.5	91.9	530	4	US-09-409-006A-4
14	1611.5	91.9	530	4	US-08-484-681-4
15	1611.5	91.9	530	5	PCT-US93-07422-4
16	1604.5	91.5	468	4	US-09-485-737B-67
17	1604.5	91.5	711	4	US-09-485-737B-90
18	1599.5	91.2	473	3	US-09-049-672A-4
19	1596.5	91.0	330	4	US-09-301-593-22
20	1596.5	91.0	451	2	US-08-887-352B-14
21	1596.5	91.0	451	2	US-08-887-352B-16
22	1596.5	91.0	451	2	US-08-887-352B-18
23	1596.5	91.0	451	3	US-08-466-151-65
24	1596.5	91.0	451	3	US-09-109-207C-14
25	1596.5	91.0	451	3	US-09-109-207C-16
26	1596.5	91.0	451	3	US-09-109-207C-18
27	1596.5	91.0	451	3	US-09-282-505-2

28	1596.5	91.0	451	3	US-09-054-255-2	Sequence 2, Appli
29	1596.5	91.0	451	3	US-09-296-005-14	Sequence 14, Appli
30	1596.5	91.0	451	3	US-09-296-005-16	Sequence 16, Appli
31	1596.5	91.0	451	3	US-09-296-005-18	Sequence 18, Appli
32	1596.5	91.0	451	4	US-09-282-846-2	Sequence 2, Appli
33	1596.5	91.0	451	4	US-09-680-145-2	Sequence 2, Appli
34	1596.5	91.0	452	3	US-09-027-449-71	Sequence 71, Appli
35	1596.5	91.0	452	3	US-09-026-985-71	Sequence 71, Appli
36	1596.5	91.0	452	4	US-09-121-952A-71	Sequence 71, Appli
37	1596.5	91.0	452	4	US-09-234-340A-71	Sequence 71, Appli
38	1596.5	91.0	453	4	US-09-301-593-18	Sequence 18, Appli
39	1596.5	91.0	454	2	US-07-934-373C-22	Sequence 22, Appli
40	1596.5	91.0	454	3	US-08-437-642B-22	Sequence 22, Appli
41	1596.5	91.0	454	4	US-08-146-205C-22	Sequence 22, Appli
42	1596.5	91.0	454	5	PCT-US93-07832-22	Sequence 22, Appli
43	1596.5	91.0	467	3	US-09-049-672A-8	Sequence 8, Appli
44	1594.5	90.9	450	2	US-08-788-800-12	Sequence 12, Appli
45	1594.5	90.9	469	2	US-07-934-373C-23	Sequence 23, Appli

ALIGNMENTS

RESULT 1  
US-08-761-277A-47  
; Sequence 47, Application US/08761277A  
; Patent No. 5972334  
; GENERAL INFORMATION:  
; APPLICANT: Denney Jr., Dan W.  
; TITLE OF INVENTION: Vaccines For Treatment Of Lymphoma And  
; TITLE OF INVENTION: Leukemia  
; NUMBER OF SEQUENCES: 80  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Medlen & Carroll, LLP  
; STREET: 220 Montgomery Street, Suite 2200  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: United States Of America  
; ZIP: 94104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION NUMBER: US/08/761,277A  
; FILING DATE: 06-DEC-1996  
; CLASSIFICATION: 424  
; PRIOR APPLICATION NUMBER: US 08/644,664  
; FILING DATE: 01-MAY-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MacKnight, Kamrin T.  
; REGISTRATION NUMBER: 38,230  
; REFERENCE/DOCKET NUMBER: GENITOPE-02406  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 705-8410  
; TELEFAX: (415) 397-8338  
; INFORMATION FOR SEQ ID NO: 47:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 327 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-761-277A-47

Query Match 99.4%; Score 1743; DB 2; Length 327;  
Best Local Similarity 100.0%; Pred. No. 7.8e-158;  
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 3 ASTKGSVPFLAPCSRSTSTAAALCCLVKDYFPEPTVSWNSGALTSVHTFPVQLQSS 62  
Db 1 ASTKGSVPFLAPCSRSTSTAAALCCLVKDYFPEPTVSWNSGALTSVHTFPVQLQSS 60

QY 63 GLYSLSSVTVFPSSSLGKTKTYTCNVDHKPSNTKVDKRVESKYGPPCPSCPAPEFLGGPSV 122  
Db 61 GLYSLSSVTVFPSSSLGKTKTYTCNVDHKPSNTKVDKRVESKYGPPCPSCPAPEFLGGPSV 120  
QY 123 FLFPKPDKTLMISRTPEVTCVVDVDSQEDPEVQFNWYDGVVHNATKPREQFNSTY 182  
Db 121 FLFPKPDKTLMISRTPEVTCVVDVDSQEDPEVQFNWYDGVVHNATKPREQFNSTY 180  
QY 183 RVVSVLTVLHQDLWNGKEYCKVSNKGLPSSIEKTSKAKGQPREPQVYTLPPSQEEMTK 242  
Db 181 RVVSVLTVLHQDLWNGKEYCKVSNKGLPSSIEKTSKAKGQPREPQVYTLPPSQEEMTK 240  
QY 243 NOVSLTCLVKGFYPSDIAVWESNGOPENNYKTTTPVLDSDGSPFLYSRLTVDKSRWQEG 302  
Db 241 NOVSLTCLVKGFYPSDIAVWESNGOPENNYKTTTPVLDSDGSPFLYSRLTVDKSRWQEG 300  
QY 303 NVFSCSVMEALHNHYTQKLSLSLGGK 329  
Db 301 NVFSCSVMEALHNHYTQKLSLSLGGK 327

## RESULT 2

US-09-313-942-12  
; Sequence 12, Application US/09313942  
; Patent No. 6472179  
; GENERAL INFORMATION:  
; APPLICANT: REGENERON PHARMACEUTICALS, INC.  
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING  
; FILE REFERENCE: REG 203-A  
; CURRENT FILING DATE: 1999-05-19  
; PRIOR FILING DATE: 1999-05-19  
; PRIOR FILING DATE: 1999-05-19  
; PRIOR FILING DATE: 1999-05-19  
; PRIOR FILING DATE: 1999-05-19  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: FASTSEQ for Windows Version 3.0  
; SEQ ID NO 12  
; LENGTH: 329  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-313-942-12

Query Match 99.4%; Score 1743; DB 4; Length 329;  
Best Local Similarity 100.0%; Pred. No. 7.8e-158;  
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ASTKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 62  
Db 3 ASTKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 62  
QY 63 GLYSLSSVTVFPSSSLGKTKTYTCNVDHKPSNTKVDKRVESKYGPPCPSCPAPEFLGGPSV 122  
Db 63 GLYSLSSVTVFPSSSLGKTKTYTCNVDHKPSNTKVDKRVESKYGPPCPSCPAPEFLGGPSV 122  
QY 123 FLFPKPDKTLMISRTPEVTCVVDVDSQEDPEVQFNWYDGVVHNATKPREQFNSTY 182  
Db 123 FLFPKPDKTLMISRTPEVTCVVDVDSQEDPEVQFNWYDGVVHNATKPREQFNSTY 182  
QY 183 RVVSVLTVLHQDLWNGKEYCKVSNKGLPSSIEKTSKAKGQPREPQVYTLPPSQEEMTK 242  
Db 183 RVVSVLTVLHQDLWNGKEYCKVSNKGLPSSIEKTSKAKGQPREPQVYTLPPSQEEMTK 242  
QY 243 NOVSLTCLVKGFYPSDIAVWESNGOPENNYKTTTPVLDSDGSPFLYSRLTVDKSRWQEG 302  
Db 243 NOVSLTCLVKGFYPSDIAVWESNGOPENNYKTTTPVLDSDGSPFLYSRLTVDKSRWQEG 302  
QY 303 NVFSCSVMEALHNHYTQKLSLSLGGK 329  
Db 303 NVFSCSVMEALHNHYTQKLSLSLGGK 329

RESULT 3  
PCT-US96-13152-4  
; Sequence 4, Application PC/TUS9613152  
; GENERAL INFORMATION:  
; APPLICANT: Martin, Ulrich, et al.  
; TITLE OF INVENTION: Anti-selectin antibodies for prevention of multiple organ fai  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Felle & Lynch  
; ADDRESSEE: Attn: Norman D. Hanson  
; STREET: 805 Third Avenue  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10022  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Computer Disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US96/13152  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION NUMBER: 08/578,953  
; FILING DATE: 27-Dec-95  
; APPLICATION NUMBER: EP 95 112 895.8  
; FILING DATE: 17-Aug-95  
; APPLICATION NUMBER: EP 95 114 969.9  
; FILING DATE: 19-Sep-95  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Norman D. Hanson  
; REGISTRATION NUMBER: 30,946  
; REFERENCE/DOCKET NUMBER: BOER 1059-PCT-PFF/NDH  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 688-9200  
; TELEFAX: (212) 838-3884  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 443  
; TYPE: amino acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
PCT-US96-13152-4

Query Match 99.4%; Score 1743; DB 5; Length 443;

Best Local Similarity 100.0%; Pred. No. 1.2e-157;  
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ASTKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 62  
Db 117 ASTKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 176  
QY 63 GLYSLSSVTVFPSSSLGKTKTYTCNVDHKPSNTKVDKRVESKYGPPCPSCPAPEFLGGPSV 122  
Db 177 GLYSLSSVTVFPSSSLGKTKTYTCNVDHKPSNTKVDKRVESKYGPPCPSCPAPEFLGGPSV 236  
QY 123 FLFPKPDKTLMISRTPEVTCVVDVDSQEDPEVQFNWYDGVVHNATKPREQFNSTY 182  
Db 237 FLFPKPDKTLMISRTPEVTCVVDVDSQEDPEVQFNWYDGVVHNATKPREQFNSTY 296  
QY 183 RVVSVLTVLHQDLWNGKEYCKVSNKGLPSSIEKTSKAKGQPREPQVYTLPPSQEEMTK 242  
Db 297 RVVSVLTVLHQDLWNGKEYCKVSNKGLPSSIEKTSKAKGQPREPQVYTLPPSQEEMTK 356  
QY 243 NOVSLTCLVKGFYPSDIAVWESNGOPENNYKTTTPVLDSDGSPFLYSRLTVDKSRWQEG 302  
Db 357 NOVSLTCLVKGFYPSDIAVWESNGOPENNYKTTTPVLDSDGSPFLYSRLTVDKSRWQEG 416  
QY 303 NVFSCSVMEALHNHYTQKLSLSLGGK 329



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Db 417 NVFSCVMHEALHNHYTKSLSLGK 443
|||||
RESULT 4
US-08-704-744-81
; Sequence 81, Application US/08704744
; Patent No. 5705154
; GENERAL INFORMATION:
; APPLICANT: Dalie, Barbara
; APPLICANT: Miller, Kenneth
; APPLICANT: Murgolo, Nicholas
; APPLICANT: Tindall, Stephen
; TITLE OF INVENTION: Humanized Monoclonal Antibodies Against Human Interleukin-4
; NUMBER OF SEQUENCES: 90
; CORRESPONDENCE ADDRESS:
; ADDRESS: Schering-plough Corporation
; STREET: 2000 Galloping Hill Road
; CITY: Kenilworth
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07033-0530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: Macintosh 7.5.3
; SOFTWARE: Microsoft Word 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/704,744
; FILING DATE: 06-SEP-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/208886
; FILING DATE: 10-MAR-1994
; APPLICATION NUMBER: PCT/US/95/02400
; FILING DATE: 08-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Foulke, Cynthia L.
; REGISTRATION NUMBER: 32,364
; REFERENCE/DOCKET NUMBER: JB0429K
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 298-2987
; TELEFAX: (908) 298-5388
; TELEX:
; INFORMATION FOR SEQ ID NO: 81:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 467 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-704-744-81
Query Match 99.4%; Score 1743; DB 1; Length 467;
Best Local Similarity 100.0%; Pred. No. 1.3e-157;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 ASTKGSVPFLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 62
Db 141 ASTKGSVPFLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 200
Qy 63 GLYSLSSVTVPSSSLGTTKTYTCNVDPKPSNTKVDKRVESKYGPPCPSPCPAPELLGPPSV 122
Db 201 GLYSLSSVTVPSSSLGTTKTYTCNVDPKPSNTKVDKRVESKYGPPCPSPCPAPELLGPPSV 260
Qy 123 FLPPPKPDTLMISRTPEVTCVVVDVSDPEVQFNWYVDGVEVHNAKTKPREEQFNSTY 182
Db 261 FLPPPKPDTLMISRTPEVTCVVVDVSDPEVQFNWYVDGVEVHNAKTKPREEQFNSTY 320
Qy 183 RVSVSLTVLHODWLNGKEYCKVSNKGLPSSIEKTTISKAKGQPRPQVYVTLPPSQEEMTK 242
Db 321 RVSVSLTVLHODWLNGKEYCKVSNKGLPSSIEKTTISKAKGQPRPQVYVTLPPSQEEMTK 380
Qy 243 NVSVLTCLVKGFVPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSLRTVDKSRWQEG 302
Db 417 NVFSCVMHEALHNHYTKSLSLGK 443
|||||
RESULT 5
US-08-523-894-8
; Sequence 8, Application US/08523894
; Patent No. 6136310
; GENERAL INFORMATION:
; APPLICANT: Hanna, Nabil
; APPLICANT: Newman, Roland A.
; APPLICANT: Reiff, Mitchell E.
; TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
; TITLE OF INVENTION: Therapy
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314-3187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/523,894
; FILING DATE: 06-SEP-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-165
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 467 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-523-894-8
Query Match 99.4%; Score 1743; DB 3; Length 467;
Best Local Similarity 100.0%; Pred. No. 1.3e-157;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 ASTKGSVPFLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 62
Db 141 ASTKGSVPFLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 200
Qy 63 GLYSLSSVTVPSSSLGTTKTYTCNVDPKPSNTKVDKRVESKYGPPCPSPCPAPELLGPPSV 122
Db 201 GLYSLSSVTVPSSSLGTTKTYTCNVDPKPSNTKVDKRVESKYGPPCPSPCPAPELLGPPSV 260
Qy 123 FLPPPKPDTLMISRTPEVTCVVVDVSDPEVQFNWYVDGVEVHNAKTKPREEQFNSTY 182
Db 261 FLPPPKPDTLMISRTPEVTCVVVDVSDPEVQFNWYVDGVEVHNAKTKPREEQFNSTY 320
Qy 183 RVSVSLTVLHODWLNGKEYCKVSNKGLPSSIEKTTISKAKGQPRPQVYVTLPPSQEEMTK 242
Db 321 RVSVSLTVLHODWLNGKEYCKVSNKGLPSSIEKTTISKAKGQPRPQVYVTLPPSQEEMTK 380
Qy 243 NVSVLTCLVKGFVPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSLRTVDKSRWQEG 302
Db 381 NVSVLTCLVKGFVPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSLRTVDKSRWQEG 440
```

Db 441 NVFSCVMHEALHNYTKSLSLGK 467

RESULT 7

US-08-523-894-12

Sequence 12, Application US/08523894

Patent No. 6136310

GENERAL INFORMATION:

APPLICANT: Hanna, Nabil

APPLICANT: Newman, Roland A.

APPLICANT: Reff, Mitchell E.

TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human

TITLE OF INVENTION: Therapy

NUMBER OF SEQUENCES: 59

CORRESPONDENCE ADDRESS:

ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS

STREET: 699 Prince Street

CITY: Alexandria

STATE: VA

COUNTRY: USA

ZIP: 22314-3187

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/523,894

FILING DATE: 06-SEP-1995

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Teskin, Robin L.

REGISTRATION NUMBER: 35,030

REFERENCE/DOCKET NUMBER: 012712-165

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-836-6620

TELEFAX: 703-836-2021

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 467 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-523-894-12

Query Match 98.7%; Score 1731; DB 3; Length 467;

Best Local Similarity 99.4%; Pred. No. 1.8e-156;

Matches 325; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 ASTKGSPVPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 62

Db 141 ASTKGSPVPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 200

QY 63 GLYSLSVVTVFSSSLGKTYTCNVDRKPSNTKVDKRVESKYGPPCPSPCPAPEFLGGPSV 122

Db 201 GLYSLSVVTVFSSSLGKTYTCNVDRKPSNTKVDKRVESKYGPPCPSPCPAPEFLGGPSV 260

QY 123 FLFPPKPKDTLMISRTPEVTCVVVDVSDQEDPEVFQFNWYVDGVEVHNAKTKPREEQFNSTY 182

Db 261 FLFPPKPKDTLMISRTPEVTCVVVDVSDQEDPEVFQFNWYVDGVEVHNAKTKPREEQFNSTY 320

QY 183 RVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAQGPSPQVYTLPPSQEEMTK 242

Db 321 RVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAQGPSPQVYTLPPSQEEMTK 380

QY 243 NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSRLTVDKSRWQEG 302

Db 381 NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSRLTVDKSRWQEG 440

QY 303 NVFSCVMHEALHNYTKSLSLGK 329

Db 441 NVFSCVMHEALHNYTKSLSLGK 467

QY 303 NVFSCVMHEALHNYTKSLSLGK 329

Db 441 NVFSCVMHEALHNYTKSLSLGK 467

RESULT 6

US-08-523-894-10

Sequence 10, Application US/08523894

Patent No. 6136310

GENERAL INFORMATION:

APPLICANT: Hanna, Nabil

APPLICANT: Newman, Roland A.

APPLICANT: Reff, Mitchell E.

TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human

TITLE OF INVENTION: Therapy

NUMBER OF SEQUENCES: 59

CORRESPONDENCE ADDRESS:

ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS

STREET: 699 Prince Street

CITY: Alexandria

STATE: VA

COUNTRY: USA

ZIP: 22314-3187

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/523,894

FILING DATE: 06-SEP-1995

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Teskin, Robin L.

REGISTRATION NUMBER: 35,030

REFERENCE/DOCKET NUMBER: 012712-165

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-836-6620

TELEFAX: 703-836-2021

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 467 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-523-894-10

Query Match 99.0%; Score 1736; DB 3; Length 467;

Best Local Similarity 99.7%; Pred. No. 6.2e-157;

Matches 326; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 ASTKGSPVPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 62

Db 141 ASTKGSPVPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 200

QY 63 GLYSLSVVTVFSSSLGKTYTCNVDRKPSNTKVDKRVESKYGPPCPSPCPAPEFLGGPSV 122

Db 201 GLYSLSVVTVFSSSLGKTYTCNVDRKPSNTKVDKRVESKYGPPCPSPCPAPEFLGGPSV 260

QY 123 FLFPPKPKDTLMISRTPEVTCVVVDVSDQEDPEVFQFNWYVDGVEVHNAKTKPREEQFNSTY 182

Db 261 FLFPPKPKDTLMISRTPEVTCVVVDVSDQEDPEVFQFNWYVDGVEVHNAKTKPREEQFNSTY 320

QY 183 RVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAQGPSPQVYTLPPSQEEMTK 242

Db 321 RVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAQGPSPQVYTLPPSQEEMTK 380

QY 243 NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSRLTVDKSRWQEG 302

Db 381 NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSRLTVDKSRWQEG 440

QY 303 NVFSCVMHEALHNYTKSLSLGK 329

## RESULT 8

US-07-916-098A-45  
 ; Sequence 45, Application US/07916098A  
 ; Patent No. 5871732  
 ; GENERAL INFORMATION:  
 ; APPLICANT: BURKLY, LINDA C.  
 ; APPLICANT: CHISHOLM, PATRICIA L.  
 ; APPLICANT: THOMAS, DAVID W.  
 ; APPLICANT: ROSA, MARGARET D.  
 ; APPLICANT: ROSA, JOSEPH J.  
 ; TITLE OF INVENTION: ANTI-CD4 ANTIBODY HOMOLOGS USEFUL IN  
 ; TITLE OF INVENTION: PROPHYLAXIS AND TREATMENT OF AIDS, ARC AND HIV INFECTION  
 ; NUMBER OF SEQUENCES: 61  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: ALLEGRETTI & WITCOFF, LTD.  
 ; STREET: 10 SOUTH WACKER DRIVE  
 ; CITY: CHICAGO  
 ; STATE: ILLINOIS  
 ; COUNTRY: U.S.A.  
 ; ZIP: 60606  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: WORD PERFECT 5.1  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/07/916,098A  
 ; FILING DATE: July 24, 1992  
 ; CLASSIFICATION: 424  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: PCT/US91/08843  
 ; FILING DATE: No. 5871732ember 27, 1991  
 ; CLASSIFICATION: 424  
 ; APPLICATION NUMBER: 07/618,542  
 ; FILING DATE: No. 5871732ember 27, 1990  
 ; CLASSIFICATION: 424  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: JOHN J. MC DONNELL  
 ; REGISTRATION NUMBER: 26,949  
 ; REFERENCE/DOCKET NUMBER: 92.310-G  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (312) 715-1000  
 ; TELEFAX: (312) 715-1234  
 ; TELEX: 910/221-5317  
 ; INFORMATION FOR SEQ ID NO: 45:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 467 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-07-916-098A-45

Query Match 98.4%; Score 1726.5; DB 2; Length 467;  
 Best Local Similarity 99.7%; Pred. No. 58-156; 0; Mismatches 0; Indels 1; Gaps 1;  
 Matches 326; Conservative 0;  
 QY 3 ASTKGPSVFLPACSRSTSESTAALGCLVKDYFPEPTVMSNSGALTSGVHTFPAVLQSS 62  
 DB 142 ASTKGPSVFLPACSRSTSESTAALGCLVKDYFPEPTVMSNSGALTSGVHTFPAVLQSS 201  
 QY 63 GLYSLSVVTVPSSSLGTYTCNVVDHSPNTKVDKRVESKYGPCCPCPAPEFLGGPSV 122  
 DB 202 GLYSLSVVTVPSSSLGTYTCNVVDHSPNTKVDKRVESKYGPCCPCPAPEFLGGPSV 261  
 QY 123 FLPPPPKDTLMISRPETVTCVVDVSDPEVQFNWYVDGVEVHNATKKREEOFNSTY 182  
 DB 262 FLPPPPKDTLMISRPETVTCVVDVSDPEVQFNWYVDGVEVHNATKKREEOFNSTY 321  
 QY 183 RVVSVLTVLHQDLNKGKCKVSNKGLPSSIEKTSIKAKGPRFPQVYTLPPSQEEMTK 242  
 DB 322 RVVSVLTVLHQDLNKGKCKVSNKGLPSSIEKTSIKAK-QPRFPQVYTLPPSQEEMTK 380

QY 243 NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPFVLDSDGSGFFLYSLTVDKSRWQEG 302  
 DB 381 NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPFVLDSDGSGFFLYSLTVDKSRWQEG 440  
 QY 303 NVFSCSVMEALHNHYTQKSLSLGLK 329  
 DB 441 NVFSCSVMEALHNHYTQKSLSLGLK 467  
 RESULT 9  
 US-08-477-460B-4  
 ; Sequence 4, Application US/08477460B  
 ; Patent No. 6034223  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Progenics Pharmaceuticals, Inc.  
 ; TITLE OF INVENTION: NON-PEPTIDYL MOIETY-CONJUGATED  
 ; TITLE OF INVENTION: CD4-GAMMA2 AND CD4-1gG2 IMMUNOCONJUGATES, AND USES THEREOF  
 ; NUMBER OF SEQUENCES: 9  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Cooper & Dunham  
 ; STREET: 30 Rockefeller Plaza  
 ; CITY: New York  
 ; STATE: New York  
 ; COUNTRY: USA  
 ; ZIP: 10112  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.24  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/477,460B  
 ; FILING DATE: 07-JUN-1995  
 ; CLASSIFICATION: 530  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/927,931  
 ; FILING DATE: 07-AUG-1992  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: White, John P.  
 ; REGISTRATION NUMBER: 28,678  
 ; REFERENCE/DOCKET NUMBER: 41215-A-PCT/JFW/AJM  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (212) 977-9550  
 ; TELEFAX: (212) 977-9809  
 ; TELEX: 422523 COOP UI  
 ; INFORMATION FOR SEQ ID NO: 4:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 530 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: unknown  
 ; TOPOLOGY: unknown  
 ; MOLECULE TYPE: cDNA  
 ; ORIGINAL SOURCE:  
 ; ORGANISM: homo sapien  
 ; CELL TYPE: lymphocyte  
 ; US-08-477-460B-4

Query Match 91.9%; Score 1611.5; DB 3; Length 530;  
 Best Local Similarity 92.4%; Pred. No. 5-4e-145;  
 Matches 303; Conservative 10; Mismatches 14; Indels 1; Gaps 1;  
 QY 2 FASTKGPSVFLPACSRSTSESTAALGCLVKDYFPEPTVMSNSGALTSGVHTFPAVLQSS 61  
 DB 204 FASTKGPSVFLPACSRSTSESTAALGCLVKDYFPEPTVMSNSGALTSGVHTFPAVLQSS 263  
 QY 62 SGYLSVVTVPSSSLGTYTCNVVDHSPNTKVDKRVESKYGPCCPCPAPEFLGGPS 121  
 DB 264 SGYLSVVTVPSSSLGTYTCNVVDHSPNTKVDKRVESKYGPCCPCPAPEFLGGPS 322  
 QY 122 VFLPPPKDTLMISRPETVTCVVDVSDPEVQFNWYVDGVEVHNATKKREEOFNST 181  
 DB 323 VFLPPPKDTLMISRPETVTCVVDVSDPEVQFNWYVDGVEVHNATKKREEOFNST 382

QY 182 YRVSVLTVLHODWLNKGYKCKVSNKGLPSSIEKTSKAGOPRPPQVYTLPPSOEEMT 241  
DB 383 FRVSVLTVVHODWLNKGYKCKVSNKGLPAPIEKTSKAGOPRPPQVYTLPPSOEEMT 442  
QY 242 KQVSLTCLVKGFYPSDIAVWESNGQPENNYKTPPVLDSDGSGFFLYSLRTVDKSRWQE 301  
DB 443 KQVSLTCLVKGFYPSDIAVWESNGQPENNYKTPPVLDSDGSGFFLYSLRTVDKSRWQE 502  
QY 302 GNVFSCSVNHEALHNHYTQKSLSLGK 329  
DB 503 GNVFSCSVNHEALHNHYTQKSLSLSPGK 530  
RESULT 10  
US-08-379-516-4  
; Sequence 4, Application US/08379516  
; Patent No. 6083478  
; GENERAL INFORMATION:  
; APPLICANT: Allaway, Graham P.  
; APPLICANT: Maddon, Paul J.  
; TITLE OF INVENTION: No. 6083478-Peptidyl Moiety-Conjugated CD4-Gamma2 and CD4-IgG2  
; TITLE OF INVENTION: Immunoconjugates and Uses Thereof  
; FILE REFERENCE: 41215-A-PCT-US  
; CURRENT APPLICATION NUMBER: US/08/379,516  
; CURRENT FILING DATE: 1996-06-10  
; EARLIER APPLICATION NUMBER: PCT/US93/07422  
; EARLIER FILING DATE: 1993-08-06  
; EARLIER APPLICATION NUMBER: 07/927,931  
; EARLIER FILING DATE: 1992-08-07  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: Patent in Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 530  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-08-379-516-4  
Query Match 91.9%; Score 1611.5; DB 3; Length 530;  
Best Local Similarity 92.4%; Pred. No. 5.4e-145;  
Matches 303; Conservative 10; Mismatches 14; Indels 1; Gaps 1;  
QY 2 FASTKGPSVFFPLAPCSRSTSESTAALGCLVKDYFPEPTVSNWNSGALTSGVHTFPAVLQ 61  
DB 204 FASTKGPSVFFPLAPCSRSTSESTAALGCLVKDYFPEPTVSNWNSGALTSGVHTFPAVLQ 263  
QY 62 SGLYSLSSVTVTPSSSLGTTKTYTCNVDHKPSNTKVDKVESKYGPPCPCPAPPEFLGSPS 121  
DB 264 SGLYSLSSVTVTPSSNFGTQTYTCNVDHKPSNTKVDKVERKCCVECPAPP-VAGPS 322  
QY 122 VLFPPPKDPTLMISRTPEVTCVVDVSDQEDPEVQFNWYDGVVHNAKTKPREEQNST 181  
DB 323 VLFPPPKDPTLMISRTPEVTCVVDVSDQEDPEVQFNWYDGVVHNAKTKPREEQNST 382  
QY 182 YRVSVLTVLHODWLNKGYKCKVSNKGLPSSIEKTSKAGOPRPPQVYTLPPSOEEMT 241  
DB 383 FRVSVLTVVHODWLNKGYKCKVSNKGLPAPIEKTSKAGOPRPPQVYTLPPSOEEMT 442  
QY 242 KQVSLTCLVKGFYPSDIAVWESNGQPENNYKTPPVLDSDGSGFFLYSLRTVDKSRWQE 301  
DB 443 KQVSLTCLVKGFYPSDIAVWESNGQPENNYKTPPVLDSDGSGFFLYSLRTVDKSRWQE 502  
QY 302 GNVFSCSVNHEALHNHYTQKSLSLGK 329  
DB 503 GNVFSCSVNHEALHNHYTQKSLSLSPGK 530  
RESULT 11  
US-09-329-916-4  
; Sequence 4, Application US/09329916  
; Patent No. 6177549  
; GENERAL INFORMATION:  
; APPLICANT: Progenics Pharmaceuticals, Inc.

; TITLE OF INVENTION: NON-PEPTIDYL MOIETY-CONJUGATED  
; TITLE OF INVENTION: CD4-GAMMA2 AND CD4-IGG2 IMMUNOCONJUGATES, AND USES THEREOF  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper & Dunham  
; STREET: 30 Rockefeller Plaza  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10112  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.24  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/329,916  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/477,460  
; FILING DATE: 07-JUN-1995  
; APPLICATION NUMBER: US 07/927,931  
; FILING DATE: 07-AUG-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P.  
; REGISTRATION NUMBER: 28,678  
; REFERENCE/DOCKET NUMBER: 41215-A-PCT/JPW/AJM  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 977-9550  
; TELEFAX: (212) 977-9809  
; TELEX: 422523 COOP UI  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 530 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: cDNA  
; ORIGINAL SOURCE:  
; ORGANISM: homo sapien  
; CELL TYPE: lymphocyte  
US-09-329-916-4  
Query Match 91.9%; Score 1611.5; DB 3; Length 530;  
Best Local Similarity 92.4%; Pred. No. 5.4e-145;  
Matches 303; Conservative 10; Mismatches 14; Indels 1; Gaps 1;  
QY 2 FASTKGPSVFFPLAPCSRSTSESTAALGCLVKDYFPEPTVSNWNSGALTSGVHTFPAVLQ 61  
DB 204 FASTKGPSVFFPLAPCSRSTSESTAALGCLVKDYFPEPTVSNWNSGALTSGVHTFPAVLQ 263  
QY 62 SGLYSLSSVTVTPSSSLGTTKTYTCNVDHKPSNTKVDKVESKYGPPCPCPAPPEFLGSPS 121  
DB 264 SGLYSLSSVTVTPSSNFGTQTYTCNVDHKPSNTKVDKVERKCCVECPAPP-VAGPS 322  
QY 122 VLFPPPKDPTLMISRTPEVTCVVDVSDQEDPEVQFNWYDGVVHNAKTKPREEQNST 181  
DB 323 VLFPPPKDPTLMISRTPEVTCVVDVSDQEDPEVQFNWYDGVVHNAKTKPREEQNST 382  
QY 182 YRVSVLTVLHODWLNKGYKCKVSNKGLPSSIEKTSKAGOPRPPQVYTLPPSOEEMT 241  
DB 383 FRVSVLTVVHODWLNKGYKCKVSNKGLPAPIEKTSKAGOPRPPQVYTLPPSOEEMT 442  
QY 242 KQVSLTCLVKGFYPSDIAVWESNGQPENNYKTPPVLDSDGSGFFLYSLRTVDKSRWQE 301  
DB 443 KQVSLTCLVKGFYPSDIAVWESNGQPENNYKTPPVLDSDGSGFFLYSLRTVDKSRWQE 502  
QY 302 GNVFSCSVNHEALHNHYTQKSLSLGK 329  
DB 503 GNVFSCSVNHEALHNHYTQKSLSLSPGK 530

## RESULT 12

US-08-485-372A-4  
; Sequence 4, Application US/08485372A  
; Patent No. 6187748  
; GENERAL INFORMATION:  
; APPLICANT: Beaudry, Gary A.  
; APPLICANT: Maddon, Paul G.  
; TITLE OF INVENTION: CD4-GAMMA2 CD4-IgG2 CHIMERAS  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper & Dunham LLP  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.24  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/485,372A  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/476,227  
; FILING DATE: 07-JUN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P.  
; REGISTRATION NUMBER: 28,678  
; REFERENCE/DOCKET NUMBER: 37690-II-A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 278-0400  
; TELEFAX: (212) 391-0525  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 530 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: cDNA  
; ORIGINAL SOURCE:  
; ORGANISM: homo sapien  
; CELL TYPE: lymphocyte  
US-08-485-372A-4

Query Match 91.9%; Score 1611.5; DB 3; Length 530;  
Best Local Similarity 92.4%; Pred. No. 5.4e-145;  
Matches 303; Conservative 10; Mismatches 14; Indels 1; Gaps 1;  
QY 2 FASTKGPSVFPPLAPCSRSTSESTAALGCLVKDYRPEPTVWSNLSGALTSGVHTTFAVLQS 61  
DB 204 FASTKGPSVFPPLAPCSRSTSESTAALGCLVKDYRPEPTVWSNLSGALTSGVHTTFAVLQS 263  
QY 62 SGLYSLSSVTVVPSNFGTQYTCNVDPKPSNTKVDKRVESKYGPPCPSCPAPEFLGQPS 121  
DB 264 SGLYSLSSVTVVPSNFGTQYTCNVDPKPSNTKVDKRVESKYGPPCPSCPAPEFLGQPS 322  
QY 122 VFLFPKPKDLMISRTPEVTCVVDVSDQEDPEVQFNWYDGVVHNATKPREQFNST 181  
DB 323 VFLFPKPKDLMISRTPEVTCVVDVSDQEDPEVQFNWYDGVVHNATKPREQFNST 382  
QY 182 YRVVSVLTVLHODWLNKGEYKCKVSNKGLPAPIETISIKAKGQPREPQVYTLPPSSEMT 241  
DB 383 FRVSVLTVWHDWLNKGEYKCKVSNKGLPAPIETISIKAKGQPREPQVYTLPPSSEMT 442  
QY 242 KQVSLTCLVKGFYPSDIAVEHESGQPENNYKTTTPVLDSDGSFPLYSLRTVDKSRWQE 301  
DB 443 KQVSLTCLVKGFYPSDIAVEHESGQPENNYKTTTPVLDSDGSFPLYSLRTVDKSRWQE 502  
QY 302 GNVFSCSVNHEALHNHYTQKSLSLIGK 329

## Db 503

GNVFSCSVNHEALHNHYTQKSLSLSPGK 530

## RESULT 13

US-09-409-006A-4  
; Sequence 4, Application US/09409006A  
; Patent No. 6342586  
; GENERAL INFORMATION:  
; APPLICANT: Progenics Pharmaceuticals, Inc.  
; TITLE OF INVENTION: NON-PEPTIDYL MOISTY-CONJUGATED  
; TITLE OF INVENTION: CD4-GAMMA2 AND CD4-IgG2 IMMUNOCONJUGATES, AND USES THEREOF  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper & Dunham  
; STREET: 30 Rockefeller Plaza  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10112  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.24  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/409,006A  
; FILING DATE: 23-SEP-1999  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/927,931  
; FILING DATE: 07-AUG-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P.  
; REGISTRATION NUMBER: 28,678  
; REFERENCE/DOCKET NUMBER: 41215-A-PCT/JPW/AJM  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 977-9550  
; TELEFAX: (212) 977-9809  
; TELEX: 422523 COOP UI  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 530 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: cDNA  
; ORIGINAL SOURCE:  
; ORGANISM: homo sapien  
; CELL TYPE: lymphocyte  
US-09-409-006A-4

Query Match 91.9%; Score 1611.5; DB 4; Length 530;  
Best Local Similarity 92.4%; Pred. No. 5.4e-145;  
Matches 303; Conservative 10; Mismatches 14; Indels 1; Gaps 1;  
QY 2 FASTKGPSVFPPLAPCSRSTSESTAALGCLVKDYRPEPTVWSNLSGALTSGVHTTFAVLQS 61  
DB 204 FASTKGPSVFPPLAPCSRSTSESTAALGCLVKDYRPEPTVWSNLSGALTSGVHTTFAVLQS 263  
QY 62 SGLYSLSSVTVVPSNFGTQYTCNVDPKPSNTKVDKRVESKYGPPCPSCPAPEFLGQPS 121  
DB 264 SGLYSLSSVTVVPSNFGTQYTCNVDPKPSNTKVDKRVESKYGPPCPSCPAPEFLGQPS 322  
QY 122 VFLFPKPKDLMISRTPEVTCVVDVSDQEDPEVQFNWYDGVVHNATKPREQFNST 181  
DB 323 VFLFPKPKDLMISRTPEVTCVVDVSDQEDPEVQFNWYDGVVHNATKPREQFNST 382  
QY 182 YRVVSVLTVLHODWLNKGEYKCKVSNKGLPAPIETISIKAKGQPREPQVYTLPPSSEMT 241  
DB 383 FRVSVLTVWHDWLNKGEYKCKVSNKGLPAPIETISIKAKGQPREPQVYTLPPSSEMT 442  
QY 242 KQVSLTCLVKGFYPSDIAVEHESGQPENNYKTTTPVLDSDGSFPLYSLRTVDKSRWQE 301

Db 443 KNOVSLTCLVKGFPDIAVWESNGQPENNYKTTTPMLDSGSGFFLYSKLTVDKSRWQ 502  
QY 302 GNVFSCSVWHEALHNHYTKSLSLKG 329  
Db 503 GNVFSCSVWHEALHNHYTKSLSLSPGK 530

## RESULT 14

US-08-484-681-4  
; Sequence 4, Application US/08484681  
; Patent No. 6451313  
; GENERAL INFORMATION:  
; APPLICANT: Beaudry, Gary A.  
; APPLICANT: Maddon, Paul J.  
; TITLE OF INVENTION: CD4-GAMMA2 CD4-IgG2 CHIMERAS  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper & Dunham LLP  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.24  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/484,681  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P.  
; REGISTRATION NUMBER: 28,678  
; REFERENCE/DOCKET NUMBER: 37690-II-B  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 278-0400  
; TELEFAX: (212) 391-0525  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 530 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: cDNA  
; ORGANISM: homo sapien  
; CELL TYPE: lymphocyte  
US-08-484-681-4

Query Match 91.9%; Score 1611.5; DB 4; Length 530;  
Best Local Similarity 92.4%; Pred. No. 5.4e-145; Indels 1; Gaps 1;  
Matches 303; Conservative 10; Mismatches 14; Indels 1; Gaps 1;  
QY 2 FASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSNWNSGALTSGVHTFPAVLQ 61  
Db 204 FASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSNWNSGALTSGVHTFPAVLQ 263  
QY 62 SGYLSLVVTVPSSSLGTTKTYTCNVDHKPSNTKVDKRVESKVGPPCPCPAPFLGGPS 121  
Db 264 SGYLSLVVTVPSNFGTQTYTCNVDHKPSNTKVDKRVESKVGPPCPCPAPFLGGPS 322  
QY 122 VFLFPPKPKDITLMISRTPEVTCVVDVSDQEDPEVQFNWYVDGVEVHNATKPREEQFNST 181  
Db 323 VFLFPPKPKDITLMISRTPEVTCVVDVSDQEDPEVQFNWYVDGVEVHNATKPREEQFNST 382  
QY 182 YRVVSVLTVLHQDWLNGKEYCKVSNKGLPAPIEKTIISKAKGQPREPQVYTLPPSQEEMT 241  
Db 383 YRVVSVLTVLHQDWLNGKEYCKVSNKGLPAPIEKTIISKAKGQPREPQVYTLPPSQEEMT 442

QY 242 KNOVSLTCLVKGFPDIAVWESNGQPENNYKTTTPMLDSGSGFFLYSKLTVDKSRWQ 301  
Db 443 KNOVSLTCLVKGFPDIAVWESNGQPENNYKTTTPMLDSGSGFFLYSKLTVDKSRWQ 502  
QY 302 GNVFSCSVWHEALHNHYTKSLSLKG 329  
Db 503 GNVFSCSVWHEALHNHYTKSLSLSPGK 530

## RESULT 15

PCT-US93-07422-4  
; Sequence 4, Application PC/TUS9307422  
; GENERAL INFORMATION:  
; APPLICANT: Progenics Pharmaceuticals, Inc.  
; TITLE OF INVENTION: NON-PEPTIDYL MOIETY-CONJUGATED  
; TITLE OF INVENTION: CD4-GAMMA2 AND CD4-IgG2 IMMUNOCONJUGATES, AND USES THEREOF  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper & Dunham  
; STREET: 30 Rockefeller Plaza  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10112  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.24  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US93/07422  
; FILING DATE: 19930806  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/927,931  
; FILING DATE: 07-AUG-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P.  
; REGISTRATION NUMBER: 28,678  
; REFERENCE/DOCKET NUMBER: 41215-A-PCT/JPW/AJM  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 977-9550  
; TELEFAX: (212) 977-9809  
; TELEX: 422523 COOP UI  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 530 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: cDNA  
; ORIGINAL SOURCE:  
; ORGANISM: homo sapien  
; CELL TYPE: lymphocyte  
PCT-US93-07422-4

Query Match 91.9%; Score 1611.5; DB 5; Length 530;  
Best Local Similarity 92.4%; Pred. No. 5.4e-145; Indels 1; Gaps 1;  
Matches 303; Conservative 10; Mismatches 14; Indels 1; Gaps 1;  
QY 2 FASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSNWNSGALTSGVHTFPAVLQ 61  
Db 204 FASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSNWNSGALTSGVHTFPAVLQ 263  
QY 62 SGYLSLVVTVPSSSLGTTKTYTCNVDHKPSNTKVDKRVESKVGPPCPCPAPFLGGPS 121  
Db 264 SGYLSLVVTVPSNFGTQTYTCNVDHKPSNTKVDKRVESKVGPPCPCPAPFLGGPS 322  
QY 122 VFLFPPKPKDITLMISRTPEVTCVVDVSDQEDPEVQFNWYVDGVEVHNATKPREEQFNST 181  
Db 323 VFLFPPKPKDITLMISRTPEVTCVVDVSDQEDPEVQFNWYVDGVEVHNATKPREEQFNST 382  
QY 182 YRVVSVLTVLHQDWLNGKEYCKVSNKGLPSSIEKTIISKAKGQPREPQVYTLPPSQEEMT 241







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Db      50 HISPYNQATTYNQFK 65

RESULT 3
S17604
IG heavy chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: S17604
R:Clackson, T.; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G.
Nature 352, 624-628, 1991
A:Title: Making antibody fragments using phage display libraries.
A:Reference number: S17230; MUID:91326098; PMID:1907718
A:Accession: S17604
A>Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-36 <CLA>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:8-31/Domain: immunoglobulin homology <IMM>

Query Match      60.0%; Score 57; DB 2; Length 98;
Best Local Similarity 62.5%; Pred. No. 0.043;
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY      2 IDPYNGITTYDQNLKG 17
       |:|||||:|:|:|
Db      44 INPYNGDTFYNQKPKG 59

RESULT 4
S26320
IG heavy chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
C:Accession: S26320
R:Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A:Title: Antibodies that are specific for a single amino acid interchange in a protein
A:Reference number: S26309; MUID:91341421; PMID:1908510
A:Accession: S26320
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-107 <STA>
A:Cross-references: EMBL:X59206
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:3-86/Domain: immunoglobulin homology <IMM>

Query Match      60.0%; Score 57; DB 2; Length 107;
Best Local Similarity 66.7%; Pred. No. 0.047;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      2 IDPYNGITTYDQNLK 16
       |:|||||:|:|:|
Db      39 INPYNGATSYNQNF 53

RESULT 5
S26319
IG heavy chain V region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 19-Mar-1998 #sequence_revision 19-Mar-1998 #text_change 21-Jan-2000
C:Accession: S26319
R:Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A:Title: Antibodies that are specific for a single amino acid interchange in a protein
A:Reference number: S26309; MUID:91341421; PMID:1908510
A:Accession: S26319
A:Molecule type: mRNA
A:Residues: 1-114 <STA>
A:Cross-references: EMBL:X59172
C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin
F:11-94/Domain: immunoglobulin homology <IMM>

Query Match      60.0%; Score 57; DB 2; Length 114;
Best Local Similarity 62.5%; Pred. No. 0.05;
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY      2 IDPYNGITTYDQNLKG 17
       |:|||||:|:|:|
Db      47 INPYNGDTFYNQKPKG 62

RESULT 6
PS0057
IG heavy chain precursor V region (PAR) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 20-Jun-2000
C:Accession: PS0057
R:Yasuda, Y.; Takahashi, M.; Azuma, C.; Kanai, Y.; Honjo, T.
J. Biochem. 104, 337-343, 1988
A:Title: Biased expression of variable region gene families of the immunoglobulin heavy
A:Reference number: PS0057; MUID:89197817; PMID:2467902
A:Accession: PS0057
A:Molecule type: DNA
A:Residues: 1-135 <YAO>
A:Cross-references: GB:D00307; NID:9220448; PIDN:BAA00213.1; PID:9220449
A:Note: The authors translated the codon AAG for residue 32 as Asn and GAC for 92 as Gl.
C:Comment: The gene encoding this protein was isolated from a hybridoma that produces a
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-135/Product: Ig heavy chain V region PAR #status predicted <MAT>
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match      60.0%; Score 57; DB 2; Length 135;
Best Local Similarity 62.5%; Pred. No. 0.061;
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY      2 IDPYNGITTYDQNLKG 17
       |:|||||:|:|:|
Db      70 INPYNGDTFYNQKPKG 85

RESULT 7
A27609
IG heavy chain precursor V region (I29) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 15-Dec-1988 #sequence_revision 30-Jun-1991 #text_change 23-Jul-1999
C:Accession: A27609
R:Klein, D.; Nietupski, J.; Sirlin, S.; Stavnezer, J.
J. Immunol. 140, 1676-1684, 1988
A:Title: I.29 lymphoma cells express a nonmutated V-H gene before and after H chain swi
A:Reference number: A27609; MUID:88154467; PMID:3126234
A:Accession: A27609
A:Molecule type: DNA
A:Residues: 1-139 <KLE>
A:Cross-references: EMBL:M19401; NID:9195441; PIDN:AAA38303.1; PID:9553992
C:Genetics:
A:Introns: 16/1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-139/Product: Ig heavy chain V region I29 #status predicted <VAR>
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match      60.0%; Score 57; DB 2; Length 139;
Best Local Similarity 58.8%; Pred. No. 0.063;
Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY      1 YIDPYNGITTYDQNLKG 17
       |:|||||:|:|:|
Db      69 YINPYNDYTSYNQKPKG 85
```



R:Berdoz, J.; Krachenbuhl, J.P.  
submitted to the EMBL Data Library, November 1994  
A:Description: Specific amplification by the polymerase chain reaction of rearranged genes  
A:Reference number: S52445  
A:Accession: S52445  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-137 <BER>  
A:Cross-references: EMBL:X82690; NID:g673439; PIDN:CAA58011.1; PID:g673440  
C:Genetics:  
A:Introns: 16/1  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:34-115/Domain: immunoglobulin homology <IMM>

QY 2 IDPYNGITIIYDQNLKG 17  
DB 43 IDPESGGTAYNQNFPG 58

Search completed: January 13, 2004, 12:44:44  
Job time : 2.23231 secs

Query Match 55.8%; Score 53; DB 2; Length 137;  
Best Local Similarity 52.9%; Pred. No. 0.28;  
Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 YIDPYNGITIIYDQNLKG 17  
DB 59 WIDPENGNTYIDPKFQG 85

RESULT 14  
A37263  
IG heavy chain V region (4A9) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C>Date: 30-Aug-1991 #sequence\_revision 03-Apr-1992 #text\_change 16-Aug-1996  
C:Accession: A37263  
R:Goshorn, S.C.; Retzel, E.; Jermerson, R.  
J. Biol. Chem. 266, 2134-2142, 1991  
A:Title: Common structural features among monoclonal antibodies binding the same antigen  
A:Reference number: A38601; MUID:91115823; PMID:1703527  
A:Accession: A37263  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-93 <GOS>  
A:Cross-references: GB:M57996  
A:Note: the authors translated the codon CAA for residue 38 as His, AGA for residue 39 as  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin

Query Match 54.7%; Score 52; DB 2; Length 93;  
Best Local Similarity 52.5%; Pred. No. 0.26;  
Matches 10; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2 IDPYNGITIIYDQNLKG 17  
DB 35 IDPQGGTAYNQNFPG 50

RESULT 15  
I37262  
IG heavy chain V region (1G1) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C>Date: 30-Aug-1991 #sequence\_revision 30-Aug-1991 #text\_change 23-Jul-1999  
C:Accession: I37262  
R:Goshorn, S.C.; Retzel, E.; Jermerson, R.  
J. Biol. Chem. 266, 2134-2142, 1991  
A:Title: Common structural features among monoclonal antibodies binding the same antigen  
A:Reference number: A38601; MUID:91115823; PMID:1703527  
A:Accession: I37262  
A:Status: preliminary; not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-101 <GOS>  
A:Cross-references: GB:M57995; NID:g195375; PIDN:AA63334.1; PID:g195376  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin

Query Match 54.7%; Score 52; DB 2; Length 101;  
Best Local Similarity 52.5%; Pred. No. 0.29;  
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

GenCore version 5.1.1.6  
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OM protein - protein search, using sw model

Run on: January 13, 2004, 12:19:34 ; Search time 0.742358 Seconds  
(without alignments)  
1076.912 Million cell updates/sec

Title: US-09-990-586-101  
Perfect score: 95  
Sequence: 1 YIDPYNIGITVDQLKG 17

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	50	52.6	120	1 HV03 MOUSE	P01747 mus musculus
2	49	51.6	117	1 HV14 MOUSE	P01758 mus musculus
3	47	49.5	1302	1 RPOB SPIC1	P47767 spiroplasma
4	46	48.4	136	1 HV15 MOUSE	P01759 mus musculus
5	45	47.4	113	1 FLIT BACSU	P39740 bacillus su
6	45	47.4	117	1 HV12 MOUSE	P01756 mus musculus
7	45	47.4	117	1 HV13 MOUSE	P01757 mus musculus
8	45	47.4	118	1 HV51 MOUSE	P06330 mus musculus
9	45	47.4	505	1 VLI1 HPV13	P27964 human papil
10	44	46.3	140	1 HV02 MOUSE	P01746 mus musculus
11	44	46.3	335	1 YO94 CAEEL	P41844 caenorhabdi
12	44	46.3	450	1 PMBA ECOLI	P24231 escherichia
13	44	46.3	499	1 VLI1 HPV13	Q02273 human papil
14	44	46.3	502	1 VLI1 PCPV1	Q02274 pygmy chimp
15	44	46.3	1286	1 RPOD GUITH	O78483 guillardi
16	43	45.3	137	1 RECR FUSN1	Q8r956 fusobacteri
17	43	45.3	423	1 EATS CAEEL	Q27295 caenorhabdi
18	43	45.3	611	1 GLMS BRUME	Q8yc47 b glucosani
19	43	45.3	733	1 PURL METJA	Q58660 methanococ
20	42	44.2	14	1 UN37 CLOPA	P81358 clostridium
21	42	44.2	121	1 HV01 MOUSE	P01745 mus musculus
22	42	44.2	501	1 VLI1 FAPVE	P11326 european el
23	42	44.2	504	1 ATIN HSVBP	P30020 bovine herp
24	42	44.2	518	1 ATPA MYCGE	P47641 mycoplasma
25	42	44.2	715	1 PURL METAC	Q8tit6 methanosarc
26	42	44.2	716	1 PURL METMA	Q8tyk1 methanosarc
27	42	44.2	724	1 PURL METKA	Q8ty09 methanopyru
28	41	43.2	286	1 SUOE CAVPO	P49887 cavia porce
29	41	43.2	300	1 PHAC_PSEAE	Q51553 pseudomonas
30	41	43.2	466	1 NMT SCHPO	Q43010 schizosacch
31	41	43.2	501	1 ATPA ACEWO	P50000 acetobacter
32	41	43.2	518	1 ATPA MYCPN	Q50329 mycoplasma
33	41	43.2	1976	1 MYHA_BOVIN	Q27991 bos taurus

## ALIGNMENTS

## RESULT 1

HV03 MOUSE STANDARD; PRT; 120 AA.  
 ID HV03 MOUSE  
 AC P01747; 1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Ig heavy chain V region 36-65.  
 OS Mus musculus (Mouse)  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=83131846; PubMed=6186498;  
 RA Siekevitz M., Geffer M.L., Brodeur P., Riblet R.,  
 RA Marshak-Rothstein A.;  
 RT "The genetic basis of antibody production: the dominant anti-arsonate  
 RT idiotypic response of the strain A mouse."  
 RL Eur. J. Immunol. 12:1023-1032(1982).  
 CC -!- MISCELLANEOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER  
 CC DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE AUTHORS  
 CC CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED TO THE SAME J  
 CC SEGMENT, JH2.  
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.  
 DR HSSP; P01789; IMCP.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 KW Immunoglobulin V region; Hybridoma.  
 FT DOMAIN 1  
 FT NON TER 120 120  
 FT IG-LIKE.  
 SQ SEQUENCE 120 AA; 13307 MW; FF04E4A167B654AF CRC64;

Query Match 52.6%; Score 50; DB 1; Length 120;

Best Local Similarity 52.9%; Pred. No. 0.36;

Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 YIDPYNIGITVDQLKG 17

DB 49 YINFGNGVTKYNEKFKG 65

## RESULT 2

HV14 MOUSE STANDARD; PRT; 117 AA.  
 ID HV14 MOUSE  
 AC P01758;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Ig heavy chain V region 108A precursor.  
 GN IGH-VJ558.  
 OS Mus musculus (Mouse).

```

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81245215; PubMed=6789211;
RA Givold D., Zakut R., Efron K., Rechavi G., Ram D., Cohen J.B.;
RT "Diversity of germ-line immunoglobulin VH genes.";
RL Nature 292:426-430(1981).
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC
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CC
CC EMBL; J00488; AAA38519.1; -
DR PIR; A02041; HVMS8A.
DR HSP; P01810; 2FBJ.
DR MGD; MGI:96486; Igh-VJ558.
DR InterPro; IPR007110; I9-like.
DR InterPro; IPR003006; I9_MHC.
DR Pfam; PF00047; I9; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; I9 LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 108A.
FT DOMAIN 20 >117 IG-LIKE.
FT NON_TER 117 117
FT SEQUENCE 117 AA; 12972 MW; 428CB44DF25D1BC2 CRC64;
SQ
Query Match 51.6%; Score 49; DB 1; Length 117;
Best Local Similarity 62.5%; Pred. No. 0.51;
Matches 10; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
QY 1 YIDPYNGITTYDQNLK 16
Db 69 YIYPYNGGTYNQKFK 84
RESULT 3
RPOB SPICI STANDARD; PRT; 1302 AA.
AC P47767;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE DNA-directed RNA polymerase beta chain (EC 2.7.7.6) (Transcriptase
DE beta chain) (RNA polymerase beta subunit).
GN RPOB.
OS Spiroplasma citri.
OC Bacteria; Firmicutes; Mollicutes; Entomoplasmatales;
OC Spiroplasmataceae; Spiroplasma.
OX NCBI_TaxID=2133;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=R8A2HP;
RX MEDLINE=96257200; PubMed=8675039;
RA Laigret P., Gaurivaud P., Bove J.;
RT "The unique organization of the rpoB region of Spiroplasma citri: a
RT restriction and modification system gene is adjacent to rpoB.";
RL Gene 171:95-98 (1996)
CC -1- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
CC OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
CC SUBSTRATES.
CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
CC {RNA}(N).
CC -1- SUBUNIT: THE ENZYME CONSISTS OF THE SIGMA CHAIN AND THE CORE

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CC ENZYME WHICH IS COMPOSED OF 2 ALPHA CHAINS, 1 BETA CHAIN, AND 1
CC BETA' CHAIN.
CC -1- SIMILARITY: Belongs to the RNA polymerase beta chain family.
CC
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CC
CC EMBL; U25815; AAC4217.1; -
DR PIR; T43230; T43230.
DR HSP; O9KWU7; 1HQM.
DR InterPro; IPR001572; RNA_pol_B.
DR Pfam; PF04563; RNA_pol_Rpb2_1; 1.
DR Pfam; PF04561; RNA_pol_Rpb2_2; 2.
DR Pfam; PF04565; RNA_pol_Rpb2_3; 1.
DR Pfam; PF00562; RNA_pol_Rpb2_6; 1.
DR Pfam; PF04560; RNA_pol_Rpb2_7; 1.
DR PROSITE; PS01166; RNA_POL_BETA; 1.
DR Transferrase; Transcription; DNA-directed RNA polymerase.
KW TRANSFERASE; 1302 AA; 146533 MW; 8D971C23EB9FEB2F CRC64;
SQ
Query Match 49.5%; Score 47; DB 1; Length 1302;
Best Local Similarity 50.0%; Pred. No. 15;
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
QY 2 IDPYNGITTYDQNL 15
Db 301 LDPTGTGDIYDQSI 314
RESULT 4
HV15 MOUSE STANDARD; PRT; 136 AA.
ID HV15 MOUSE
AC P01759;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region BCL1 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=82222262; PubMed=6806821;
RX Knapp M.R., Liu C.-P., Newell N., Ward R.B., Tucker P.W., Strober S.,
RX Blattner F.R.;
RT "Simultaneous expression of immunoglobulin mu and delta heavy chains
RT by a cloned B-cell lymphoma: a single copy of the VH gene is shared
RT by two adjacent CH genes.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:2996-3000(1982).
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC
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CC
CC EMBL; J00494; AAA38130.1; -
DR PIR; A02042; HVMSB1.
DR HSP; P01772; 2FB4.
DR InterPro; IPR007110; I9-like.
DR InterPro; IPR003006; I9_MHC.
DR Pfam; PF00047; I9; 1.
DR SMART; SM00406; IGV; 1.

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DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 136 IG HEAVY CHAIN V REGION BC11.
FT DOMAIN 20 135 IG-LIKE.
FT NON_TER 136 136
SQ SEQUENCE 136 AA; 15078 MW; 6827CFBC6DB3F35E CRC64;

Query Match 48.4%; Score 46; DB 1; Length 136;
Best Local Similarity 56.2%; Pred. No. 1.8;
Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 2 IDPYNGITIDYDQNLKG 17
Db 70 ISTYNGTSTYQKFKG 85

RESULT 5
FLIT_BACSU STANDARD; PRT; 113 AA.
ID FLIT_BACSU STANDARD; PRT; 117 AA.
AC P39740;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Flagellar protein flit.
GN FLIT.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=168 / HE2038;
RA Soldo B., Lazarevic V., Maue C., Karamata D.;
RX MEDLINE=94252974; PubMed=8195064;
RT "The Bacillus subtilis sigma D-dependent operon encoding the
RT flagellar proteins FlitD, FlitS, and FlitT."
RL J. Bacteriol. 176:3093-3101(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RA Soldo B., Lazarevic V., Maue C., Karamata D.;
RX MEDLINE=98044033; PubMed=9384377;
RT "Sequence of the Bacillus subtilis 168 chromosomal region from 305
RT to 307 degree."
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RA Kunst F., Ogasawara N., Moser I., Albertini A.M., Alloni G.,
RA Avevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriass R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell S., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Conterton I.F., Cummings N.J., Daniel R.A.,
RA Denicot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
RA Etikian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Funa S., Galizzi A., Galleron N.,
RA Gim S.Y., Glaser P., Goffeau A., Gollightly B.J., Grandi G.,
RA Giuseppe G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hocono S., Hullo M.F., Itaya M., Jones L.,
RA Coris B., Karamata D., Kasahara Y., Klaere-Blanchard M., Klein C.,
RA Kobayashi Y., Koetter P., Konigstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Maue C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Presecan E., Fujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Roche E., Roche B., Rose M., Sadale Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sekiguchi J., Sekowska A., Seror S.J., Seror P., Shin B.S., Soldo B.,
RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Tanakoshi A., Tanaka T., Terpetra P., Tognoni A.,
RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,

```

```
Query Match 47.4%; Score 45; DB 1; Length 117;
Best Local Similarity 56.2%; Pred. No. 2.3;
Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 IDPYNIGITTYDQNLKG 17
DB 51 INPNNGGTSYNQKFKG 66

RESULT 7
HV13 MOUSE
ID HV13 MOUSE STANDARD; PRT; 117 AA.
AC P01757;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region J558.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_
RP SEQUENCE.
RX MEDLINE=80078170; PubMed=6765983;
RA Schilling J., Clevinger B., Davie J.M., Hood L.;
RT "Amino acid sequence of homogeneous antibodies to dextran and DNA
RT rearrangements in heavy chain V-region gene segments.";
RL Nature 283:35-40(1980).
CC -!- MISCELLANEOUS: THE SEQUENCES OF 10 HYBRIDOMA PROTEINS THAT ALSO
CC BIND DEXTRAN DIFFER FROM THAT SHOWN AT 1-7 POSITIONS, MANY OF
CC WHICH OCCUR IN THE D AND J SEGMENTS.
CC -!- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A26242; MHMSJ5.
DR HSSP; P01789; IMCP.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 98
FT DOMAIN 99 104
FT DOMAIN 105 118
FT DISULFID 22 96
FT NON_TER 118 118
SQ SEQUENCE 118 AA; 12934 MW; 94F7BEE4C762A018 CRC64;

Query Match 47.4%; Score 45; DB 1; Length 118;
Best Local Similarity 56.2%; Pred. No. 2.3;
Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 IDPYNIGITTYDQNLKG 17
DB 51 INPNNGGTSYNQKFKG 66

RESULT 9
VL1 HPVME
ID VL1 HPVME STANDARD; PRT; 505 AA.
AC P27564;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Major capsid protein L1.
GN L1.
OS Human papillomavirus type ME180.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10602;
RN [1]_
RP SEQUENCE FROM N.A.
RX MEDLINE=91374616; PubMed=1716694;
RA Reuter S., Delius H., Kahn T., Hofmann B., Zur Hausen H., Schwarz E.;
RA "Characterization of a novel human papillomavirus DNA in the cervical
RA carcinoma cell line ME180.";
RL J. Virol. 65:5564-5568(1991).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M73258; AAF14010.1; -.
CC PIR; B40509; PIWLPR.
CC InterPro; IPR002210; PV_capsid_L1.
CC Pfam; PF00500; late protein L1; 1.
CC PRINTS; PR00865; HPVcapsidLI.
CC ProDom; PD000544; PV_capsid_L1; 1.
KW Coat protein; late protein.
SQ SEQUENCE 505 AA; 56805 MW; 595DE493B708207B CRC64;

Query Match 47.4%; Score 45; DB 1; Length 505;
Best Local Similarity 50.0%; Pred. No. 11;
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 3 DPYNGITTYDQNLK 16
DB 440 DPYDGLNFMVNLK 453
```

```
RESULT 10
HV02 MOUSE
ID HV02 MOUSE STANDARD; PRT; 140 AA.
AC P01746;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region 93G7 precursor.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RP STRAIN=A/J;
RX MEDLINE=82152818; PubMed=6801765;
RA Sims J., Rabbitts T.H., Estess P., Slaughter C., Tucker P.W.,
RA Capra J.D.;
RT "Somatic mutation in genes for the variable portion of the
RT immunoglobulin heavy chain."
RL Science 216:309-311(1982).
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC -----
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CC or send an email to license@isb-sib.ch)
CC -----
CC EMBL; J00493; AAA38128.1; -.
DR PIR; A94264; HVMSG7.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Hybridsoma; Signal.
FT SIGNAL 1
FT CHAIN 20 140 IG HEAVY CHAIN V REGION 93G7.
FT DOMAIN 20 139 IG-LIKE.
FT NON_TER 140 140
SQ SEQUENCE 140 AA; 15514 MW; 25A4CBBE31DA5CE3 CRC64;

Query Match 46.3%; Score 44; DB 1; Length 140;
Best Local Similarity 47.1%; Pred. No. 4;
Matches 8; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 YIDPYNGITIYDQNLKG 17
||:|||||:|:|
Db 69 YINPGNGYINYNKPKG 85

RESULT 11
Y094 CAEEL
ID Y094 CAEEL STANDARD; PRT; 335 AA.
AC F41844;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Hypothetical 40.1 kDa protein T20B12.4 in chromosome III.
GN T20B12.4.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabdita; Rhabditoidea;
OC Rhabditidae; Felodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
SEQUENCE FROM N.A.
RP STRAIN=Bristol N2;
```

```
Waterston R.;
Submitted (JUN-1994) to the EMBL/GenBank/DBJ databases.
-!- SIMILARITY: STRONG, TO C.ELEGANS K06H7.2.
-----
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CC -----
CC EMBL; U10401; AAA19057.1; -.
DR PIR; T16904; T16904.
DR WormPep; T20B12.4; CE01410.
KW Hypothetical protein.
SQ SEQUENCE 335 AA; 40139 MW; 9DE51B219062BE8E7 CRC64;

Query Match 46.3%; Score 44; DB 1; Length 335;
Best Local Similarity 80.0%; Pred. No. 10;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 IDPYNGITIV 11
|||||
Db 298 IDPYESITIV 307

RESULT 12
PMBE.ECOLI
ID PMBE.ECOLI STANDARD; PRT; 450 AA.
AC P24231;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE PMBE protein (Tlde protein).
GN PMBE OR TLDE OR B4235 OR Z5845 OR ECS5212.
OS Escherichia coli, and
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562, 83334;
RN [1]
SEQUENCE FROM N.A.
RP STRAIN=K12;
RX MEDLINE=91186828; PubMed=2082149;
RA Rodriguez-Sainz M.C., Hernandez-Chico C., Moreno F.;
RT "Molecular characterization of pmbe, an Escherichia coli chromosomal
RT gene required for the production of the antibiotic peptide MccB17."
RL Mol. Microbiol. 4:1921-1932(1990).
RN [2]
SEQUENCE FROM N.A., AND CHARACTERIZATION.
RP STRAIN=K12;
RX MEDLINE=96177756; PubMed=8604133;
RA Murayama N., Shimizu H., Takiguchi S., Baba Y., Amino H.,
RA Horiuchi T., Sekimizu K., Miki T.;
RT "Evidence for involvement of Escherichia coli genes pmbeA, csrA and a
RT previously unrecognized gene tldD, in the control of DNA gyrase by
RT lctD (ccdB) of sex factor F."
RL J. Mol. Biol. 256:483-502(1996).
RN [3]
SEQUENCE FROM N.A.
RP STRAIN=K12;
RX MEDLINE=95334362; PubMed=7610040;
RA Burland V.D., Plunkett G. III, Sofia H.J., Daniels D.L.,
RA Blattner F.R.;
RT "Analysis of the Escherichia coli genome VI: DNA sequence of the
RT region from 92.8 through 100 minutes."
RL Nucleic Acids Res. 23:2105-2119(1995).
RN [4]
SEQUENCE FROM N.A.
RP STRAIN=0157:H7 / EDL933 / ATCC 700927;
RX MEDLINE=21074935; PubMed=11206551;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
```



RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,  
RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,  
RA Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamouis K.,  
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,  
RA Welch R.A., Blattner F.R.,  
RA "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7,"  
RL Nature 409:529-533(2001).  
RN (5)  
RP SEQUENCE FROM N.A.  
RC STRAIN=O157:H7 / RMD 0509952;  
RX MEDLINE=21156231; PubMed=11258796;  
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,  
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., T.,  
RA Iida T., Takami H., Honda T., Sasaki C., Ogasawara N., Yasunaga  
RA Kuhara S., Shiba T., Hattori M., Shinagawa H.,  
RA "Complete genome sequence of enterohaemorrhagic Escherichia coli  
RT O157:H7 and genomic comparison with a laboratory strain K-12,"  
RL DNA Res. 8:11-22(2001).  
CC -1- FUNCTION: MAY FACILITATE THE SECRETION OF THE PEPTIDE ANTIBIOTIC  
CC MICROBIN B17 (MCCB17) BY COMPLETING ITS MATURATION. SUPPRESSES THE  
CC INHIBITORY ACTIVITY OF THE CARBON STORAGE REGULATOR (CSRA).  
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
CC -1- SIMILARITY: BELONGS TO THE T1DD/PMBA FAMILY.  
CC -----  
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CC -----  
CC EMBL; X54152; CAA38091.1; -  
CC EMBL; D44452; BAA07915.1; -  
CC EMBL; U14003; AAA97132.1; -  
CC EMBL; AE000494; AAC77192.1; -  
CC EMBL; AE005655; AAG59432.1; -  
CC EMBL; AP002568; BAB38635.1; -  
CC PIR; D86121; D86121.  
CC PIR; D91280; D91280.  
CC PIR; S13730; S13730.  
CC EcoGene; EG10741; pmBA.  
CC InterPro; IPR002510; PmbA\_T1dd.  
CC Pfam; PF01523; PmbA\_T1dd; 1.  
KW Complete proteome.  
SQ SEQUENCE 450 AA; 48369 MW; A062969197B52B3E CRC64;  
  
Query Match 46.3%; Score 44; DB 1; Length 450;  
Best Local Similarity 72.7%; Pred. No. 14;  
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
  
QY 7 GITVYDQNLKG 17  
DB 67 GITVYDQNRKG 77  
  
RESULT 13  
VLI HPV13  
ID VLI HPV13 STANDARD; PRT; 499 AA.  
AC Q02273;  
DT 01-APR-1993 (Rel. 25, Created)  
DT 01-APR-1993 (Rel. 25, Last sequence update)  
DE 01-OCT-1996 (Rel. 34, Last annotation update)  
DE Major capsid protein L1.  
GN L1.  
OS Human papillomavirus type 13.  
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
OC Papillomavirus.  
OX NCBI\_TaxID=10573;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92391075; PubMed=1325697;  
RA van Ranst M., Fuse A., Fiten P., Beuken E., Pfister H., Burk R.D.,  
RA "Human papillomavirus type 13 and pygmy chimpanzee papillomavirus  
RT type 1: comparison of the genome organizations.";  
RL Virology 190:587-596(1992).  
CC -----  
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CC -----  
CC EMBL; X62844; CAA44662.1; -  
CC InterPro; IPR002210; PV capsid L1.  
CC Pfam; PF00500; late protein L1; 1.  
CC PRINTS; PR00865; HPVcapsidL1.  
CC ProDom; PD000544; PV capsid L1; 1.  
CC Coat protein; Late protein.  
KW Coat protein; Late protein.  
SQ SEQUENCE 502 AA; 55718 MW; A22D1980E9A4BA3 CRC64;  
  
Query Match 46.3%; Score 44; DB 1; Length 502;  
Best Local Similarity 50.0%; Pred. No. 16;  
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

RA Opendakker G.;  
RT "Human papillomavirus type 13 and pygmy chimpanzee papillomavirus  
RT type 1: comparison of the genome organizations.";  
RL Virology 190:587-596(1992).  
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CC -----  
CC EMBL; X62843; CAA44654.1; -  
CC PIR; H42955; P1WLI3.  
CC InterPro; IPR002210; PV capsid L1.  
CC Pfam; PF00500; late protein L1; 1.  
CC PRINTS; PR00865; HPVcapsidL1.  
CC ProDom; PD000544; PV capsid L1; 1.  
CC Coat protein; Late protein.  
KW Coat protein; Late protein.  
SQ SEQUENCE 499 AA; 55773 MW; AA6D5F7FFFD24759 CRC64;  
  
Query Match 46.3%; Score 44; DB 1; Length 499;  
Best Local Similarity 50.0%; Pred. No. 16;  
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;  
  
QY 3 DPYNGITIVDQNLK 16  
DB 434 DPYAGLSFWENLK 447  
  
RESULT 14  
VLI PCPV1  
ID VLI PCPV1 STANDARD; PRT; 502 AA.  
AC Q02274;  
DT 01-APR-1993 (Rel. 25, Created)  
DT 01-APR-1993 (Rel. 25, Last sequence update)  
DT 01-OCT-1996 (Rel. 34, Last annotation update)  
DE Major capsid protein L1.  
GN L1.  
OS Pygmy chimpanzee papillomavirus type 1.  
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
OC Papillomavirus.  
OX NCBI\_TaxID=10576;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92391075; PubMed=1325697;  
RA van Ranst M., Fuse A., Fiten P., Beuken E., Pfister H., Burk R.D.,  
RA Opendakker G.;  
RT "Human papillomavirus type 13 and pygmy chimpanzee papillomavirus  
RT type 1: comparison of the genome organizations.";  
RL Virology 190:587-596(1992).  
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CC -----  
CC EMBL; X62844; CAA44662.1; -  
CC InterPro; IPR002210; PV capsid L1.  
CC Pfam; PF00500; late protein L1; 1.  
CC PRINTS; PR00865; HPVcapsidL1.  
CC ProDom; PD000544; PV capsid L1; 1.  
CC Coat protein; Late protein.  
KW Coat protein; Late protein.  
SQ SEQUENCE 502 AA; 55718 MW; A22D1980E9A4BA3 CRC64;  
  
Query Match 46.3%; Score 44; DB 1; Length 502;  
Best Local Similarity 50.0%; Pred. No. 16;  
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 3 DPYNGITTYDQNLK 16  
 Db 437 DRYAGLSFEVNLK 450

## RESULT 15

```

RPOD_GUITH
ID RPOD_GUITH STANDARD; PRT; 1286 AA.
AC 078483;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE DNA-directed RNA polymerase beta" Chain (EC 2.7.7.6).
GN RPOC2.
OS Guillardia theta (Cryptomonas phi).
OG Chloroplast.
OC Eukaryota; Cryptophyta; Cryptomonadaceae; Guillardia.
OX NCBI_TaxID=55529;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99128221; PubMed=99293932;
RA Douglas S.E., Penny S.L.;
RT "The plastid genome of the cryptophyte alga, Guillardia theta:
RT complete sequence and conserved syntenic groups confirm its common
RT ancestry with red algae."
RL J. Mol. Evol. 48:236-244(1999).
CC -!- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
CC OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
CC SUBSTRATES.
CC -!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
CC (RNA)(N).
CC -!- SUBUNIT: In chloroplasts, the RNA polymerase is composed of four
CC subunits: alpha, beta, beta', and beta".
CC
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CC
CC -----
CC EMBL; AF041468; AAC35674.1; -.
CC HSP; Q9KMU6; 1HQW.
CC InterPro; IPR000722; RNA_pol_A.
CC InterPro; IPR007066; RNA_pol_Rpb1_3.
CC InterPro; IPR007083; RNA_pol_Rpb1_4.
CC InterPro; IPR007081; RNA_pol_Rpb1_5.
CC Pfam; PF04983; RNA_pol_Rpb1_3; 1.
CC Pfam; PF05000; RNA_pol_Rpb1_4; 1.
CC Pfam; PF04998; RNA_pol_Rpb1_5; 2.
CC Transferrase; Transcription; DNA-directed RNA polymerase; Chloroplast.
CC SEQUENCE 1286 AA; 145044 MW; BEFF46PEF5522C73 CRC64;
CC
CC Query Match 46.3%; Score 44; DB 1; Length 1286;
CC Best Local Similarity 61.5%; Pred. No. 44;
CC Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
CC
CC Y 4 PYNGITTYDQNLK 16
CC Db 363 PFNGIIRYKLNK 375

```

Search completed: January 13, 2004, 12:39:32  
 Job time : 3.74236 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 13, 2004, 12:20:44 ; Search time 3.04367 Seconds  
(without alignments)  
1441.318 Million cell updates/sec

Title: US-09-990-586-101  
Perfect score: 95  
Sequence: 1 YIDPYNGITTYDQNLKG 17

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL 23:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phase:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_rvirus:\*
- 16: sp\_bacteriap:\*
- 17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	62	65.3	481	11 Q8VCV5	Q8VCV5 mus musculus
2	54	56.8	488	11 Q91WR1	Q91WR1 mus musculus
3	51	53.7	120	11 Q920E8	Q920E8 mus musculus
4	51	53.7	148	12 Q11401	Q11401 reindeer pa
5	50	52.6	109	11 Q9JL75	Q9JL75 mus musculus
6	48	50.5	243	17 Q28486	Q28486 archaeoglob
7	47.5	50.0	954	5 Q8IC07	Q8IC07 plasmodium
8	47	49.5	481	11 Q91WT3	Q91WT3 mus musculus
9	47	49.5	595	16 Q8YCE9	Q8YCE9 anabaena sp
10	46	48.4	385	16 Q9PQ56	Q9PQ56 ureaplasma
11	46	48.4	675	10 Q9FNM5	Q9FNM5 arabidopsis
12	46	48.4	681	10 Q8RWP3	Q8RWP3 arabidopsis
13	45	47.4	117	11 Q9QXE9	Q9QXE9 mus musculus
14	45	47.4	117	11 Q9QXF0	Q9QXF0 mus musculus
15	45	47.4	152	12 Q81070	Q81070 human papil
16	45	47.4	152	12 Q9MIV1	Q9MIV1 human papil

17	45	47.4	238	5 Q17518	Q17518 caenorhabdi
18	45	47.4	501	12 Q8BDQ8	Q8BDQ8 reindeer pa
19	45	47.4	1092	8 Q8HTL4	Q8HTL4 chlamydomon
20	44	46.3	170	17 Q96XK1	Q96XK1 sulfolobus
21	44	46.3	223	2 Q50398	Q50398 mycoplasma
22	44	46.3	261	16 Q8UB53	Q8UB53 agrobacteri
23	44	46.3	450	16 Q8XGJ7	Q8XGJ7 salmonella
24	44	46.3	450	16 Q8FAP2	Q8FAP2 escherichia
25	44	46.3	501	12 Q37391	Q37391 common chim
26	44	46.3	889	10 Q9FXA5	Q9FXA5 arabidopsis
27	44	46.3	897	10 Q9C7W9	Q9C7W9 arabidopsis
28	44	46.3	938	16 Q8FP27	Q8FP27 corynebacte
29	44	46.3	1007	10 Q9C7X0	Q9C7X0 arabidopsis
30	44	46.3	3574	5 Q8IDA8	Q8IDA8 plasmodium
31	43.5	45.8	403	16 Q8D2W4	Q8D2W4 wiggleswort
32	43	45.3	162	2 Q93SR7	Q93SR7 pseudomonas
33	43	45.3	162	16 Q910W5	Q910W5 pseudomonas
34	43	45.3	580	12 Q91LH9	Q91LH9 white spot
35	43	45.3	581	12 Q8VB97	Q8VB97 white spot
36	43	45.3	607	16 Q8CY30	Q8CY30 bruceella su
37	43	45.3	775	16 Q8XNT7	Q8XNT7 clostridium
38	43	45.3	878	16 Q8P6M3	Q8P6M3 xanthomonas
39	43	45.3	2110	5 Q8IB35	Q8IB35 plasmodium
40	42	44.2	119	5 Q9GY22	Q9GY22 schistosoma
41	42	44.2	151	12 Q84227	Q84227 human papil
42	42	44.2	364	2 Q93QW3	Q93QW3 bacteroides
43	42	44.2	476	17 Q97XC8	Q97XC8 sulfolobus
44	42	44.2	482	12 Q91HD9	Q91HD9 bovine herp
45	42	44.2	503	12 Q99FW7	Q99FW7 human papil

## ALIGNMENTS

## RESULT 1

Q8VCV5 PRELIMINARY; PRT; 481 AA.

AC Q8VCV5; DT 01-MAR-2002 (TRENBLrel. 20, Created)

DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)

DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)

DE Hypothetical 52.3 kDa protein.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]\_

RP SEQUENCE FROM N.A.

RC TISSUE=breast tumor;

RA Strausberg R.;

RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC018455; AAH18455.1; -

DR InterPro; IPR007110; IG-like.

DR InterPro; IPR003006; IG\_MHC.

DR InterPro; IPR003596; IG\_LV.

DR Pfam; PF00047; IG; 4.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS00835; IG\_LIKE; 4.

DR PROSITE; PS00290; IG\_MHC; 2.

KW Hypothetical protein.

SQ SEQUENCE 481 AA; 52326 MW; 52B44C5826807143 CRC64;

Query Match 65.3%; Score 62; DB 11; Length 481;

Best Local Similarity 64.7%; Pred. NO. 0.16; Mismatches 4; Indels 0; Gaps 0;

Matches 11; Conservative 2;

QY 1 YIDPYNGITTYDQNLKG 17

|||||:|

69 YIDPYNGSSYNQKFG 85

## RESULT 2

Q91WR1

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ID Q91WR1 PRELIMINARY; PRT; 488 AA.
AC Q91WR1; 2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical 53.0 kDa protein.
GN IGH-VJ558 OR AI893585.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC Straussberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC013539; AAH13539.1; -.
DR MGI; 96486; IGH-VJ558.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 2.
KW Hypothetical protein_IG_MHC;
SQ SEQUENCE 488 AA; 52964 MW; F12068460B400B9D CRC64;

Query Match 56.8%; Score 54; DB 11; Length 488;
Best Local Similarity 62.5%; Pred. No. 3.3;
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 IDPVNGITTYDQNLKG 17
|:|||||:|:|
DB 70 INFNGTSTYNQKFKG 85

RESULT 3
Q920E8 PRELIMINARY; PRT; 120 AA.
AC Q920E8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Pterin-mimicking anti-idiotypic heavy chain variable region
DE (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Atkin J.D., Iape A., Jennings I.G., Horaitis O., Cotton R.G.H.;
RT "Definition of the Idiotype of Pterin-Mimicking Antibodies Expressed
in Mammalian Cells";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF307936; AAJ09420.1; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG_LIKE; 1.
FT NON_TER 120
FT SEQUENCE 120 AA; 13204 MW; DC4834AB1DE56F3C CRC64;

Query Match 53.7%; Score 51; DB 11; Length 120;
Best Local Similarity 62.5%; Pred. No. 2.3;
Matches 10; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2 IDPVNGITTYDQNLKG 17
|:|||||:|:|

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Db 51 IDPVYGGTSTYNQKFKG 66

RESULT 4
O11401 PRELIMINARY; PRT; 148 AA.
AC O11401;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Reindeer papillomavirus L1 (Fragment).
GN L1.
OS Reindeer papillomavirus (RPV).
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
CX NCBI_TaxID=10569;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97332322; PubMed=9188556;
RA Chan S.Y., Bernard H.U., Ratterree M., Birkebak T.A., Faras A.J.,
RA Ostrow R.S.;
RT "Genomic diversity and evolution of papillomaviruses in rhesus
monkeys";
RL J. Virol. 71:4938-4943(1997).
DR EMBL; U89670; AA863856.1; -.
DR InterPro; IPR002210; PV_capsid_L1.
DR Pfam; PF00500; late_protein_L1; 1.
DR PRINTS; PD00865; HPVCAFSIDL1.
DR ProDom; PD000544; PV_capsid_L1; 1.
FT NON_TER 148
FT SEQUENCE 148 AA; 16623 MW; 56C5A7C98A785928 CRC64;

Query Match 53.7%; Score 51; DB 12; Length 148;
Best Local Similarity 53.3%; Pred. No. 2.8;
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 3 DPYNGITTYDQNLKG 17
|:|||||:|:|
DB 127 DPYSGLKFWEVNLKG 141

RESULT 5
Q9JL75 PRELIMINARY; PRT; 109 AA.
ID Q9JL75
AC Q9JL75;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Anti-myosin immunoglobulin heavy chain variable region
DE (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RX MEDLINE=20448942; PubMed=10992488;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "T-Cell-dependent antibody response to the dominant epitope of
streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
with cardiac myosin";
RL Infect. Immun. 68:5803-5808(2000).
DR EMBL; AF206031; AAF69329.1; -.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 109
FT SEQUENCE 109 AA; 11811 MW; 56C5A7C98A785928 CRC64;

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RP SEQUENCE FROM N.A.
RA Seeger K., Murphy L., Harris D., Berriman M., Pain A., Hall N.,
RA Quail M., Barrrell B.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL844506; CAD50834.1; -.
KW Hypothetical protein.
SQ SEQUENCE 954 AA; 115329 MW; 25417952D67DD6C4 CRC64;

Query Match          50.0%; Score 47.5; DB 5; Length 954;
Best Local Similarity 52.6%; Pred. No. 72;
Matches 10; Conservative 3; Mismatches 3; Indels 3; Gaps 1;

QY 1 YIDPYNG---ITTYDQNLK 16
    |||:|||||:|:|:|
DB 462 YIQPHNGIHIITNYQNIR 480

RESULT 8
Q91WT3 PRELIMINARY; PRT; 481 AA.
ID Q91WT3
AC Q91WT3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical 52.0 kDa protein.
DE IGH-VJ558 OR AI893585.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC013488; AAH13488.1; -.
DR MGI; 96486; Igh-VJ558.
DR InterPro; IPR007110; IG-Like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 2.
KW Hypothetical protein.
SQ SEQUENCE 481 AA; 52022 MW; 4EB5C253038B718 CRC64;

Query Match          49.5%; Score 47; DB 11; Length 481;
Best Local Similarity 50.0%; Pred. No. 42;
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 2 IDPYNGITTYDQNLKG 17
    |||:|:|:|:|
DB 70 IDPDSYTSYNOKFKG 85

RESULT 9
Q8YQE9 PRELIMINARY; PRT; 595 AA.
ID Q8YQE9;
AC Q8YQE9;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Periplasmic oligopeptide-binding protein of oligopeptide ABC
DE transporter.
DE DE
GN ALR3884.
OS Anabaena sp. (strain PCC 7120).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
OX NCBI_TaxID=103690;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE+21595285; PubMed+11759840;
RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,

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RA Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,  
 RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,  
 RA Nakazaki N., Shimo S., Sugimoto M., Takazawa M., Yamada M.,  
 RA Yasuda M., Tabata S.,  
 RT "Complete genomic sequence of the filamentous nitrogen-fixing  
 RT cyanobacterium *Anabaena* sp. strain PCC 7120.",  
 RL DNA Res. 8:205-213(2001).  
 DR EMBL; AP003594; BAB75583.1; -.  
 DR InterPro; IPR000914; SBP\_bac\_5.  
 DR Pfam; PF00496; SBP\_bac\_5; 3.  
 KW Complete proteome.  
 SQ SEQUENCE 595 AA; 67165 MW; D7070EBAB85F0D17 CRC64;  
 Query Match 49.5%; Score 47; DB 16; Length 595;  
 Best Local Similarity 43.8%; Pred.No. 53;  
 Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;  
 QY 1 YIDPYNGITTYDQNLK 16  
 DB 379 YLSPEGLKVIDYNLE 394  
 RESULT 10  
 Q9PQ56 PRELIMINARY; PRT; 386 AA.  
 ID Q9PQ56  
 AC Q9PQ56  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Serine/threonine kinase.  
 GN PKN OR U0216.  
 OS Ureaplasma parvum (Ureaplasma urealyticum biotype 1).  
 OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Ureaplasma.  
 OX NCBI\_TaxID=134821;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Serovar 3;  
 RX MEDLINE=20500219; PubMed=11048724;  
 RA Glass J.I., Lefkowitz B.J., Glass J.S., Heiner C.R., Chen E.Y.,  
 RA Cassell G.H.;  
 RT "The complete sequence of the mucosal pathogen *Ureaplasma*  
 RT *urealyticum*.",  
 RL Nature 407:757-762(2000).  
 DR EMBL; AE002120; AAF30624.1; -.  
 DR InterPro; IPR000719; Prot\_kinase.  
 DR InterPro; IPR002290; Ser\_thr\_pkinase.  
 DR Pfam; PF00069; pkinase; 1.  
 DR ProDom; PD000001; Prot\_kinase; 1.  
 DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
 KW ATP-binding; Transferase; Complete proteome.  
 SQ SEQUENCE 386 AA; 45241 MW; 789374CC15D1CAD9 CRC64;  
 Query Match 48.4%; Score 46; DB 16; Length 386;  
 Best Local Similarity 52.9%; Pred.No. 48;  
 Matches 9; Conservative 2; Mismatches 6; Indels 0; Gaps 0;  
 QY 1 YIDPYNGITTYDQNLK 17  
 DB 326 YIKPLNKLIRYKNLAG 342  
 RESULT 11  
 Q9FNMS PRELIMINARY; PRT; 675 AA.  
 ID Q9FNMS  
 AC Q9FNMS  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE GTP-binding protein LepA homolog  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Columbia;  
 RX MEDLINE=98069011; PubMed=9405937;  
 RA Kotani H., Nakamura Y., Sato S., Kaneko T., Asamizu E., Miyajima N.,  
 RA Tabata S.;  
 RT "Structural analysis of Arabidopsis thaliana chromosome 5. II.  
 RT Sequence features of the regions of 1,044,062 bp covered by thirteen  
 RT physically assigned P1 clones.",  
 RL DNA Res. 4:291-300(1997).  
 DR EMBL; AB066697; BAB10014.1; -.  
 DR HSP; P13551; IDAR.  
 DR InterPro; IPR000640; EFG\_C.  
 DR InterPro; IPR004161; EFTU\_D2.  
 DR InterPro; IPR000795; EF\_GTPbind.  
 DR InterPro; IPR006297; LepA.  
 DR InterPro; IPR005225; Small\_GTP.  
 DR Pfam; PF00679; EFG\_C; 1.  
 DR Pfam; PF00009; GTP\_EFTU; 1.  
 DR Pfam; PF03144; GTP\_EFTU\_D2; 1.  
 DR PRINTS; PR00315; ELONGATNCT.  
 DR TIGRFAMs; TIGR01393; LepA; 1.  
 DR TIGRFAMs; TIGR00231; small\_GTP; 1.  
 DR PROSITE; PS00301; EFATOR\_GTP; 1.  
 KW GTP-binding; Protein biosynthesis  
 SQ SEQUENCE 675 AA; 74874 MW; 824A3D0B093497E5 CRC64;  
 Query Match 48.4%; Score 46; DB 10; Length 675;  
 Best Local Similarity 41.2%; Pred.No. 87;  
 Matches 7; Conservative 4; Mismatches 6; Indels 0; Gaps 0;  
 QY 1 YIDPYNGITTYDQNLK 17  
 DB 274 YIDPYRGVIVYFRVIDG 290  
 RESULT 12  
 Q8RWP3 PRELIMINARY; PRT; 681 AA.  
 ID Q8RWP3  
 AC Q8RWP3  
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE GTP-binding protein LepA-like protein.  
 GN AT5G08650.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Southwick A., Karlin-Neumann G., Nguyen M., Lam B., Miranda M.,  
 RA Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,  
 RA Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,  
 RA Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,  
 RA Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,  
 RA Ecker J., Theologis A., Davis R.W.;  
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Tripp M., Southwick A., Karlin-Neumann G., Nguyen M., Miranda M.,  
 RA Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,  
 RA Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,  
 RA Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,  
 RA Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,  
 RA Ecker J., Theologis A., Davis R.W.;  
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY029298; AAM12957.1; -.  
 DR EMBL; AY128719; AAM91119.1; -.  
 DR InterPro; IPR000640; EFG\_C.

DR InterPro; IPR004161; EFTU D2.  
 DR InterPro; IPR000795; EF\_GTPbind.  
 DR InterPro; IPR006297; LepA.  
 DR InterPro; IPR005225; Small\_GTP.  
 DR Pfam; PF00679; ERG\_C; 1.  
 DR Pfam; PF00009; GTP\_EFTU; 1.  
 DR Pfam; PF03144; GTP\_EFTU D2; 1.  
 DR TIGRFAMs; TIGR01393; lepA; 1.  
 DR TIGRFAMs; TIGR00231; small\_GTP; 1.  
 DR PROSITE; PS00301; EFACOR\_GTP; 1.  
 KW GTP-binding; Protein biosynthesis.  
 SQ SEQUENCE 681 AA; 75424 MW; 0C850E50DC5B9C4C CRC64;

Query Match 48.4%; Score 46; DB 10; Length 681;  
 Best Local Similarity 41.2%; Pred. No. 87;  
 Matches 7; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 YIDPYNGITIVDQNLKG 17  
 |||||:|:|:|:  
 Db 280 YIDPYRGVIVFVIDG 296

## RESULT 13

Q9QXE9 PRELIMINARY; PRT; 117 AA.  
 AC Q9QXE9;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
 DE Immunoglobulin heavy chain V-D-J region (Fragment).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RA Clemens A., Rademaekers A., Specht C., Koelsch E.;  
 RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AJ225174; CAB65237.1; -.  
 DR HSSP; P01810; 2FBJ

DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_v.  
 DR Pfam; PF00047; IG; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG LIKE; 1.  
 FT NON\_TER 1  
 FT NON\_TER 117  
 SQ SEQUENCE 117 AA; 13000 MW; CDDE2AF84D499734 CRC64;

Query Match 47.4%; Score 45; DB 11; Length 117;  
 Best Local Similarity 56.2%; Pred. No. 20;  
 Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 IDPYNGITIVDQNLKG 17  
 |||||:|:|:|:  
 Db 51 INPNNGGTSYNQKFKG 66

## RESULT 14

Q9QXF0 PRELIMINARY; PRT; 117 AA.  
 AC Q9QXF0;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
 DE Immunoglobulin heavy chain V-D-J region (Fragment).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RA Clemens A., Rademaekers A., Specht C., Koelsch E.;  
 RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AJ225174; CAB65236.1; -.  
 DR HSSP; P01789; 1MCP.

DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_v.  
 DR Pfam; PF00047; IG; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG LIKE; 1.  
 FT NON\_TER 1  
 FT NON\_TER 117  
 SQ SEQUENCE 117 AA; 13060 MW; D816AD0858A47E4C CRC64;

Query Match 47.4%; Score 45; DB 11; Length 117;  
 Best Local Similarity 56.2%; Pred. No. 20;  
 Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 IDPYNGITIVDQNLKG 17  
 |||||:|:|:|:  
 Db 51 INPNNGGTSYNQKFKG 66

## RESULT 15

Q81070 PRELIMINARY; PRT; 152 AA.  
 AC Q81070;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
 DE Major capsid protein L1 (Fragment).  
 GN L1.  
 OS Human papillomavirus type 68.  
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
 OC Papillomavirus  
 OX NCBI\_TaxID=45240;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RC STRAIN=IS362;  
 RX MEDLINE=96186743; PubMed=8627792;  
 RA Stewart A.C., Eriksson A.M., Munoz N., Bosch F.X.,  
 RA Peto J., Wheeler C.M.;  
 RT "Intratype variation in 12 human papillomavirus types: a worldwide  
 perspective.";  
 RL J. Virol. 70:3127-3136 (1996).  
 RN [2]  
 RP SEQUENCE FROM N.A.

RC STRAIN=IS362;  
 RA Farmer A.D.;  
 RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; U45934; AAB19169.1; -.  
 DR InterPro; IPR002210; PV\_capsid\_L1.  
 DR Pfam; PF00500; late\_protein\_L1; 1.  
 DR PRINTS; PR00865; HPVcapsidL1.  
 DR ProDom; PD000544; PV\_capsid\_L1; 1.  
 FT NON\_TER 1  
 FT NON\_TER 152  
 SQ SEQUENCE 152 AA; 17331 MW; CCF76574491F7D2D CRC64;

Query Match 47.4%; Score 45; DB 12; Length 152;  
 Best Local Similarity 50.0%; Pred. No. 26;  
 Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 3 DPYNGITIVDQNLK 16  
 |||||:|:|:|:  
 Db 125 DPYDGLNFWNVNLK 138

Search completed: January 13, 2004, 12:43:13  
 Job time : 5.04367 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 13, 2004, 12:18:44 ; Search time 3.96419 Seconds  
(without alignments)  
680.681 Million cell updates/sec

Title: US-09-990-586-101

Perfect score: 95

Sequence: 1 YIDPYNGITTYDQNLKG 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A.Geneseq 19Jun03:  
1: /SIDSI/gcgdata/geneseq/geneseq-embl/AA1980.DAT:  
2: /SIDSI/gcgdata/geneseq/geneseq-embl/AA1981.DAT:  
3: /SIDSI/gcgdata/geneseq/geneseq-embl/AA1982.DAT:  
4: /SIDSI/gcgdata/geneseq/geneseq-embl/AA1983.DAT:  
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6: /SIDSI/gcgdata/geneseq/geneseq-embl/AA1985.DAT:  
7: /SIDSI/gcgdata/geneseq/geneseq-embl/AA1986.DAT:  
8: /SIDSI/gcgdata/geneseq/geneseq-embl/AA1987.DAT:  
9: /SIDSI/gcgdata/geneseq/geneseq-embl/AA1988.DAT:  
10: /SIDSI/gcgdata/geneseq/geneseq-embl/AA1989.DAT:  
11: /SIDSI/gcgdata/geneseq/geneseq-embl/AA1990.DAT:  
12: /SIDSI/gcgdata/geneseq/geneseq-embl/AA1991.DAT:  
13: /SIDSI/gcgdata/geneseq/geneseq-embl/AA1992.DAT:  
14: /SIDSI/gcgdata/geneseq/geneseq-embl/AA1993.DAT:  
15: /SIDSI/gcgdata/geneseq/geneseq-embl/AA1994.DAT:  
16: /SIDSI/gcgdata/geneseq/geneseq-embl/AA1995.DAT:  
17: /SIDSI/gcgdata/geneseq/geneseq-embl/AA1996.DAT:  
18: /SIDSI/gcgdata/geneseq/geneseq-embl/AA1997.DAT:  
19: /SIDSI/gcgdata/geneseq/geneseq-embl/AA1998.DAT:  
20: /SIDSI/gcgdata/geneseq/geneseq-embl/AA1999.DAT:  
21: /SIDSI/gcgdata/geneseq/geneseq-embl/AA2000.DAT:  
22: /SIDSI/gcgdata/geneseq/geneseq-embl/AA2001.DAT:  
23: /SIDSI/gcgdata/geneseq/geneseq-embl/AA2002.DAT:  
24: /SIDSI/gcgdata/geneseq/geneseq-embl/AA2003.DAT:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	91	95.8	17	AAW71859	Human anti-tissue
2	91	95.8	117	AAW71288	Human anti-tissue
3	72	75.8	118	AAV52755	Anti-tissue factor
4	72	75.8	118	AAV52756	Anti-tissue factor
5	69	72.6	110	AAW84099	Vitronectin alpha
6	69	72.6	117	AAW84093	Murine vitronectin
7	69	72.6	117	AAW84097	Humanised anti-alp
8	62	65.3	116	AAW22418	Reshaped human AUK
9	62	65.3	135	AAW29016	pUC-RVh-1220b. Sy

10	62	65.3	135	AAW29017	pUC-RVh-1220d. Sy
11	62	65.3	135	AAW28669	p12-h2. Synthetic
12	62	65.3	214	ABP96759	TSH receptor antib
13	62	65.3	214	ABP96760	TSH receptor antib
14	60	63.2	119	AAW34570	VH Fv fragment of
15	60	63.2	119	AAW35886	Antidigoxin monocl
16	60	63.2	119	AAW62294	Murine monoclonal
17	60	63.2	121	AAW81363	Heavy chain variab
18	60	63.2	123	AAW62298	Murine monoclonal
19	60	63.2	214	ABP96763	TSH receptor antib
20	60	63.2	214	ABP96764	TSH receptor antib
21	60	63.2	214	AAW80153	Binding site. Hom
22	60	63.2	246	AAW27245	Sequence of the AA
23	60	63.2	246	AAW44229	Chimeric Ig superf
24	60	63.2	251	AAW80152	Multifunctional pr
25	60	63.2	252	AAW02279	26-10 anti-digoxin
26	60	63.2	252	AAW53169	26-10 anti-digoxin
27	60	63.2	252	AAW80423	Anti-digoxin sfv
28	60	63.2	260	AAW95600	Anti-digoxin scfv
29	60	63.2	260	AAW83101	Anti-digoxin singl
30	60	63.2	261	AAW44230	Chimeric Ig superf
31	60	63.2	267	AAW44227	Chimeric Ig superf
32	60	63.2	269	AAW60567	Anti-digoxin singl
33	60	63.2	272	AAW34672	26-10 sfv. Synthe
34	60	63.2	274	AAW44228	Chimeric Ig superf
35	60	63.2	311	AAW80151	Multifunctional pr
36	60	63.2	311	AAW05378	Multifunctional pr
37	60	63.2	313	AAW62305	Single chain antib
38	60	63.2	367	AAW27244	Sequence encoded b
39	59	62.1	117	AAW29450	Murine 6G425 heavy
40	59	62.1	117	AAW29451	Humanised 6G425 F
41	59	62.1	117	AAW30310	Humanised murine 6
42	59	62.1	117	AAW30311	Humanised murine 6
43	59	62.1	117	AAW77753	Murine 6G425 heavy
44	59	62.1	117	AAW77754	Humanised 6G425 F
45	59	62.1	117	ABU59500	Mouse antibody 6G4

#### ALIGNMENTS

RESULT 1  
AAW71859  
ID AAW71859 standard; peptide; 17 AA.  
XX  
XX  
AC  
AAW71859:  
XX  
DT 10-DEC-1998 (first entry)  
XX  
DE Human anti-tissue factor antibody hypervariable region #5.  
XX  
KW Human; anti-tissue factor light chain variable region; H36.D2.B7;  
KW anti-tissue factor heavy chain variable region; inhibition; antibody;  
KW blood coagulation; thrombosis; restenosis; thromboembolic condition;  
KW cardiovascular; infection; neoplastic disease; clot; diagnosis.  
XX  
OS Homo sapiens.  
XX  
XX  
FN WO9840408-A1.  
XX  
PD 17-SEP-1998.  
XX  
FF 10-MAR-1998; 98WO-US04644.  
XX  
PR 10-MAR-1997; 97US-0814806.  
XX  
PA (SUNO-) SUNOL MOLECULAR CORP.  
XX  
PI Jiao J, Luopschen L, Nieves EL, Wong HC;  
XX  
DR WPI; 1998-520804/44.  
DR N-PSDB; AAV61138.  
XX



PT New antibody to human tissue factor - used for, e.g. treating  
 PT thrombosis or restenosis or thromboembolic conditions associated  
 PT with cardiovascular, infectious or neoplastic disease  
 XX  
 PS  
 XX Claim 13; Page 31; 53pp; English.

CC The present sequence represents a hypervariable region from the human  
 CC anti-tissue factor antibody that binds native human tissue factor (TF)  
 CC and does not bind non-native TF. The antibody capable of specifically  
 CC binding native TF may be used for inhibiting blood coagulation and also  
 CC for reducing TF levels in a mammal. The antibodies can be used, e.g. to  
 CC treat thromboses, particularly to prevent or inhibit restenosis, or  
 CC other thromboses following an invasive medical procedure such as  
 CC arterial or cardiac surgery (e.g. angioplasty, endarterectomy,  
 CC deployment of a stent, use of catheter, graft implantation or use of an  
 CC arteriovenous shunt). The antibodies can also be used as a carrier for  
 CC blood clot such as streptokinase, tissue plasminogen activator (t-PA)  
 CC or urokinase, or a cytotoxic agent by conjugating a suitable toxin to  
 CC the antibody. Further the antibodies can be used for treating a  
 CC thromboembolic condition associated with cardiovascular disease, an  
 CC infectious disease, a neoplastic disease or as a thrombolytic agent.  
 CC The antibodies can also be used for detection and diagnosis.

XX Sequence 17 AA;

Query Match 95.8%; Score 91; DB 19; Length 17;  
 Best Local Similarity 94.1%; Pred. No. 3.5e-08;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YIDPYNGITTYDQNLKG 17  
 |||||  
 DB 1 YIDPYNGITTYDQNFPG 17

# RESULT 2

ID AAW71288 standard; Protein; 117 AA.

XX AAW71288;

DT 10-DEC-1998 (first entry)

XX Human anti-tissue factor heavy chain variable region.

XX Human; anti-tissue factor light chain variable region; H36.D2.B7;  
 KW anti-tissue factor heavy chain variable region; inhibition; antibody;  
 KW blood coagulation; thrombosis; restenosis; thromboembolic condition;  
 KW cardiovascular; infection; neoplastic disease; clot; diagnosis.

XX Homo sapiens.

XX WO9840408-A1.

XX 17-SEP-1998.

XX 10-MAR-1998; 98WO-US04644.

XX 10-MAR-1997; 97US-0814806.

XX (SUNO-) SUNOL MOLECULAR CORP.

XX Jiao J, Luepschen L, Nieves EL, Wong HC;

XX WPI; 1998-520804/44.

XX N-PSDB; AAV54962.

XX New antibody to human tissue factor - used for, e.g. treating  
 PT thrombosis or restenosis or thromboembolic conditions associated  
 PT with cardiovascular, infectious or neoplastic disease  
 XX  
 PS  
 XX Claim 12; Fig 1B; 53pp; English.

CC The present sequence represents the human anti-tissue factor heavy chain  
 CC variable region from an antibody that binds native human tissue factor  
 CC (TF) and does not bind non-native TF. The antibody capable of  
 CC specifically binding native TF may be used for inhibiting blood  
 CC coagulation and also for reducing TF levels in a mammal. The antibodies  
 CC can be used, e.g. to treat thromboses, particularly to prevent or  
 CC inhibit restenosis, or other thromboses following an invasive medical  
 CC procedure such as arterial or cardiac surgery (e.g. angioplasty,  
 CC endarterectomy, deployment of a stent, use of catheter, graft  
 CC implantation or use of an arteriovenous shunt). The antibodies can also  
 CC be used as a carrier for drugs, particularly pharmaceuticals targeted  
 CC for interaction with a blood clot such as streptokinase, tissue  
 CC plasminogen activator (t-PA) or urokinase, or a cytotoxic agent by  
 CC conjugating a suitable toxin to the antibody. Further the antibodies  
 CC can be used for treating a thromboembolic condition associated with  
 CC cardiovascular disease, an infectious disease, a neoplastic disease or  
 CC as a thrombolytic agent. The antibodies can also be used for detection  
 CC and diagnosis.

XX Sequence 117 AA;

Query Match 95.8%; Score 91; DB 19; Length 117;  
 Best Local Similarity 94.1%; Pred. No. 3.5e-07;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YIDPYNGITTYDQNLKG 17  
 |||||  
 DB 50 YIDPYNGITTYDQNFPG 66

# RESULT 3

AAV52755 standard; Protein; 118 AA.

XX AAV52755;

DT 26-JAN-2000 (first entry)

DE Anti-tissue factor mouse monoclonal antibody ATR-2 H chain V region.

KW Human tissue factor; TF; humanised; antibody; mouse monoclonal antibody;  
 KW ATR-2; ATR-3; ATR-4; ATR-5; ATR-7; ATR-8; thrombotic disease; DIC;  
 KW disseminated intravascular coagulation; immunogenicity; chimeric.

XX Synthetic.

XX Mus sp.

XX WO9951743-A1.

XX 14-OCT-1999.

XX 02-APR-1999; 99WO-JF01768.

XX 03-APR-1998; 98JP-0091850.

XX (CHUS) CHUGAI SEIYAKU KK.

XX Sato K, Adachi H, Yabuta N;

XX WPI; 1999-620204/53.

XX N-PSDB; AAZ33006.

PT Humanised antibody recognizing human tissue factor, used for treatment

PT of disseminated intravascular coagulation -

XX Claim 1; Page 274; 291pp; Japanese.

XX The present invention describes chimeric antibody (Ab) heavy (H) chains  
 CC containing the variable region of the H chain of a mouse monoclonal Ab  
 CC recognising human tissue factor (hTF) and the constant region of the H  
 CC chain of a human Ab. The variable region is one of six specified  
 CC sequences (which are the H chain variable regions from mouse monoclonal  
 CC Ab's ATR-2,3,4,5,7 or 8). Also described are chimeric Ab light (L)

CC chains containing the variable region of the L chain of a mouse  
 CC monoclonal Ab recognising human tissue factor (hTF) and the constant  
 CC region of the L chain of a human Ab, the variable region being one of six  
 CC specified sequences (which are the L chain variable regions from mouse  
 CC monoclonal Ab's ATR-2,3,4,5,7 or 8). The chimeric Ab's can be used for  
 CC the treatment and prevention of thrombotic disease, especially of  
 CC disseminated intravascular coagulation (DIC). The humanised antibody has  
 CC the high hTF binding activity of the mouse monoclonal antibody but  
 CC greatly reduced immunogenicity. AA233001 to AA233091 and Y527007 to  
 CC AA52767 represent sequences used in the exemplification of the present  
 CC invention.

XX Sequence 118 AA;  
 SQ Query Match 75.8%; Score 72; DB 20; Length 118;  
 Best Local Similarity 76.5%; Pred. No. 0.00048;  
 Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 YIDPYNGTIIYDQNLKG 17  
 DB 50 YIDPYNGGTIYNQKFKG 66

RESULT 4  
 AA52756  
 ID AA52756 standard; Protein; 118 AA.

XX AA52756;  
 AC AA52756;  
 DT 26-JAN-2000 (first entry)  
 XX Anti-tissue factor mouse monoclonal antibody ATR-3 H chain V region.

XX Human tissue factor; TF; humanised; antibody; mouse monoclonal antibody;  
 KW ATR-2; ATR-3; ATR-4; ATR-5; ATR-7; ATR-8; thrombotic disease; DIC;  
 KW disseminated intravascular coagulation; immunogenicity; chimeric.

XX Synthetic.  
 OS Mus sp.

PN WO9951743-A1.  
 XX 14-OCT-1999.

XX 02-APR-1999; 99WO-JP01768.  
 XX 03-APR-1998; 98JP-0091850.

XX (CHUS) CHUGAI SEIYAKU KK.  
 XX Sato K, Adachi H, Yabuta N;

XX WPI; 1999-520204/53.  
 XX N-PSDB; AA233007.

XX Humanised antibody recognising human tissue factor, used for treatment  
 PT of disseminated intravascular coagulation -

XX Claim 1; Page 275; 291pp; Japanese.

XX The present invention describes chimeric antibody (Ab) heavy (H) chains  
 CC containing the variable region of the H chain of a mouse monoclonal Ab  
 CC recognising human tissue factor (hTF) and the constant region of the H  
 CC chain of a human Ab. The variable region is one of six specified  
 CC sequences (which are the H chain variable regions from mouse monoclonal  
 CC Ab's ATR-2,3,4,5,7 or 8). Also described are chimeric Ab light (L)  
 CC chains containing the variable region of the L chain of a mouse  
 CC monoclonal Ab recognising human tissue factor (hTF) and the constant  
 CC region of the L chain of a human Ab, the variable region being one of six  
 CC specified sequences (which are the L chain variable regions from mouse  
 CC monoclonal Ab's ATR-2,3,4,5,7 or 8). The chimeric Ab's can be used for  
 CC the treatment and prevention of thrombotic disease, especially of  
 CC disseminated intravascular coagulation (DIC). The humanised antibody has

CC the high hTF binding activity of the mouse monoclonal antibody but  
 CC greatly reduced immunogenicity. AA233001 to AA233091 and Y527007 to  
 CC AA52767 represent sequences used in the exemplification of the present  
 CC invention.

XX Sequence 118 AA;  
 SQ Query Match 75.8%; Score 72; DB 20; Length 118;  
 Best Local Similarity 76.5%; Pred. No. 0.00048;  
 Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 YIDPYNGTIIYDQNLKG 17  
 DB 50 YIDPYNGGTIYNQKFKG 66

RESULT 5  
 AA52756  
 ID AA52756 standard; Protein; 110 AA.

XX AA52756;  
 AC AA52756;  
 DT 15-MAR-1999 (first entry)  
 XX Vitronectin alpha-v beta-3 MAB VH.

XX Humanised antibody; monoclonal antibody; MAB; antibody engineering;  
 KW mouse; human; vitronectin; alpha-v beta-3; receptor; restenosis;  
 KW cancer; metastasis; rheumatoid arthritis; atherosclerosis;  
 KW angiogenesis; diabetic retinopathy; inflammation;  
 KW macular degeneration; osteoporosis; Paget's disease;  
 KW hyperparathyroidism; hypercalcaemia; therapy; immunotherapy.

XX Mus sp.  
 OS WO9840488-A1.

PN 17-SEP-1998.  
 XX 12-MAR-1998; 98WO-US04987.

XX 12-MAR-1997; 97US-0039609.  
 XX (SMIX) SMITHKLINE BEECHAM CORP.

XX Johanson KO, Jonak ZL, Taylor AH;  
 XX WPI; 1999-034590/03.

XX N-PSDB; AA71801.  
 XX New anti alpha-v beta-3 vitronectin receptor antibodies - used for

PT immunotherapeutic treatment of e.g. diabetic retinopathy,  
 PT inflammatory disorders, atherosclerosis, restenosis, cancers or

PT osteoporosis  
 XX Example 13; Page 63; 97pp; English.

XX This is the amino acid sequence of the region of the murine  
 CC monoclonal antibody (MAB) D12 heavy chain variable region (VH)  
 CC that is altered in humanised D12 VH (see also AA52756). A  
 CC synthetic gene (see AA52756) encoding the protein was prepared  
 CC from synthetic oligonucleotides and used to prepare an expression  
 CC vector for humanised D12 VH. D12 is an anti-human alpha-v beta-3  
 CC vitronectin receptor MAB. Humanised D12 MABs can be used for  
 CC passive immunotherapy of disorders mediated by the alpha-v beta-3  
 CC vitronectin receptor, e.g. restenosis and angiogenic associated  
 CC diseases.

XX Sequence 110 AA;  
 SQ Query Match 72.6%; Score 69; DB 20; Length 110;  
 Best Local Similarity 70.6%; Pred. No. 0.0014;  
 Matches 12; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

This is the amino acid sequence of the heavy chain variable region (VH) of the anti-human alpha-v beta-3 vitronectin receptor murine monoclonal antibody D12, as deduced from isolated cDNA (see KAV171297). D12 VH and VL (see AA043094) show sequence similarity to Kabat VH subgroup I (see AA043095) and Kabat VK subgroup III (see AA043096), respectively. Humanised VH (see AA043097) and VL (see AA043098) were constructed by combining the framework regions of the human V region consensus sequences with complementarity determining regions of D12 (keeping some preferred murine framework residues). The humanised antibodies are specifically reactive with the human alpha-v beta-3 protein receptor and capable of neutralising the receptor. They can be used for passive immunotherapy of a disorders mediated by the alpha-v beta-3 receptor, e.g. cardiovascular disorders or angiogenic-related disorders, such as angiogenesis associated with diabetic retinopathy, atherosclerosis and restenosis, chronic inflammatory disorders, macular degeneration, rheumatoid arthritis and cancer, e.g. solid tumour metastasis, and diseases where bone resorption is associated with pathology such as osteoporosis, hyperparathyroidism, Paget's disease, hypercalcaemia

CC are retained. The humanised heavy chain can be expressed in host  
 CC cells using nucleic acid molecules (see AAV71799) of the invention.  
 CC Humanised D12 VL is also provided (see AAW84098)). The humanised  
 CC antibodies can be used for passive immunotherapy of disorders  
 CC mediated by the alpha-v beta-3 receptor, e.g. cardiovascular or  
 CC angiogenic-related disorders, such as angiogenesis associated  
 CC with diabetic retinopathy, atherosclerosis and restenosis, chronic  
 CC inflammatory disorders, macular degeneration, rheumatoid arthritis  
 CC and cancer, e.g. solid tumour metastasis, and diseases where bone  
 CC resorption is associated with pathology such as osteoporosis,  
 CC hyperparathyroidism, Paget's disease, hypercalcaemia of malignancy,  
 CC osteolytic lesions produced by bone metastasis, bone loss due to  
 CC immobilisation or sex hormone deficiency. They can also be used for  
 CC targeted drug therapy, and for detection and diagnosis.

XX Sequence 117 AA;  
 SQ Query Match 72.6%; Score 69; DB 20; Length 117;  
 Best Local Similarity 70.6%; Pred. No. 0.0015; Gaps 0;  
 Matches 12; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 YIDPYNIGITFDQNLKG 17  
 Db 50 YIDPYNIGITFDQNLKG 66

RESULT 8  
 AAW22418  
 ID AAW22418 standard; Protein; 116 AA.

XX AC AAW22418;

DT 08-DEC-1997 (first entry)

XX DE Reshaped human AUK12-20 VH.

XX Alpha-4 integrin; humanised antibody; monoclonal antibody 21.6;  
 KW asthma; atherosclerosis; AIDS; dementia; diabetes; tumour;  
 KW metastasis; inflammatory bowel disease; rheumatoid arthritis;  
 KW transplant rejection; graft versus host disease; nephritis;  
 KW atopic dermatitis; psoriasis; myocardial ischaemia;  
 XX acute leukocyte mediated lung injury; therapy; AUK12-20.

XX Chimeric Homo sapiens;  
 OS Chimeric synthetic.

Key	Location/Qualifiers
FT Region	1..30
FT Region	/label= FR1
FT Region	31..35
FT Region	/label= CDR1
FT Region	36..49
FT Region	/label= FR2
FT Region	50..66
FT Region	/label= CDR2
FT Region	67..98
FT Region	/label= FR3
FT Region	99..105
FT Region	/label= CDR3
FT Region	106..116
FT Region	/label= FR4

XX WO9718838-A1.

XX 29-MAY-1997.

XX 21-NOV-1996; 96WO-US18807.

XX 21-NOV-1995; 95US-0561521.

XX (ATHE-) ATHENA NEUROSCIENCES INC.

XX Bendig MW, Jones ST, Leger OJ, Saldanha J, Vednock TA;

XX WPI; 1997-297879/27.  
 DR Uses of humanised alpha-4 integrin antibody - for treatment of  
 PT asthma, atherosclerosis, AIDS, dementia, etc.  
 XX Example 6; Page 44; 107pp; English.

XX This polypeptide comprises version 'b', of a reshaped human  
 CC antibody AUK12-20 VH region. A DNA fragment encoding the  
 CC polypeptide was subcloned into vector pUC19 for use as a template  
 CC for PCR amplification and production of version 'a' of a reshaped  
 CC human 21.6 VH region (see AAW22413) that can be used in the  
 CC construction of novel humanised anti-alpha-4 integrin antibodies.  
 CC Claimed humanised antibodies are useful in the treatment of  
 CC asthma, atherosclerosis, AIDS, dementia, diabetes, inflammatory  
 CC bowel disease, rheumatoid arthritis, transplant rejection, graft  
 CC versus host disease, tumour metastasis, nephritis, atopic  
 CC dermatitis, psoriasis, myocardial ischaemia, and acute leukocyte  
 CC mediated lung injury.

SQ Sequence 116 AA;

Query Match 65.3%; Score 62; DB 18; Length 116;  
 Best Local Similarity 64.7%; Pred. No. 0.021;  
 Matches 11; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 YIDPYNIGITFDQNLKG 17  
 Db 50 YIDPYNIGITFDQNLKG 66

RESULT 9

AAW29016

ID AAW29016 standard; Protein; 135 AA.

XX AC AAW29016;

XX 25-MAR-2003 (updated)

DT 30-MAR-1993 (first entry)

XX pUC-RVh-1220b.

XX Human; antibody; interleukin-6; receptor; IL-6R; CDR; PCR; mouse;  
 KW complementarity determining region; monoclonal; hybridoma; PCR;  
 KW plasmid; polymerase chain reaction; amplify.

XX Synthetic.

Key	Location/Qualifiers
FT Peptide	1..19
FT Region	/note= "Leader peptide"
FT Region	20..49
FT Region	/label= FR1
FT Region	50..54
FT Region	/label= CDR1
FT Region	55..68
FT Region	/label= FR2
FT Region	69..85
FT Region	/label= CDR2
FT Region	86..117
FT Region	/label= FR3
FT Region	118..124
FT Region	/label= CDR3
FT Region	125..135
FT Region	/label= FR4

XX WO9219759-A1.

XX 12-NOV-1992.

XX 24-APR-1992; 92WO-JP00544.

PR 25-APR-1991; 91JP-0095476.  
 PR 19-FEB-1992; 92JP-0032084.  
 XX (CHUS ) CHUGAI SEIYAKU KK.  
 PA Bendig MM, Jones ST, Saldanha JW, Sato K, Tsuchiya M;  
 PI WPI; 1992-398882/48.  
 XX N-PSDB; AAQ31391.  
 DR Reconstituted human antibody to human interleukin-6 receptor -  
 PT has low antigenicity and contains mouse V-region complementarity  
 PT determining regions  
 XX Disclosure; Page 157-8; 207pp; Japanese.  
 XX The sequences given in AAR29016-17 are portions of monoclonal antibodies  
 CC which were encoded by plasmids contained within the mouse hybridoma,  
 CC AUK12-20. The DNA encoding the complementarity determining regions  
 CC (CDR's) was isolated by polymerase chain reaction. These antibodies  
 CC recognise human interleukin-6 receptor (IL-6R). The hybridoma cells  
 CC were transformed with plasmids containing fragments of the antibody  
 CC gene which caused the production of the antibody from the hybridoma  
 CC cell line.  
 CC (Updated on 25-MAR-2003 to correct PN field.)  
 CC Sequence 135 AA;

Query Match 65.3%; Score 62; DB 13; Length 135;  
 Best Local Similarity 64.7%; Pred. No. 0.025;  
 Matches 11; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 YIDPYNGITIYDQNLKG 17  
 |||||:|:|:|:  
 DB 69 YIDPFNGGTSYNQKFKG 85

RESULT 10  
 AAR29017  
 ID AAR29017 standard; Protein; 135 AA.  
 XX AAR29017;  
 AC  
 XX 25-MAR-2003 (updated)  
 DT 30-MAR-1993 (first entry)  
 DE PUC-RVh-1220d.  
 XX Human; antibody; interleukin-6; receptor; IL-6R; CDR; PCR; mouse;  
 KW complementarity determining region; monoclonal; hybridoma; PCR;  
 KW plasmid; polymerase chain reaction; amplify.  
 XX Synthetic.

Key	Location/Qualifiers
Peptide	1..19 /note= "Leader peptide"
Region	20..49 /label= FR1
Region	50..54 /label= FR1
Region	55..68 /label= CDR1
Region	69..85 /label= FR2
Region	86..117 /label= CDR2
Region	118..124 /label= FR3
Region	125..135 /label= CDR3
Region	136..149 /label= FR4

PN WO9219759-A1.

XX 12-NOV-1992.  
 XX 24-APR-1992; 92WO-JP00544.  
 XX 25-APR-1991; 91JP-0095476.  
 PR 19-FEB-1992; 92JP-0032084.  
 XX (CHUS ) CHUGAI SEIYAKU KK.  
 PA Bendig MM, Jones ST, Saldanha JW, Sato K, Tsuchiya M;  
 PI WPI; 1992-398882/48.  
 XX N-PSDB; AAQ31391.  
 DR Reconstituted human antibody to human interleukin-6 receptor -  
 PT has low antigenicity and contains mouse V-region complementarity  
 PT determining regions  
 XX Disclosure; Page 159-60; 207pp; Japanese.  
 XX The sequences given in AAR29016-17 are portions of monoclonal antibodies  
 CC which were encoded by plasmids contained within the mouse hybridoma,  
 CC AUK12-20. The DNA encoding the complementarity determining regions  
 CC (CDR's) was isolated by polymerase chain reaction. These antibodies  
 CC recognise human interleukin-6 receptor (IL-6R). The hybridoma cells  
 CC were transformed with plasmids containing fragments of the antibody  
 CC gene which caused the production of the antibody from the hybridoma  
 CC cell line.  
 CC (Updated on 25-MAR-2003 to correct PN field.)  
 CC Sequence 135 AA;

Query Match 65.3%; Score 62; DB 13; Length 135;  
 Best Local Similarity 64.7%; Pred. No. 0.025;  
 Matches 11; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 YIDPYNGITIYDQNLKG 17  
 |||||:|:|:|:  
 DB 69 YIDPFNGGTSYNQKFKG 85

RESULT 11  
 AAR28669  
 ID AAR28669 standard; Protein; 135 AA.  
 XX AAR28669;

XX 25-MAR-2003 (updated)  
 DT 30-MAR-1993 (first entry)  
 DE p12-h2.

XX Human; antibody; interleukin-6; receptor; IL-6R; light chain; L; H;  
 KW heavy chain; variable region; mouse; monoclonal; hybridoma; AUK12-20;  
 KW plasmid; p12-h2; p12-h2.

Key	Location/Qualifiers
Peptide	1..19 /note= "Signal peptide"
Protein	20..135 /note= "Mature peptide"

XX WO9219759-A1.  
 XX 12-NOV-1992.  
 XX 24-APR-1992; 92WO-JP00544.  
 XX 25-APR-1991; 91JP-0095476.  
 PR 19-FEB-1992; 92JP-0032084.

XX (CHUS ) CHUGAI SEIYAKU KK.  
 XX Bendig MM, Jones ST, Saldanha JW, Sato K, Tsuchiya M;  
 XX WPI; 1992-398882/48.  
 XX N-PSDB; AAQ30754.  
 XX Reconstituted human antibody to human interleukin-6 receptor -  
 PT has low antigenicity and contains mouse V-region complementarity  
 PT determining regions  
 XX Disclosure; Page 119-20; 207pp; Japanese.  
 XX The sequences given in AAR28668-69 were encoded by plasmid sequences  
 CC which were used in example to illustrate the production of a human  
 CC antibody which recognises human interleukin-6 receptor (IL-6R). The  
 CC antibody comprises light (L) chain and heavy (H) chain variable  
 CC regions which were derived from a mouse monoclonal antibody produced  
 CC from the hybridoma AUK12-20 which contained the plasmids p12-K2 and  
 CC p12-h2.  
 CC (Updated on 25-MAR-2003 to correct PN field.)  
 XX SQ Sequence 135 AA;  
 Query Match 65.3%; Score 62; DB 13; Length 135;  
 Best Local Similarity 64.7%; Pred. No. 0.025;  
 Matches 11; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 YIDPYNGITTYDQNLKG 17  
 DB 69 YIDPFNGGTSYNKPKG 85  
 RESULT 12  
 ABP96759  
 ID ABP96759 standard; Protein; 214 AA.  
 AC ABP96759;  
 XX 05-JUN-2003 (first entry)  
 DT TSH receptor antibody 17D2 heavy chain amino acid sequence.  
 DE  
 XX Thyrotropin receptor; TSH receptor; epitope region; antibody;  
 KW autoantibody; autoimmune disease; thyroid tissue; cytostatic;  
 KW gene therapy; immune reaction; thyroid cancer.  
 XX Synthetic.  
 OS  
 XX WO2003018632-A2.  
 PN 06-MAR-2003.  
 PD  
 XX 21-AUG-2002; 2002WO-GB03831.  
 PF  
 XX 23-AUG-2001; 2001GB-0020649.  
 PR 01-JUL-2002; 2002GB-0015212.  
 XX (RSRR-) RSR LTD.  
 PA  
 XX Smith BR, Furmaniak J, Sanders JF;  
 PI WPI; 2003-290051/28.  
 XX N-PSDB; ACC44914.  
 DR New polypeptide sequence having part or all of the primary structural  
 XX conformation of one or more TSH receptor epitopes, useful for treating  
 PT an autoimmune disease associated with an immune reaction to a TSH  
 PT receptor, e.g. thyroid cancer -  
 XX Claim 71; Fig 17; 196pp; English.  
 PS  
 XX

CC The present invention describes a polypeptide sequence comprising part  
 CC or all of the primary structural conformation of one or more thyrotropin  
 CC (TSH) receptor epitopes with which autoantibodies and/or lymphocytes  
 CC produced in response to a TSH receptor interact. Also described: (1) one  
 CC or more receptor TSH epitopes with which the autoantibodies and/or  
 CC lymphocytes interact, as with the polypeptide sequence described above;  
 CC (2) a method of screening for autoantibodies or lymphocytes produced in  
 CC response to a TSH receptor in a sample of body fluid obtained from a  
 CC subject suspected of suffering from, susceptible to, having or recovering  
 CC from autoimmune disease associated with an immune reaction to a TSH  
 CC receptor; (3) a binding partner for a TSH receptor, which is capable of  
 CC binding to a TSH receptor to stimulate the TSH receptor, where the  
 CC binding partner does not comprise TSH or naturally produced antibodies to  
 CC the TSH receptor; and (4) a combination comprising the binding partner  
 CC and one or more further agents capable of stimulating thyroid tissue,  
 CC and/or tissue containing a TSH receptor, for simultaneous, separate or  
 CC sequential use in stimulating thyroid tissue, and/or tissue containing a  
 CC TSH receptor. A TSH receptor has cytostatic activity and can be used in  
 CC gene therapy. The polypeptide, compositions and methods from the present  
 CC invention can be used for treating an autoimmune disease associated with  
 CC an immune reaction to a TSH receptor. The specific binding partner is  
 CC useful for the manufacture of a medicament for stimulating thyroid cancer.  
 CC or tissue containing a TSH receptor, and for treating thyroid cancer.  
 CC ACC44874 to ACC44905 and ABP96719 to ABP96750 represent TSH receptor  
 CC sequences, and ACC44910 to ACC44933 encode the TSH receptor antibody VH  
 CC and VL domains given in ABP96751 to ABP96778, which are used in the  
 CC exemplification of the present invention.  
 XX SQ Sequence 214 AA;  
 Query Match 65.3%; Score 62; DB 24; Length 214;  
 Best Local Similarity 64.7%; Pred. No. 0.044;  
 Matches 11; Conservative 1; Mismatches 5; Indels 0; Gaps 0;  
 QY 1 YIDPYNGITTYDQNLKG 17  
 DB 50 YIDPYSGATSYHQKFG 66  
 RESULT 13  
 ABP96760  
 ID ABP96760 standard; Protein; 214 AA.  
 AC ABP96760;  
 XX 05-JUN-2003 (first entry)  
 DT TSH receptor antibody 17D2 heavy chain amino acid sequence.  
 DE  
 XX Thyrotropin receptor; TSH receptor; epitope region; antibody;  
 KW autoantibody; autoimmune disease; thyroid tissue; cytostatic;  
 KW gene therapy; immune reaction; thyroid cancer.  
 XX Synthetic.  
 OS  
 XX WO2003018632-A2.  
 PN 06-MAR-2003.  
 PD  
 XX 21-AUG-2002; 2002WO-GB03831.  
 PF  
 XX 23-AUG-2001; 2001GB-0020649.  
 PR 01-JUL-2002; 2002GB-0015212.  
 XX (RSRR-) RSR LTD.  
 PA  
 XX Smith BR, Furmaniak J, Sanders JF;  
 PI WPI; 2003-290051/28.  
 XX N-PSDB; ACC44915.  
 DR New polypeptide sequence having part or all of the primary structural  
 XX conformation of one or more TSH receptor epitopes, useful for treating  
 PT an autoimmune disease associated with an immune reaction to a TSH  
 PT receptor, e.g. thyroid cancer -  
 XX Claim 71; Fig 17; 196pp; English.  
 PS  
 XX

PT an autoimmune disease associated with an immune reaction to a TSH  
 PT receptor, e.g. thyroid cancer -  
 XX  
 PS Claim 67; Fig 18; 196pp; English.  
 CC  
 CC The present invention describes a polypeptide sequence comprising part  
 CC or all of the primary structural conformation of one or more thyrotropin  
 CC (TSH) receptor epitopes with which autoantibodies and/or lymphocytes  
 CC produced in response to a TSH receptor interact. Also described: (1) one  
 CC or more receptor TSH epitopes with which the autoantibodies and/or  
 CC lymphocytes interact, as with the polypeptide sequence described above;  
 CC (2) a method of screening for autoantibodies or lymphocytes produced in  
 CC response to a TSH receptor in a sample of body fluid obtained from a  
 CC subject suspected of suffering from, susceptible to, having or recovering  
 CC from autoimmune disease associated with an immune reaction to a TSH  
 CC receptor; (3) a binding partner for a TSH receptor, which is capable of  
 CC binding to a TSH receptor to stimulate the TSH receptor, where the  
 CC binding partner does not comprise TSH or naturally produced antibodies to  
 CC the TSH receptor; and (4) a combination comprising the binding partner  
 CC and one or more further agents capable of stimulating thyroid tissue,  
 CC and/or tissue containing a TSH receptor, for simultaneous, separate or  
 CC sequential use in stimulating thyroid tissue, and/or tissue containing a  
 CC TSH receptor. A TSH receptor has cytostatic activity and can be used in  
 CC gene therapy. The polypeptide, compositions and methods from the present  
 CC invention can be used for treating an autoimmune disease associated with  
 CC an immune reaction to a TSH receptor. The specific binding partner is  
 CC useful for the manufacture of a medicament for stimulating thyroid tissue  
 CC or tissue containing a TSH receptor, and for treating thyroid cancer.  
 CC ACC44874 to ACC44905 and ABP96719 to ABP96750 represent TSH receptor  
 CC sequences, and ACC44910 to ACC44933 encode the TSH receptor antibody VH  
 CC and VL domains given in ABP96751 to ABP96778, which are used in the  
 CC exemplification of the present invention.

XX SQ Sequence 214 AA;

Query Match 65.3%; Score 62; DB 24; Length 214;  
 Best Local Similarity 64.7%; Pred. No. 0.044;  
 Matches 11; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 1 YIDPYNGITIDONLKG 17  
 |||||:|:|:|:|:  
 Db 50 YIDPYSGATYHQKPKG 66

RESULT 14  
 AAR34670  
 ID AAR34670 standard; Protein; 119 AA.

XX AAR34670;  
 XX  
 XX 25-MAR-2003 (updated)  
 DT 25-AUG-1993 (first entry)  
 XX  
 XX VH Fv fragment of antidigitoxin monoclonal antibody 26-10.  
 XX  
 XX Heavy; light; variable; VH; VL; region; antidigitoxin; monoclonal;  
 KW antibody; Mab; 26-10; Fv; fragment; antigen; binding site; linker;  
 KW expression-secretion system; T7 promoter; signal peptide; molecule;  
 KW polymerase chain reaction; PCR; single chain.  
 XX  
 XX Synthetic.  
 OS  
 XX WO9308300-A1.  
 PN  
 XX 29-APR-1993.  
 XX  
 XX 16-OCT-1992; 92WO-US08881.  
 XX  
 XX 18-OCT-1991; 91US-0777709.  
 XX  
 XX (UYCA-) UNIV CALGARY.  
 PA  
 XX Anthony JG, Ng SC, Wong S;  
 PI

XX  
 DR WPI: 1993-152491/18.  
 DR N-PSDB; AAQ41065.  
 XX  
 PT Expression-secretion vectors - for prodn. of biologically active  
 PT antibody Fv fragments or single chain Fv molecules  
 PS  
 PS Disclosure; Fig 1A; 51pp; English.

XX The sequences given in AAR34670-71 represent the heavy and light  
 CC variable portions (VH and VL) of antidigitoxin monoclonal antibody (Mab)  
 CC 26-10. These VH and VL peptide fragments are examples of Fv fragments.  
 CC Fv fragments are the smallest complete antigen binding sites presently  
 CC known. The DNA fragments encoding these Fv fragments were used in the  
 CC construction of an expression-secretion system for the production  
 CC of biologically active Fv fragments. The system also contains a DNA  
 CC sequence encoding the T7 promoter and one or DNA sequences encoding  
 CC one or more signal peptides (see also AAR38527-28). The secretion-  
 CC expression vector was produced by polymerase chain reaction. Fv  
 CC fragments may also be produced as single chain Fv molecules (see  
 CC also AAR34672) which contain the VH and VL regions, a signal sequence  
 CC and a linker between the two variable regions. Fv fragments and  
 CC single chain molecules may be used to specifically bind one or more  
 CC of the same antigens as the full length antibody from which it is  
 CC derived.  
 CC (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 119 AA;

Query Match 63.2%; Score 60; DB 14; Length 119;  
 Best Local Similarity 58.8%; Pred. No. 0.046;  
 Matches 10; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 1 YIDPYNGITIDONLKG 17  
 |||||:|:|:|:|:  
 Db 50 YISPSGVGTGYNQKPKG 66

RESULT 15

AAR38586  
 ID AAR38586 standard; Protein; 119 AA.

XX AAR38586;  
 XX  
 XX 25-MAR-2003 (updated)  
 DT 28-JUL-1995 (first entry)  
 XX  
 XX Antidigoxin monoclonal antibody 26-10 heavy chain variable region.  
 DE  
 XX Single chain antibody Fv fragment; monoclonal antibody 26-10;  
 KW anti-digoxin; scFv; heavy chain variable region.  
 KW  
 XX Homo sapiens.  
 OS  
 XX WO9312246-A1.  
 PN  
 XX 24-JUN-1993.  
 PD  
 XX 18-DEC-1991; 91WO-US07625.  
 XX  
 XX 18-DEC-1991; 91WO-US07625.  
 PR  
 XX 18-DEC-1991; 91EP-0923150.  
 XX  
 XX (ANTH/) ANTHONY J G.  
 PA (NGSC/) NG S C.  
 PA (UYCA-) UNIV CALGARY.  
 PA (WONG/) WONG S.  
 XX  
 XX Anthony JG, Ng S, Wong S, Ng SC;  
 PI

WPI: 1993-214187/26.  
 DR N-PSDB; AAQ44036.  
 XX

PT Expression-secretion vectors for prodn. of Fv fragments - used  
PT for similar applications as whole antibodies and specifically  
PT bind digoxin

XX Claim 13; Fig 1A; 55pp; English.

XX Antidigoxin monoclonal antibody 26-10 is a high affinity antibody  
CC produced against digoxin conjugated to BSA. cDNA clones of the genes  
CC encoding the VH and VL portions of the 26-10 antibody were made by  
CC PCR amplification of cDNA generated by reverse transcription of mRNA  
CC isolated from 2610 hybridoma. The VH and VL clones (encoding AAR38586  
CC and AAR38587, respectively) were used in the construction of plasmids  
CC for the expression of single-chain Fv fragments.  
CC (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 119 AA;

Query Match 63.2%; Score 60; DB 14; Length 119;  
Best Local Similarity 58.8%; Pred. No. 0.046;  
Matches 10; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 YIDPYNGITIVDNLKG 17  
|||:|:|:|:  
Db 50 YISPSGVTCYNQKPKG 66

Search completed: January 13, 2004, 12:38:29  
Job time : 3.96419 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 13, 2004, 12:43:20 ; Search time 2.71703 Seconds  
(without alignments)  
1360.812 Million cell updates/sec

Title: US-09-990-586-101

Perfect score: 95

Sequence: 1 YIDPVGITIDQNLKG 17

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 747907 seqs, 201509753 residues

Total number of hits satisfying chosen parameters: 747907

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

## RESULT 1

```

US-09-990-586-101
/ Sequence 101, Application US/09909586
/ Publication No. US20030109680A1
/ GENERAL INFORMATION:
/ APPLICANT: J'RAO, JIN-AN
/ APPLICANT: WONG, HING C.
/ TITLE OF INVENTION: ANTIBODIES FOR IN
/ TITLE OF INVENTION: OF USE THEREOF
/ FILE REFERENCE: 71758/46943-CIP2
/ CURRENT APPLICATION NUMBER: US/09/990
/ CURRENT FILING DATE: 2001.11.21
/ PRIOR APPLICATION NUMBER: 09/293,854
/ PRIOR FILING DATE: 1999-04-16
/ NUMBER OF SEQ ID NOS: 102
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 101
/ LENGTH: 17
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-990-586-101

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Query Match 100.0%: Score 95; DB 11; Length 17;

Best Local Similarity	100.0%;	Pred. No. 5.5e-09;	
Conservative	0;	Mismatches	0;
Indels	0;	Gaps	0;

Qy 1 YIDPYNGITIIDQNLKG 17  
|||  
Db 1 YIDPYNGITIIDQNLKG 17

RESULT 2  
US-10-310-113-164  
; Sequence 164; Application US/10310113  
; Publication No. US20030176664A1  
; GENERAL INFORMATION:  
; APPLICANT: JIAO, JIN-AN  
; APPLICANT: WONG, HING C.

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	95	100.0	17	11	US-09-990-586-101	Sequence 101, App	
2	95	100.0	17	12	US-10-310-113-164	Sequence 164, App	
3	95	100.0	17	12	US-10-330-880-101	Sequence 101, App	
4	91	95.8	17	10	US-09-933-854-9	Sequence 9, Appli	
5	91	95.8	17	11	US-09-990-586-9	Sequence 9, Appli	
6	91	95.8	17	12	US-10-310-113-9	Sequence 9, Appli	
7	91	95.8	17	12	US-10-310-113-161	Sequence 161, App	
8	91	95.8	17	12	US-10-330-880-9	Sequence 9, Appli	
9	91	95.8	17	15	US-10-933-417-9	Sequence 9, Appli	
10	91	95.8	117	10	US-09-933-854-4	Sequence 4, Appli	
11	91	95.8	117	11	US-09-990-586-4	Sequence 4, Appli	
12	91	95.8	117	12	US-10-310-113-4	Sequence 4, Appli	
13	91	95.8	117	12	US-10-330-880-4	Sequence 4, Appli	
14	91	95.8	117	15	US-10-933-417-4	Sequence 4, Appli	
15	69	73.6	110	12	US-10-933-880-12	Sequence 12, Appli	

APPLICANT: NIEVES, ESPERANZA LILIANA  
APPLICANT: MOSQUERA, LUIS A.  
TITLE OF INVENTION: USE OF ANTI-TISSUE FACTOR ANTIBODIES FOR TREATING  
TITLE OF INVENTION: THROMBOSES  
FILE REFERENCE: 58122(71758)  
CURRENT APPLICATION NUMBER: US/10/310,113  
CURRENT FILING DATE: 2002-12-04  
PRIOR APPLICATION NUMBER: 09/990,586  
PRIOR FILING DATE: 2001-11-21  
PRIOR APPLICATION NUMBER: 60/343,306  
PRIOR FILING DATE: 2001-10-29  
PRIOR APPLICATION NUMBER: 09/293,854  
PRIOR FILING DATE: 1999-04-16  
PRIOR APPLICATION NUMBER: 08/814,806  
PRIOR FILING DATE: 1997-03-10  
NUMBER OF SEQ ID NOS: 169  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 164  
LENGTH: 17  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
OTHER INFORMATION: humanized HC-08 CDR2 amino acid sequence  
US-10-310-113-164

Query Match 100.0%; Score 95; DB 12; Length 17;  
Best Local Similarity 100.0%; Pred. No. 5.5e-09;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YIDPYNGITIYDQNLKG 17  
Db 1 YIDPYNGITIYDQNLKG 17

RESULT 3  
US-10-230-880-101  
Sequence 101, Application US/10230880  
Publication No. US20030190705A1  
GENERAL INFORMATION:  
APPLICANT: WONG, HING C.  
APPLICANT: STINSON, JEFFREY L.  
TITLE OF INVENTION: METHOD OF HUMANIZING IMMUNE SYSTEM MOLECULES  
FILE REFERENCE: 71758/58066  
CURRENT APPLICATION NUMBER: US/10/230,880  
CURRENT FILING DATE: 2002-12-23  
PRIOR APPLICATION NUMBER: 09/990,586  
PRIOR FILING DATE: 2001-11-21  
PRIOR APPLICATION NUMBER: 60/343,306  
PRIOR FILING DATE: 2001-10-29  
PRIOR APPLICATION NUMBER: 09/293,854  
PRIOR FILING DATE: 1999-04-16  
NUMBER OF SEQ ID NOS: 174  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 101  
LENGTH: 17  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-230-880-101

Query Match 100.0%; Score 95; DB 12; Length 17;  
Best Local Similarity 100.0%; Pred. No. 5.5e-09;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YIDPYNGITIYDQNLKG 17  
Db 1 YIDPYNGITIYDQNLKG 17

RESULT 4  
US-09-293-854-9  
Sequence 9, Application US/09293854

Patent No. US20020168357A1  
GENERAL INFORMATION:  
APPLICANT: WONG, HING C.  
Jiao, Jin-an  
Esperanza, Nieves  
Lawrence, Luepschen  
TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD  
COAGULATION AND METHODS OF USE THEREOF  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP  
STREET: 130 WATER STREET  
CITY: BOSTON  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: DISKETTE  
COMPUTER: IBM COMPATIBLE  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ VERSION 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/293,854  
FILING DATE: 16-APR-1999  
CLASSIFICATION: <UNKNOWN>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/814,806  
FILING DATE: <UNKNOWN>  
ATTORNEY/AGENT INFORMATION:  
NAME: CORLESS, PETER F  
REGISTRATION NUMBER: 33,860  
REFERENCE/DOCKET NUMBER: 46943  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-523-3400  
TELEFAX: 617-523-6440  
TELEX: <UNKNOWN>  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: N-terminal  
ORIGINAL SOURCE:  
SEQUENCE DESCRIPTION: SEQ ID NO: 9:  
US-09-293-854-9

Query Match 95.8%; Score 91; DB 10; Length 17;  
Best Local Similarity 94.1%; Pred. No. 2.5e-08;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YIDPYNGITIYDQNLKG 17  
Db 1 YIDPYNGITIYDQNLKG 17

RESULT 5  
US-09-990-586-9  
Sequence 9, Application US/0990586  
Publication No. US20030109680A1  
GENERAL INFORMATION:  
APPLICANT: JIAO, JIN-AN  
APPLICANT: WONG, HING C.  
TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD COAGULATION AND METHODS  
OF USE THEREOF  
FILE REFERENCE: 71758/46943-CIP2  
CURRENT APPLICATION NUMBER: US/09/990,586  
CURRENT FILING DATE: 2001-11-21  
PRIOR APPLICATION NUMBER: 09/293,854  
PRIOR FILING DATE: 1999-04-16

Title of Invention: ANTIBODIES FOR INHIBITING BLOOD COAGULATION AND METHODS OF USE THEREOF  
 Number of Sequences: 26  
 Correspondence Address:  
 Addressee: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP  
 Street: 130 Water Street  
 City: Boston  
 State: MA 02109-3095  
 Country: USA

STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSEQ Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/293,417  
FILING DATE: 12-NO. US20030082636A1-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/293,854  
FILING DATE: 16-Apr-1999  
APPLICATION NUMBER: 08/814,806  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Corless, Peter F  
REGISTRATION NUMBER: 33,860  
REFERENCE/DOCKET NUMBER: 46943  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-523-3400  
TELEFAX: 617-523-6440  
TELEX: <Unknown>  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: N-terminal  
ORIGINAL SOURCE:  
SEQUENCE DESCRIPTION: SEQ ID NO: 9:  
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Query Match 95.8%; Score 91; DB 15; Length 17;  
Best Local Similarity 94.1%; Pred. No. 2.5e-08;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 YIDPYNGITIDQNFKG 17  
Db 1 YIDPYNGITIDQNFKG 17  
RESULT 10  
US-09-293-854-4  
Sequence 4, Application US/09293854  
Patent No. US20020168357A1  
GENERAL INFORMATION:  
APPLICANT: Wong, Hing C.  
Jiao, Jin-an  
Esperanza, Nieves  
Lawrence, Luepschen  
TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD COAGULATION AND METHODS OF USE THEREOF  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dike, Bronstein, Roberts & Cushman, LLP  
STREET: 130 Water Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSEQ Version 1.5  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/293,854  
FILING DATE: 16-Apr-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/814,806  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Corless, Peter F  
REGISTRATION NUMBER: 33,860  
REFERENCE/DOCKET NUMBER: 46943  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-523-3400  
TELEFAX: 617-523-6440  
TELEX: <Unknown>  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 117 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: N-terminal  
ORIGINAL SOURCE:  
SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
US-09-293-854-4  
Query Match 95.8%; Score 91; DB 10; Length 117;  
Best Local Similarity 94.1%; Pred. No. 2.2e-07;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 YIDPYNGITIDQNFKG 17  
Db 50 YIDPYNGITIDQNFKG 66  
RESULT 11  
US-09-990-586-4  
Sequence 4, Application US/09990586  
Publication No. US20030109680A1  
GENERAL INFORMATION:  
APPLICANT: JIAO, JIN-AN  
APPLICANT: WONG, HING C.  
TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD COAGULATION AND METHODS  
FILE REFERENCE: 71758/46943-CIP2  
CURRENT APPLICATION NUMBER: US/09/990,586  
CURRENT FILING DATE: 2001-11-21  
PRIOR APPLICATION NUMBER: 09/293,854  
PRIOR FILING DATE: 1999-04-16  
NUMBER OF SEQ ID NOS: 102  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 4  
LENGTH: 117  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-990-586-4  
Query Match 95.8%; Score 91; DB 11; Length 117;  
Best Local Similarity 94.1%; Pred. No. 2.2e-07;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 YIDPYNGITIDQNFKG 17  
Db 50 YIDPYNGITIDQNFKG 66  
RESULT 12  
US-10-310-113-4  
Sequence 4, Application US/10310113  
Publication No. US20030176664A1  
GENERAL INFORMATION:

APPLICANT: JIAO, JIN-AN  
APPLICANT: WONG, HING C.  
APPLICANT: NIEVES, ESPERANZA LILIANA  
APPLICANT: MOSQUERA, LUIS A.  
TITLE OF INVENTION: USE OF ANTI-TISSUE FACTOR ANTIBODIES FOR TREATING  
TITLE OF INVENTION: THROMBOSES  
FILE REFERENCE: 58122(71758)  
CURRENT APPLICATION NUMBER: US/10/310,113  
PRIOR FILING DATE: 2002-12-04  
PRIOR APPLICATION NUMBER: 09/990,586  
PRIOR FILING DATE: 2001-11-21  
PRIOR APPLICATION NUMBER: 60/343,306  
PRIOR FILING DATE: 2001-10-29  
PRIOR APPLICATION NUMBER: 09/293,854  
PRIOR FILING DATE: 1999-04-16  
PRIOR APPLICATION NUMBER: 08/814,806  
PRIOR FILING DATE: 1997-03-10  
NUMBER OF SEQ ID NOS: 169  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 4  
LENGTH: 117  
TYPE: PRT  
ORGANISM: Murine sp.  
US-10-310-113-4

Query Match 95.8%; Score 91; DB 12; Length 117;  
Best Local Similarity 94.1%; Pred. No. 2.2e-07;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YIDPYNGITTYDQNLKG 17  
Db 50 YIDPYNGITTYDQNFKG 66

RESULT 13  
US-10-230-880-4  
Sequence 4, Application US/10230880  
Publication No. US20030190705A1  
GENERAL INFORMATION:  
APPLICANT: WONG, HING C.  
APPLICANT: STINSON, JEFFREY L.  
APPLICANT: MOSQUERA, LUIS A.  
TITLE OF INVENTION: METHOD OF HUMANIZING IMMUNE SYSTEM MOLECULES  
FILE REFERENCE: 71758/58066  
CURRENT APPLICATION NUMBER: US/10/230,880  
CURRENT FILING DATE: 2002-12-23  
PRIOR APPLICATION NUMBER: 09/990,586  
PRIOR FILING DATE: 2001-11-21  
PRIOR APPLICATION NUMBER: 60/343,306  
PRIOR FILING DATE: 2001-10-29  
PRIOR APPLICATION NUMBER: 09/293,854  
PRIOR FILING DATE: 1999-04-16  
NUMBER OF SEQ ID NOS: 174  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 4  
LENGTH: 117  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-230-880-4

Query Match 95.8%; Score 91; DB 12; Length 117;  
Best Local Similarity 94.1%; Pred. No. 2.2e-07;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YIDPYNGITTYDQNLKG 17  
Db 50 YIDPYNGITTYDQNFKG 66

RESULT 14  
US-10-293-417-4  
Sequence 4, Application US/10293417  
Publication No. US20030082636A1

GENERAL INFORMATION:  
APPLICANT: Wong, Hing C.  
Jiao, Jin-an  
Esperanza, Nieves  
Lawrence, Luessenchen  
TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD  
COAGULATION AND METHODS OF USE THEREOF  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSES: DIKE, Bronstein, Roberts & Cushman, LLP  
STREET: 130 Water Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/293,417  
FILING DATE: 12-NO. US20030082636A1-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/293,854  
FILING DATE: 16-Apr-1999  
APPLICATION NUMBER: 08/814,806  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Corless, Peter F  
REGISTRATION NUMBER: 33,860  
REFERENCE/DOCKET NUMBER: 46943  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-523-3400  
TELEFAX: 617-523-6440  
TELEX: <Unknown>  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 117 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: N-terminal  
ORIGINAL SOURCE:  
SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
US-10-293-417-4

Query Match 95.8%; Score 91; DB 15; Length 117;  
Best Local Similarity 94.1%; Pred. No. 2.2e-07;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YIDPYNGITTYDQNLKG 17  
Db 50 YIDPYNGITTYDQNFKG 66

RESULT 15  
US-10-223-880-12  
Sequence 12, Application US/10223880  
Publication No. US20030152571A1  
GENERAL INFORMATION:  
APPLICANT: JONAK, ZDENKA  
APPLICANT: JOHANSON, KYUNG O.  
APPLICANT: TAYLOR, ALEXANDER  
TITLE OF INVENTION: ANIT-ALPHABETA3 HUMANIZED MONOCLONAL  
TITLE OF INVENTION: ANTIBODIES  
FILE REFERENCE: P50629C1  
CURRENT APPLICATION NUMBER: US/10/223,880  
CURRENT FILING DATE: 2002-08-20

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; PRIOR APPLICATION NUMBER: 09/380,910
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: PCT/US98/04987
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/039,609
; PRIOR FILING DATE: 1997-03-12
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-223-880-12

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Query Match      72.6%; Score 69; DB 12; Length 110;
Best Local Similarity 70.6%; Pred.No. 0.00085;
Matches 12; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
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DB      48 YIDPYNGDTFYNQKFKG 64

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Search completed: January 13, 2004, 13:13:47  
Job time : 2.71703 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 13, 2004, 12:33:50 ; Search time 1.46987 Seconds  
(without alignments)  
489.353 Million cell updates/sec

Title: US-09-990-586-101  
Perfect score: 95  
Sequence: 1 VIDPYNGITIYDQNLKG 17

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: /cgn2\_6/prodata/1/aaa/5A COMB.pep:\*  
2: /cgn2\_6/prodata/1/aaa/5B COMB.pep:\*  
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6: /cgn2\_6/prodata/1/aaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	91	95.8	17	4	US-09-293-854-9
3	91	95.8	117	2	US-08-814-806-4
4	91	95.8	117	4	US-09-293-854-4
5	62	65.3	17	1	US-08-137-117D-144
6	62	65.3	17	2	US-08-436-717-144
7	62	65.3	116	2	US-08-561-521-41
8	62	65.3	116	5	PTC-US95-01219-41
9	62	65.3	135	1	US-08-137-117D-27
10	62	65.3	135	1	US-08-137-117D-100
11	62	65.3	135	1	US-08-137-117D-102
12	62	65.3	135	1	US-08-137-117D-112
13	62	65.3	135	2	US-08-436-717-27
14	62	65.3	135	2	US-08-436-717-100
15	62	65.3	135	2	US-08-436-717-102
16	62	65.3	135	2	US-08-436-717-112
17	60	63.2	246	1	US-08-257-341-7
18	60	63.2	252	1	US-08-133-804-4
19	60	63.2	252	1	US-08-461-838-4
20	60	63.2	252	1	US-08-461-386-4
21	60	63.2	260	2	US-08-447-402-1
22	60	63.2	269	3	US-09-070-408-132
23	60	63.2	367	1	US-08-257-341-5
24	59	62.1	117	3	US-09-027-449-48
25	59	62.1	117	3	US-09-027-449-49
26	59	62.1	117	3	US-08-804-444A-48
27	59	62.1	117	3	US-08-804-444A-49

28	59	62.1	117	3	US-09-026-985-48	Sequence 48, Appl
29	59	62.1	117	3	US-09-026-985-49	Sequence 49, Appl
30	59	62.1	117	4	US-09-121-952A-48	Sequence 48, Appl
31	59	62.1	117	4	US-09-121-952A-49	Sequence 49, Appl
32	59	62.1	117	4	US-09-234-340A-48	Sequence 48, Appl
33	59	62.1	117	4	US-09-234-340A-49	Sequence 49, Appl
34	59	62.1	135	1	US-08-398-613A-50	Sequence 50, Appl
35	59	62.1	135	1	US-08-398-613A-50	Sequence 50, Appl
36	59	62.1	135	1	US-08-398-613A-50	Sequence 50, Appl
37	59	62.1	135	2	US-08-491-334A-50	Sequence 37, Appl
38	59	62.1	135	3	US-09-027-449-37	Sequence 37, Appl
39	59	62.1	135	3	US-08-804-444A-37	Sequence 37, Appl
40	59	62.1	135	3	US-09-026-985-37	Sequence 37, Appl
41	59	62.1	135	4	US-09-121-952A-37	Sequence 37, Appl
42	59	62.1	135	4	US-09-234-340A-37	Sequence 37, Appl
43	59	62.1	253	1	US-08-398-613A-58	Sequence 58, Appl
44	59	62.1	253	1	US-08-398-613A-58	Sequence 58, Appl
45	59	62.1	253	1	US-08-398-613A-58	Sequence 58, Appl

ALIGNMENTS

RESULT 1  
US-08-814-806-9  
; Sequence 9, Application US/08814806  
; Patent No. 5986065  
; GENERAL INFORMATION:  
; APPLICANT: Wong, Hing C.  
; APPLICANT: Jiao, Jin-an  
; APPLICANT: Esperanza, Nieves  
; APPLICANT: Lawrence, Luepschen  
; TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD  
; TITLE OF INVENTION: COAGULATION AND METHODS OF USE THEREOF  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: 130 Water Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA: US/08/814,806  
; FILING DATE:  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Corless, Peter F  
; REGISTRATION NUMBER: 33,860  
; REFERENCE/DOCKET NUMBER: 46943  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-523-3400  
; TELEFAX: 617-523-6440  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 17 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: N-terminal  
; ORIGINAL SOURCE:

Tue Jan 13 13:21:59 2004

US-08-814-806-9

Query Match 95.8%; Score 91; DB 2; Length 17;  
Best Local Similarity 94.1%; Pred. No. 8.5e-09;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YIDPYNGITTYDQNLKG 17  
|||  
Db 1 YIDPYNGITTYDQNLKG 17  
|||

## RESULT 2

US-09-293-854-9  
; Sequence 9, Application US/09293854  
; Patent No. 655319

GENERAL INFORMATION:  
APPLICANT: Wong, Hing C.

APPLICANT: Jiao, Jin-an  
APPLICANT: Esperanza, Nieves

APPLICANT: Lawrence, Luepschen  
APPLICANT: Lawrance, Luepschen

TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD  
COAGULATION AND METHODS OF USE THEREOF

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:

ADDRESSEE: Dike, Bronstein, Roberts & Cushman, LLP

STREET: 130 Water Street

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: Fast-SEQ Version 1.5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/293,854

FILING DATE: 16-Apr-1999

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/814,806

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Corless, Peter F

REGISTRATION NUMBER: 33,860

REFERENCE/DOCKET NUMBER: 46943

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-523-3400

TELEFAX: 617-523-6440

TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 17 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE: N-terminal

ORIGINAL SOURCE:

SEQUENCE DESCRIPTION: SEQ ID NO: 9:

US-09-293-854-9

Query Match 95.8%; Score 91; DB 4; Length 17;  
Best Local Similarity 94.1%; Pred. No. 8.5e-09;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YIDPYNGITTYDQNLKG 17  
|||  
Db 1 YIDPYNGITTYDQNLKG 17  
|||

## RESULT 3

US-08-814-806-4

; Sequence 4, Application US/08814806

; Patent No. 586065

GENERAL INFORMATION:

APPLICANT: Wong, Hing C.

APPLICANT: Jiao, Jin-an

APPLICANT: Esperanza, Nieves

APPLICANT: Lawrence, Luepschen

TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD

COAGULATION AND METHODS OF USE THEREOF

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:

ADDRESSEE: Dike, Bronstein, Roberts & Cushman, LLP

STREET: 130 Water Street

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: Fast-SEQ Version 1.5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/814,806

FILING DATE:

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Corless, Peter F

REGISTRATION NUMBER: 33,860

REFERENCE/DOCKET NUMBER: 46943

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-523-3400

TELEFAX: 617-523-6440

TELEX:

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 117 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE: N-terminal

ORIGINAL SOURCE:

US-08-814-806-4

Query Match 95.8%; Score 91; DB 2; Length 117;

Best Local Similarity 94.1%; Pred. No. 8.9e-08;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YIDPYNGITTYDQNLKG 17

|||

Db 50 YIDPYNGITTYDQNLKG 66

## RESULT 4

US-09-293-854-4

; Sequence 4, Application US/09293854

; Patent No. 655319

GENERAL INFORMATION:

APPLICANT: Wong, Hing C.

APPLICANT: Jiao, Jin-an

APPLICANT: Esperanza, Nieves

APPLICANT: Lawrence, Luepschen

TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD

COAGULATION AND METHODS OF USE THEREOF

NUMBER OF SEQUENCES: 26



;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Dike, Bronstein, Roberts & Cushman, LLP  
;; STREET: 130 Water Street  
;; CITY: Boston  
;; STATE: MA  
;; COUNTRY: USA  
;; ZIP: 02109  
;;  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Diskette  
;; COMPUTER: IBM Compatible  
;; OPERATING SYSTEM: DOS  
;; SOFTWARE: FastSeq Version 1.5  
;;  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/293,854  
;; FILING DATE: 16-Apr-1999  
;; CLASSIFICATION: <Unknown>  
;;  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/814,806  
;; FILING DATE: <Unknown>  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Corless, Peter F  
;; REGISTRATION NUMBER: 33,860  
;; REFERENCE/DOCKET NUMBER: 46943  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 617-523-3400  
;; TELEFAX: 617-523-6440  
;; TELEX: <Unknown>  
;;  
;; INFORMATION FOR SEQ ID NO: 4:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 117 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
;; HYPOTHETICAL: NO  
;; ANTI-SENSE: NO  
;; FRAGMENT TYPE: N-terminal  
;; ORIGINAL SOURCE:  
;; SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
US-09-293-854-4

Query Match 95.8%; Score 91; DB 4; Length 117;  
Best Local Similarity 94.1%; Pred. No. 8.9e-08;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 1 YIDPYNGITTYDQNLKG 17  
|||:|||||:|||||  
Db 50 YIDPYNGITTYDQNLKG 66

RESULT 5  
US-08-137-117D-144  
; Sequence 144, Application US/08137117D  
; Patent No. 5795965  
; GENERAL INFORMATION:  
; APPLICANT: TSUCHIYA, Masayuki  
; APPLICANT: SATO, Koh  
; APPLICANT: BENDIG, Mary  
; APPLICANT: JONES, Steven  
; APPLICANT: SALDANHA, Jose  
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN  
; INTERLEUKIN-6 RECEPTOR  
; NUMBER OF SEQUENCES: 158  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20007-5109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/436,717  
; FILING DATE:  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/137,117  
; FILING DATE: 20-DEC-1993  
; APPLICATION NUMBER: WO PCT/JP92/00544

;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patentin Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/137,117D  
;; FILING DATE: 20-DEC-1993  
;; CLASSIFICATION: 530  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: WO PCT/JP92/00544  
;; FILING DATE: 24-APR-1992  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: JP 4-32084  
;; FILING DATE: 19-FEB-1992  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: JP 3-95476  
;; FILING DATE: 25-APR-1991  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: WEGNER, Harold C.  
;; REGISTRATION NUMBER: 25,258  
;; REFERENCE/DOCKET NUMBER: 53466/126/AAOK  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (202)672-5300  
;; TELEFAX: (202)672-5399  
;; TELEX: 904136  
;; INFORMATION FOR SEQ ID NO: 144:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 17 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
US-08-137-117D-144  
  
Query Match 65.3%; Score 62; DB 1; Length 17;  
Best Local Similarity 64.7%; Pred. No. 0.00053;  
Matches 11; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
  
Qy 1 YIDPYNGITTYDQNLKG 17  
|||:|||||:|||||  
Db 1 YIDPFNGGTSYNQKFKG 17  
  
RESULT 6  
US-08-436-717-144  
; Sequence 144, Application US/08436717  
; Patent No. 5817790  
; GENERAL INFORMATION:  
; APPLICANT: TSUCHIYA, Masayuki  
; APPLICANT: SATO, Koh  
; APPLICANT: BENDIG, Mary  
; APPLICANT: JONES, Steven  
; APPLICANT: SALDANHA, Jose  
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN  
; INTERLEUKIN-6 RECEPTOR  
; NUMBER OF SEQUENCES: 158  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20007-5109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/436,717  
; FILING DATE:  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/137,117  
; FILING DATE: 20-DEC-1993  
; APPLICATION NUMBER: WO PCT/JP92/00544

Tue Jan 13 13:21:59 2004

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; FILING DATE: 24-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 4-32084
; FILING DATE: 19-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 3-95476
; FILING DATE: 25-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: WEGNER, Harold C.
; REGISTRATION NUMBER: 25,258
; REFERENCE/DOCKET NUMBER: S3466/126/AAOK
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 144:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-436-717-144

```

Query Match 65.3%; Score 62; DB 2; Length 17;  
 Best Local Similarity 64.7%; Pred. No. 0.00053;  
 Matches 11; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

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QY 1 YIDPYNGITTYDQNLKG 17
    |||||:|:|
Db 1 YIDPENGTSYNQKFKG 17

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RESULT 7
US-08-561-521-41
; Sequence 41, Application US/08561521
; Patent No. 5840299
; GENERAL INFORMATION:
; APPLICANT: Bendig, Mary M.
; APPLICANT: Leger, Olivier J.
; APPLICANT: Saldanha, Jose
; APPLICANT: Jones, S. Tarran
; TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
; TITLE OF INVENTION: Adhesion Molecule VLA-4
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/561,521
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/186,269A
; FILING DATE: 25-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William L.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15270-14
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-543-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 116 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
PCT-US95-01219-41

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Query Match 65.3%; Score 62; DB 5; Length 116;  
 Best Local Similarity 64.7%; Pred. No. 0.0056;  
 Matches 11; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

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QY 1 YIDPYNGITTYDQNLKG 17
    |||||:|:|
Db 5 YIDPENGTSYNQKFKG 66

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RESULT 9  
 US-08-137-117D-27  
 ; Sequence 27, Application US/08137117D

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; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-08-561-521-41

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Query Match 65.3%; Score 62; DB 2; Length 116;  
 Best Local Similarity 64.7%; Pred. No. 0.0056;  
 Matches 11; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

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QY 1 YIDPYNGITTYDQNLKG 17
    |||||:|:|
Db 50 YIDPENGTSYNQKFKG 66

```

```

RESULT 8
PCT-US95-01219-41
; Sequence 41, Application PC/TUS9501219
; GENERAL INFORMATION:
; APPLICANT: Bendig, Mary M.
; APPLICANT: Leger, Olivier J.
; APPLICANT: Saldanha, Jose
; APPLICANT: Jones, S. Tarran
; TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
; TITLE OF INVENTION: Adhesion Molecule VLA-4
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/01219
; FILING DATE: 25-JAN-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/186,269
; FILING DATE: 25-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William L.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15270-14
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-543-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 116 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
PCT-US95-01219-41

```

Query Match 65.3%; Score 62; DB 5; Length 116;  
 Best Local Similarity 64.7%; Pred. No. 0.0056;  
 Matches 11; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

```

QY 1 YIDPYNGITTYDQNLKG 17
    |||||:|:|
Db 50 YIDPENGTSYNQKFKG 66

```

RESULT 9  
 US-08-137-117D-27  
 ; Sequence 27, Application US/08137117D

Patent No. 5795965  
GENERAL INFORMATION:  
APPLICANT: TSUCHIYA, Masayuki  
APPLICANT: SAITO, Koh  
APPLICANT: BENDIG, Mary  
APPLICANT: JONES, Steven  
APPLICANT: SALDANHA, Jose  
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN  
TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR  
NUMBER OF SEQUENCES: 158  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/137.117D  
FILING DATE: 20-DEC-1993  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/JP92/00544  
FILING DATE: 24-APR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 4-32084  
FILING DATE: 19-FEB-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 3-95476  
FILING DATE: 25-APR-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: WEGNER, Harold C.  
REGISTRATION NUMBER: 25,258  
REFERENCE/DOCKET NUMBER: 53466/126/AAOK  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 135 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-137-117D-27

Query Match 65.3%; Score 62; DB 1; Length 135;  
Best Local Similarity 64.7%; Pred. No. 0.0067;  
Matches 11; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 YIDPYNGITIDQNLLKG 17  
Db 69 YIDPFNGGTSYQKFKG 85

RESULT 10  
US-08-137-117D-100  
Sequence 100, Application US/08137117D  
Patent No. 5795965  
GENERAL INFORMATION:  
APPLICANT: TSUCHIYA, Masayuki  
APPLICANT: SAITO, Koh  
APPLICANT: BENDIG, Mary  
APPLICANT: JONES, Steven  
APPLICANT: SALDANHA, Jose  
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN  
TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR  
NUMBER OF SEQUENCES: 158

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/137.117D  
FILING DATE: 20-DEC-1993  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/JP92/00544  
FILING DATE: 24-APR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 4-32084  
FILING DATE: 19-FEB-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 3-95476  
FILING DATE: 25-APR-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: WEGNER, Harold C.  
REGISTRATION NUMBER: 25,258  
REFERENCE/DOCKET NUMBER: 53466/126/AAOK  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 100:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 135 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-137-117D-100

Query Match 65.3%; Score 62; DB 1; Length 135;  
Best Local Similarity 64.7%; Pred. No. 0.0067;  
Matches 11; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 YIDPYNGITIDQNLLKG 17  
Db 69 YIDPFNGGTSYQKFKG 85

RESULT 11  
US-08-137-117D-102  
Sequence 102, Application US/08137117D  
Patent No. 5795965  
GENERAL INFORMATION:  
APPLICANT: TSUCHIYA, Masayuki  
APPLICANT: SAITO, Koh  
APPLICANT: BENDIG, Mary  
APPLICANT: JONES, Steven  
APPLICANT: SALDANHA, Jose  
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN  
TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR  
NUMBER OF SEQUENCES: 158  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA: US/08/137,117D  
APPLICATION NUMBER: JP 4-32084  
FILING DATE: 19-FEB-1992  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/JP92/00544  
FILING DATE: 24-APR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 4-32084  
FILING DATE: 19-FEB-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 3-95476  
FILING DATE: 25-APR-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: WEGNER, Harold C.  
REGISTRATION NUMBER: 25,258  
REFERENCE/DOCKET NUMBER: 53466/126/AAOK  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 102:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 135 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-137-117D-102

Query Match 65.3%; Score 62; DB 1; Length 135;  
Best Local Similarity 64.7%; Pred. No. 0.0067;  
Matches 11; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 YIDPNGITIIYDQNLKG 17  
|||||:|||||:|  
DB 69 YIDPFGGTSYNQKPKG 85

RESULT 12  
US-08-137-117D-112  
Sequence 112, Application US/08137117D  
Patent No. 5795965  
GENERAL INFORMATION:  
APPLICANT: TSUCHIYA, Masayuki  
APPLICANT: SATO, Koh  
APPLICANT: BENDIG, Mary  
APPLICANT: JONES, Steven  
APPLICANT: SALDANHA, Jose  
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN  
INTERLEUKIN-6 RECEPTOR  
NUMBER OF SEQUENCES: 158  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/137,117D  
FILING DATE: 20-DEC-1993  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/JP92/00544  
FILING DATE: 24-APR-1992  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 4-32084  
FILING DATE: 19-FEB-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 3-95476  
FILING DATE: 25-APR-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: WEGNER, Harold C.  
REGISTRATION NUMBER: 25,258  
REFERENCE/DOCKET NUMBER: 53466/126/AAOK  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 112:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 135 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-137-117D-112

Query Match 65.3%; Score 62; DB 1; Length 135;  
Best Local Similarity 64.7%; Pred. No. 0.0067;  
Matches 11; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 YIDPNGITIIYDQNLKG 17  
|||||:|||||:|  
DB 69 YIDPFGGTSYNQKPKG 85

RESULT 13  
US-08-436-717-27  
Sequence 27, Application US/08436717  
Patent No. 5817790  
GENERAL INFORMATION:  
APPLICANT: TSUCHIYA, Masayuki  
APPLICANT: SATO, Koh  
APPLICANT: BENDIG, Mary  
APPLICANT: JONES, Steven  
APPLICANT: SALDANHA, Jose  
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN  
INTERLEUKIN-6 RECEPTOR  
NUMBER OF SEQUENCES: 158  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/436,717  
FILING DATE:  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/137,117  
FILING DATE: 20-DEC-1993  
APPLICATION NUMBER: WO PCT/JP92/00544  
FILING DATE: 24-APR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 4-32084  
FILING DATE: 19-FEB-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 3-95476  
FILING DATE: 25-APR-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: WEGNER, Harold C.  
REGISTRATION NUMBER: 25,258

REFERENCE/DOCKET NUMBER: 53466/126/AAOK  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 135 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-436-717-27

Query Match 65.3%; Score 62; DB 2; Length 135;  
Best Local Similarity 64.7%; Pred. No. 0.0067;  
Matches 11; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 YIDPYNGITIVDQNLKG 17  
|||:|||||:|  
Db 69 YIDPFNGTSYNQKPKG 85

## RESULT 14

US-08-436-717-100  
Sequence 100, Application US/08436717  
Patent No. 5817790  
GENERAL INFORMATION:  
APPLICANT: TSUCHIYA, Masayuki  
APPLICANT: SATO, Koh  
APPLICANT: BENDIG, Mary  
APPLICANT: JONES, Steven  
APPLICANT: SALDANHA, Jose  
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN  
TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR  
NUMBER OF SEQUENCES: 158  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/436,717  
FILING DATE:  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/137,117  
FILING DATE: 20-DEC-1993  
APPLICATION NUMBER: WO PCT/JP92/00544  
FILING DATE: 24-APR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 4-32084  
FILING DATE: 19-FEB-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 3-95476  
FILING DATE: 25-APR-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: WEGNER, Harold C.  
REGISTRATION NUMBER: 25,258  
REFERENCE/DOCKET NUMBER: 53466/126/AAOK  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 100:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 135 amino acids

Query Match 65.3%; Score 62; DB 2; Length 135;  
Best Local Similarity 64.7%; Pred. No. 0.0067;  
Matches 11; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-436-717-100

Query Match 65.3%; Score 62; DB 2; Length 135;  
Best Local Similarity 64.7%; Pred. No. 0.0067;  
Matches 11; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 YIDPYNGITIVDQNLKG 17  
|||:|||||:|  
Db 69 YIDPFNGTSYNQKPKG 85

## RESULT 15

US-08-436-717-102  
Sequence 102, Application US/08436717  
Patent No. 5817790  
GENERAL INFORMATION:  
APPLICANT: TSUCHIYA, Masayuki  
APPLICANT: SATO, Koh  
APPLICANT: BENDIG, Mary  
APPLICANT: JONES, Steven  
APPLICANT: SALDANHA, Jose  
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN  
TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR  
NUMBER OF SEQUENCES: 158  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/436,717  
FILING DATE:  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/137,117  
FILING DATE: 20-DEC-1993  
APPLICATION NUMBER: WO PCT/JP92/00544  
FILING DATE: 24-APR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 4-32084  
FILING DATE: 19-FEB-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 3-95476  
FILING DATE: 25-APR-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: WEGNER, Harold C.  
REGISTRATION NUMBER: 25,258  
REFERENCE/DOCKET NUMBER: 53466/126/AAOK  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 102:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 135 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-436-717-102

Query Match 65.3%; Score 62; DB 2; Length 135;  
Best Local Similarity 64.7%; Pred. No. 0.0067;  
Matches 11; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Oy 1 YIDPVGITIIDNKG 17  
| | | | | : | | | |  
Db 69 YIDPVGTSYNQKFG 85

Search completed: January 13, 2004, 12:46:36  
Job time : 1.46987 secs